| | |
|---|---|
| 1312 | septation ring formation regulator EzrA |
| 1320 | hydrolase, haloacid dehalogenase-like family (gph) |
| 1340 | sensor histidine kinase (vncS) |
| 1348 | transmembrane protein Vexp3 (vex3) |
| 1352 | ABC transporter, ATP-binding protein (vex2) |
| 1358 | transmembrane protein Vexp1 (vex1) |
| 1366 | transposase |
| 1374 | integrase, phage family |
| 1390 | holin 2 |
| 1398 | minor structural protein |
| 1400 | host specificity protein |
| 1404 | minor structural protein |
| 1406 | PblA |
| 1486 | homeobox protein drg11 |
| 1488 | reverse transcriptase |
| 1496 | p22 erf-like protein |
| 1498 | gp157 |
| 1500 | tropomyosin 2 |
| 1512 | gp49 homologous |
| 1526 | transcriptional regulator-related protein |
| 1566 | chorismate mutase |
| 1572 | PTS system component |
| 1576 | PTS system, IIB component |
| 1580 | PTS system IIA component |
| 1584 | lactose phosphotransferase system repressor (lacR) |
| 1594 | adhesion lipoprotein (lmb) |
| 1602 | GTP pyrophosphokinase (relA) |
| 1606 | 2`,3`-cyclic-nucleotide 2`-phosphodiesterase (cpdB) |
| 1616 | iron ABC transporter, iron-binding protein |
| 1620 | DNA-binding response regulator |
| 1630 | PTS system component |
| 1634 | PTS system component (manM) |
| 1638 | PTS system component (manL) |
| 1642 | PTS system component |
| 1658 | response regulator BlpR (blpR) |
| 1676 | phosphate transport system regulatory protein PhoU |
| 1680 | phosphate ABC transporter, ATP-binding protein (pstB) |
| 1684 | phosphate ABC transporter, permease protein (pstA) |
| 1690 | phosphate ABC transporter, permease protein (pstC) |
| 1694 | probable hemolysin precursor |
| 1704 | ribosomal protein L11 methyltransferase (prmA) |
| 1710 | transcriptional regulator, MerR family (skgA) |
| 1714 | acetyltransferase, GNAT family |
| 1716 | MutT/nudix family protein |
| 1722 | spermidine N1-acetyltransferase |
| 1726 | ATPase, AAA family |
| 1736 | ABC transporter domain protein |
| 1738 | Helix-turn-helix domain protein |
| 1748 | integrase, phage family |
| 1756 | Helix-turn-helix domain protein |
| 1762 | bacteriophage L54a, integrase |
| 1768 | LPXTG-motif cell wall anchor domain protein |
| 1776 | membrane protein |
| 1778 | conjugal transfer protein |
| 1780 | IS1381, transposase OrfA/OrfB, truncation |
| 1802 | transcriptional regulator (rstR-1) |
| 1806 | transcriptional regulator |
| 1808 | FtsK/SpoIIIE family protein |
| 1814 | aggregation substance |

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|---|---|
| 1818 | mercuric reductase |
| 1822 | transcriptional regulator, MerR family |
| 1824 | Mn2+/Fe2+ transporter, NRAMP family |
| 1830 | ABC transporter, ATP-binding protein (epiF) |
| 1848 | Helix-turn-helix domain protein |
| 1850 | type 2 phosphatidic acid phosphatase(PAP2), family |
| 1858 | Abortive infection protein family |
| 1868 | aminotransferase, class-V |
| 1874 | glutathione reductase (gor) |
| 1882 | chorismate synthase (aroC) |
| 1886 | 3-dehydroquinate synthase (aroB) |
| 1900 | sulfatase family protein |
| 1914 | ABC transporter, ATP-binding protein |
| 1920 | smf protein (Smffamily) |
| 1924 | transferrin receptor |
| 1928 | iron compound ABC transporter, ATP-binding protein |
| 1932 | iron compound ABC transporter, permease protein |
| 1942 | acetyltransferase, CysE/LacA/LpxA/NodL family |
| 1952 | GTP-binding protein |
| 1958 | carbon starvation protein A |
| 1960 | response regulator (lytR) |
| 1962 | GAF domain protein (lytS) |
| 2000 | extracellular protein |
| 2004 | diarrheal toxin (yukA) |
| 2024 | carbamoyl-phosphate synthase, large subunit (carB) |
| 2028 | carbamoyl-phosphate synthase, small subunit (carA) |
| 2032 | aspartate carbamoyltransferase (pyrB) |
| 2036 | dihydroorotase, multifunctional complex type (pyrC) |
| 2040 | orotate phosphoribosyltransferase (pyrE) |
| 2048 | membrane protein |
| 2062 | phosphate ABC transporter, permease protein (pstA-2) |
| 2064 | phosphate ABC transporter, ATP-binding protein (pstB) |
| 2070 | phosphate transport system regulatory protein PhoU |
| 2072 | aminopeptidase N (pepN) |
| 2076 | DNA-binding response regulator (arlR) |
| 2080 | sensor histidine kinase (arlS) |
| 2088 | signal recognition particle protein (ffh) |
| 2102 | peptide ABC transporter, peptide-binding protein |
| 2104 | integrase/recombinase, phage integrase family |
| 2108 | sensor histidine kinase |
| 2112 | DNA-binding response regulator (vicR) |
| 2118 | ABC transporter, ATP-binding protein |
| 2122 | nisin-resistance protein |
| 2130 | lipoprotein |
| 2136 | gid protein (gid) |
| 2140 | transcriptional regulator, GntR family |
| 2142 | GMP synthase (guaA) |
| 2152 | branched-chain amino acid ABC transporter, permease protein (livM) |
| 2154 | branched-chain amino acid ABC transporter, ATP-binding protein (livG) |
| 2156 | branched-chain amino acid ABC transporter, ATP-binding protein (livF) |
| 2160 | acetoin utilization protein AcuB |
| 2174 | DNA polymerase III, delta prime subunit (holB) |
| 2186 | copper homeostasis protein (cutC) |
| 2190 | phosphoserine aminotransferase (serC) |
| 2202 | methylated-DNA--protein-cysteine S-methyltransferase (ogt) |
| 2208 | exodeoxyribonuclease III (xth) |
| 2214 | PTS system, IIC component |
| 2224 | tellurite resistance protein TehB (tehB) |
| 2246 | icaA protein |

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|---|---|
| 2250 | acetyltransferase, GNAT family |
| 2258 | oxidoreductase, short chain dehydrogenase/reductase family (fabG) |
| 2266 | oxidoreductase, Gfo/Idh/MocA family family |
| 2268 | glyoxalase family protein |
| 2272 | UDP-N-acetylglucosamine pyrophosphorylase (glmU) |
| 2276 | MutT/nudix family protein |
| 2284 | 5-methylthioadenosine/S-adenosylhomocysteine nucleosidase (mtf) |
| 2296 | phosphatidate cytidylyltransferase (cdsA) |
| 2300 | membrane-associated zinc metalloprotease |
| 2308 | autolysin (flgJ) |
| 2312 | DNA polymerase III, alpha subunit, Gram-positive type |
| 2320 | nitroreductase family protein superfamily |
| 2326 | 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldo |
| 2328 | carbohydrate kinase, PfkB family |
| 2336 | oxidoreductase, short chain dehydrogenase/reductase family (fabG) |
| 2338 | PTS system, IIA component (manL) |
| 2342 | glucuronyl hydrolase |
| 2346 | PTS system, IIB component (manL) |
| 2350 | PTS system, IIC component (manM) |
| 2364 | sugar binding transcriptional regulator RegR (regR) |
| 2368 | polypeptide deformylase (def) |
| 2380 | oxidoreductase, Gfo/Idh/MocA family |
| 2382 | endopeptidase O (pepO) |
| 2394 | Na+/H+ antiporter |
| 2404 | transcriptional regulator |
| 2410 | replication initiation protein RepRC |
| 2412 | bacteriophage L54a, antirepressor |
| 2416 | e11 |
| 2422 | replicative DNA helicase (dnaB) |
| 2432 | GTP-binding protein |
| 2440 | arpR protein |
| 2444 | gene 17 protein |
| 2458 | integrase/recombinase, phage integrase family |
| 2468 | bacteriophage L54a, phage D3 terminase |
| 2472 | protease |
| 2500 | PblB |
| 2504 | sensor histidine kinase |
| 2514 | N-acetylmuramoyl-L-alanine amidase |
| 2518 | KH domain protein |
| 2522 | ribosomal protein S16 (rpsP) |
| 2526 | permease |
| 2528 | ABC transporter, ATP-binding protein |
| 2538 | carbamoyl-phosphate synthase, large subunit |
| 2540 | carbamoyl-phosphate synthase, small subunit (carA) |
| 2550 | transcriptional regulator, LysR family |
| 2554 | ribosomal protein L27 (rpmA) |
| 2562 | ribosomal protein L21 (rplU) |
| 2572 | glycerophosphoryl diester phosphodiesterase |
| 2582 | nitroreductase family protein |
| 2586 | dipeptidase (pepV) |
| 2614 | GTP-binding protein HflX (hflX) |
| 2618 | galactose-1-phosphate uridylyltransferase (galT) |
| 2626 | oxidoreductase, short chain dehydrogenase/reductase family |
| 2630 | single-stranded-DNA-specific exonuclease RecJ (recJ) |
| 2638 | adenine phosphoribosyltransferase (apt) |
| 2646 | Bcl-2 family protein |
| 2654 | oxidoreductase, DadA family protein |
| 2658 | glucose-1-phosphate thymidylyltransferase (rfbA) |
| 2664 | dTDP-4-dehydrorhamnose 3,5-epimerase (rfbC) |

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|---|---|
| 2682 | hyaluronidase |
| 2686 | mutator MutT protein (mutX) |
| 2690 | MutT/nudix family protein |
| 2694 | membrane protein |
| 2702 | acetolactate synthase (ilvK) |
| 2706 | adherence and virulence protein A (pavA) |
| 2714 | ABC transporter, permease protein (rbsC) |
| 2722 | metallo-beta-lactamase superfamily protein |
| 2734 | ribose 5-phosphate isomerase (rpiA) |
| 2738 | phosphopentomutase (deoB) |
| 2742 | purine nucleoside phosphorylase, family 2 (deoD) |
| 2750 | purine nucleoside phosphorylase (deoD) |
| 2762 | capsular polysaccharide biosynthesis protein Cps4A (cps4A) |
| 2768 | cpsb protein |
| 2770 | cpsc protein |
| 2772 | CpsE |
| 2774 | CpsF |
| 2776 | CpsVG |
| 2778 | CpsVH |
| 2780 | CpsVM |
| 2782 | CpsVN |
| 2784 | glycosyl transferase domain protein |
| 2786 | glycosyl transferase, family 2/glycosyl transferase family 8 |
| 2790 | CpsVK |
| 2794 | CpsL |
| 2796 | neuB protein |
| 2798 | UDP-N-acetylglucosamine 2-epimerase |
| 2800 | hexapeptide transferase family protein |
| 2802 | NeuA |
| 2808 | uracil-DNA glycosylase (ung) |
| 2818 | DNA topoisomerase IV, B subunit (parE) |
| 2822 | DNA topoisomerase IV, A subunit (parC) |
| 2826 | branched-chain amino acid aminotransferase (ilvE) |
| 2842 | glycerol kinase (glpK) |
| 2848 | aerobic glycerol-3-phosphate dehydrogenase (glpD) |
| 2874 | ABC transporter, ATP-binding protein |
| 2882 | PTS system component (bglP) |
| 2886 | glutamate 5-kinase (proB) |
| 2890 | gamma-glutamyl phosphate reductase (proA) |
| 2898 | cell division protein FtsL (ftsL) |
| 2904 | penicillin-binding protein 2X (pbpX) |
| 2910 | phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY) |
| 2914 | ATP-dependent RNA helicase, DEAD/DEAH box family (deaD) |
| 2918 | ABC transporter, substrate-binding protein |
| 2924 | amino acid ABC transporter, permease protein |
| 2928 | amino acid ABC transporter, ATP-binding protein |
| 2932 | thioredoxin reductase (trxB) |
| 2940 | NAD+ synthetase (nadE) |
| 2944 | aminopeptidase C (pepC) |
| 2952 | recombination protein U (recU) |
| 2966 | Uncharacterized protein family UPF0020 family |
| 2974 | autoinducer-2 production protein LuxS (luxS) |
| 2978 | KH domain protein |
| 2986 | ABC transporter, ATP-binding protein |
| 2994 | DNA-binding response regulator (vraR) |
| 3000 | guanylate kinase (gmk) |
| 3004 | DNA-directed RNA polymerase, omega subunit |
| 3008 | primosomal protein N (priA) |
| 3012 | methionyl-tRNA formyltransferase (fmt) |

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|---|---|
| 3016 | Sun protein (sun) |
| 3020 | protein phosphatase 2C |
| 3032 | sensor histidine kinase |
| 3034 | DNA-binding response regulator (vraR) |
| 3036 | cof family protein/peptidyl-prolyl cis-trans isomerase, cyclophilin typ |
| 3040 | S1 RNA binding domain protein (rpsA) |
| 3044 | pyruvate formate-lyase-activating enzyme |
| 3062 | PTS system, IIB component (celA) |
| 3066 | PTS system, cellobiose-specific IIC component (celB) |
| 3068 | formate acetyltransferase (pfl) |
| 3072 | transaldolase |
| 3080 | cysteine synthase A (cysK) |
| 3088 | comF operon protein 1 (comFA) |
| 3092 | competence protein ComF |
| 3096 | ribosomal subunit interface protein (yfiA) |
| 3104 | tryptophanyl-tRNA synthetase (trpS) |
| 3108 | carbamate kinase (arcC) |
| 3116 | ornithine carbamoyltransferase (argF) |
| 3124 | arginine deiminase (arcA) |
| 3134 | transcriptional regulator, Crp/Fnr family |
| 3138 | inosine-5'-monophosphate dehydrogenase (guaB) |
| 3140 | MutR |
| 3142 | transporter |
| 3146 | recF protein (recF) |
| 3158 | peptidase, M16 family |
| 3166 | ABC transporter, ATP-binding protein |
| 3170 | ABC transporter, ATP-binding protein |
| 3178 | LysM domain protein (lytN) |
| 3180 | immunodominant antigen A (isaA) |
| 3184 | L-serine dehydratase, iron-sulfur-dependent, alpha subunit (sdhA) |
| 3188 | L-serine dehydratase, iron-sulfur-dependent, beta subunit (sdhB) |
| 3202 | DHH subfamily 1 protein |
| 3206 | ribosomal protein L9 (rplI) |
| 3210 | replicative DNA helicase (dnaB) |
| 3216 | ribosomal protein S4 (rpsD) |
| 3224 | transcriptional regulator, TetR family |
| 3236 | membrane protein |
| 3238 | choline transporter (proWX) |
| 3240 | glycine betaine/L-proline transport ATP binding subunit (proV) |
| 3242 | DNA-binding response regulator |
| 3244 | Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family |
| 3246 | ornithine carbamoyltransferase (argF) |
| 3248 | carbamate kinase (arcC) |
| 3252 | membrane protein |
| 3256 | sensory box histidine kinase VicK |
| 3258 | DNA-binding response regulator |
| 3268 | Helix-turn-helix domain protein |
| 3278 | integrase |
| 3284 | ribosomal protein L33 (rpmG) |
| 3288 | ribosomal protein L32 (rpmF) |
| 3300 | YitT family protein |
| 3304 | YitT family protein |
| 3320 | DNA mismatch repair protein MutS (mutS) |
| 3324 | cold-shock domain family protein-related protein |
| 3336 | drug transporter |
| 3340 | Holliday junction DNA helicase RuvA (ruvA) |
| 3352 | recA protein (recA) |
| 3386 | oxidoreductase, Gfo/Idh/MocA family |
| 3390 | acetyltransferase, GNAT family |

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|---|---|
| 3394 | anaerobic ribonucleoside-triphosphate reductase activating protein (nrd |
| 3412 | ABC transporter, permease protein (rbsC) |
| 3414 | ABC transporter, ATP-binding protein (nrtC) |
| 3416 | PTS system, mannose-specific IIAB components (manL) |
| 3420 | Cof family protein |
| 3432 | xanthine/uracil permease family protein |
| 3440 | acetyltransferase, GNAT family |
| 3442 | transcriptional regulator (cps4A) |
| 3448 | HIT family protein (hit) |
| 3460 | ABC transporter, permease protein |
| 3472 | Uncharacterized BCR, YhbC family COG0779 superfamily |
| 3484 | ribosomal protein L7A family |
| 3496 | esterase |
| 3500 | transcriptional repressor, CopY (copY) |
| 3504 | cation-transporting ATPase, E1-E2 family |
| 3508 | cation-binding protein-related protein |
| 3520 | DNA polymerase I (polA) |
| 3534 | DNA-binding response regulator (saeR) |
| 3536 | sensor histidine kinase (saeS) |
| 3562 | drug resistance transporter, EmrB/QacA subfamily |
| 3566 | peptidase M24 family protein |
| 3570 | peptidase M24 family protein (pepQ) |
| 3572 | cytidine/deoxycytidylate deaminase family protein |
| 3584 | translation elongation factor P (efp) |
| 3592 | N utilization substance protein B (nusB) |
| 3596 | sugar-binding transcriptional regulator, LacI family (scrR) |
| 3600 | sucrose-6-phosphate dehydrogenase (scrB) |
| 3606 | PTS system IIABC components (scrA) |
| 3610 | fructokinase (scrK) |
| 3614 | mannose-6-phosphate isomerase, class I (manA) |
| 3622 | phospho-2-dehydro-3-deoxyheptonate aldolase (aroH) |
| 3626 | holo-(acyl-carrier-protein) synthase (acpS) |
| 3630 | alanine racemase (alr) |
| 3634 | autolysin (usp45) |
| 3636 | ATP-dependent DNA helicase RecG (recG) |
| 3642 | shikimate 5-dehydrogenase (aroE) |
| 3652 | Cof family protein |
| 3668 | ferredoxin-related protein |
| 3676 | peptidase t (pepT) |
| 3684 | UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (mur |
| 3692 | iron compound ABC transporter, substrate-binding protein |
| 3698 | FecCD transport family protein (sirB) |
| 3704 | iron compound ABC transporter, permease protein (sirB) |
| 3710 | inorganic pyrophosphatase, manganese-dependent (ppaC) |
| 3714 | pyruvate formate-lyase-activating enzyme (pflA) |
| 3718 | CBS domain protein |
| 3730 | acid phosphatase |
| 3736 | LPXTG-motif cell wall anchor domain protein |
| 3738 | LPXTG-site transpeptidase family protein |
| 3742 | LPXTG-site transpeptidase family protein |
| 3744 | cell wall surface anchor family protein |
| 3746 | cell wall surface anchor family protein |
| 3752 | glycosyl transferase, group 1 family protein domain protein |
| 3754 | EpsQ protein |
| 3756 | polysaccharide extrusion protein |
| 3768 | dTDP-glucose 4-6-dehydratase |
| 3782 | glycosyl transferase domain protein |
| 3788 | dTDP-4-dehydrorhamnose reductase (rfbD) |
| 3796 | RNA polymerase sigma-70 factor (rpoD) |

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|---|---|
| 3802 | DNA primase (dnaG) |
| 3816 | ABC transporter, ATP-binding protein Vexp2 (vex2) |
| 3818 | permease |
| 3820 | transmembrane protein Vexp3 |
| 3822 | transmembrane protein Vexp3 |
| 3832 | endopeptidase O (pepO) |
| 3834 | endopeptidase O (pepO) |
| 3840 | serine protease, subtilase family |
| 3842 | exotoxin 2 |
| 3844 | CylK |
| 3854 | glycine cleavage system T protein |
| 3856 | CylE |
| 3858 | ABC transporter homolog CylB |
| 3862 | acyl carrier protein homolog AcpC (acpP) |
| 3864 | 3-oxoacyl-(acyl-carrier-protein) reductase (fabG) |
| 3868 | CylD |
| 3876 | membrane protein |
| 3912 | LPXTG-site transpeptidase family protein |
| 3916 | LPXTG-site transpeptidase family protein |
| 3918 | LPXTG-site transpeptidase family protein |
| 3920 | LPXTG-motif cell wall anchor domain protein |
| 3928 | chaperonin, 33 kDa (hslO) |
| 3932 | Tn5252, Orf 10 protein |
| 3934 | transposase OrfAB, subunit B |
| 3948 | psr protein |
| 3952 | shikimate kinase (aroK) |
| 3964 | enolase (eno) |
| 3972 | MutT/nudix family protein |
| 3976 | glycosyl transferase, group 1 |
| 3978 | preprotein translocase, SecA subunit (secA) |
| 3986 | preprotein translocase SecY family protein |
| 3990 | glycosyl transferase, family 8 |
| 3992 | glycosyl transferase, family 2 |
| 3998 | glycosyl transferase, family 8 |
| 4000 | glycosyl transferase, family 2/glycosyl transferase family 8 |
| 4002 | glycosyl transferase, family 8 |
| 4012 | LPXTG-motif cell wall anchor domain protein (clfB) |
| 4016 | transcriptional regulator |
| 4018 | excinuclease ABC, B subunit (uvrB) |
| 4022 | Abortive infection protein family |
| 4024 | amino acid ABC transporter, amino acid-binding protein/permease protein |
| 4026 | amino acid ABC transporter, ATP-binding protein |
| 4034 | GTP-binding protein, GTP1/Obg family (obg) |
| 4042 | aminopeptidase PepS (pepS) |
| 4050 | ribosomal small subunit pseudouridine synthase A (rsuA) |
| 4060 | lactoylglutathione lyase (gloA) |
| 4064 | glycosyl transferase family protein |
| 4072 | alkylphosphonate utilization operon protein PhnA (phnA) |
| 4078 | glucosamine--fructose-6-phosphate aminotransferase (isomerizing) (glmS) |
| 4090 | Phosphofructokinase |
| 4094 | DNA polymerase III, alpha subunit (dnaE) |
| 4098 | transcriptional regulator, GntR family |
| 4102 | ABC transporter, ATP-binding protein |
| 4106 | ABC transporter, ATP-binding protein |
| 4116 | FtsK/SpoIIIE family protein |
| 4122 | Helix-turn-helix domain protein |
| 4152 | Helix-turn-helix domain protein |
| 4158 | excisionase |
| 4160 | transposase |

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|---|---|
| 4166 | chloramphenicol acetyltransferase (cat) |
| 4174 | PilB-related protein |
| 4178 | acetyltransferase |
| 4182 | Leucine Rich Repeat domain protein |
| 4190 | nucleoside diphosphate kinase (ndk) |
| 4206 | Protein of unknown function superfamily |
| 4218 | hydrolase, haloacid dehalogenase-like family (pho2) |
| 4226 | oxygen-independent coproporphyrinogen III oxidase |
| 4236 | phosphoglucomutase/phosphomannomutase family protein (femD) |
| 4240 | Gram-positive signal peptide, YSIRK family domain protein |
| 4256 | cobyric acid synthase (cobQ) |
| 4260 | lipoate-protein ligase A (lplA) |
| 4264 | branched-chain alpha-keto acid dehydrogenase E3 component, lipoamide de |
| 4266 | pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltr |
| 4270 | pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase be |
| 4286 | magnesium transporter, CorA family |
| 4294 | exonuclease RexB (rexB) |
| 4302 | phenylalanyl-tRNA synthetase, beta subunit (pheT) |
| 4324 | ATP synthase F1, epsilon subunit (atpC) |
| 4328 | ATP synthase F1, beta subunit (atpD) |
| 4332 | ATP synthase F1, gamma subunit (atpG) |
| 4338 | ATP synthase F1, alpha subunit (atpA) |
| 4342 | ATP synthase F1, delta subunit (atpH) |
| 4346 | ATP synthase F0, B subunit (atpF) |
| 4350 | ATP synthase, F0 subunit A (atpB) |
| 4354 | proton-translocating ATPase, c subunit-related protein |
| 4360 | glycogen synthase (glgA) |
| 4362 | glycogen biosynthesis protein GlgD (glgD) |
| 4366 | 1,4-alpha-glucan branching enzyme (glgB) |
| 4368 | pullulanase |
| 4382 | ribonuclease BN |
| 4396 | acetyltransferase, GNAT family |
| 4398 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA) |
| 4402 | thiamine-phosphate pyrophosphorylase (thiE) |
| 4406 | phosphomethylpyrimidine kinase (thiD) |
| 4410 | transcriptional regulator, Deg family (tenA) |
| 4414 | ABC transporter, ATP-binding protein |
| 4426 | S-adenosylmethionine synthetase (metK) |
| 4440 | DNA polymerase III, gamma and tau subunits (dnaX) |
| 4444 | GAF domain protein |
| 4448 | uridine kinase (udk) |
| 4452 | ATP-dependent RNA helicase, DEAD/DEAH box family |
| 4458 | peptidoglycan GlcNAc deacetylase (pgdA) |
| 4462 | glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent (gapN) |
| 4466 | phosphoenolpyruvate-protein phosphotransferase (ptsI) |
| 4470 | phosphocarrier protein hpr |
| 4474 | NrdH-redoxin-related protein |
| 4478 | ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE) |
| 4498 | glycosyl transferase, family 8 |
| 4504 | alanyl-tRNA synthetase (alaS) |
| 4512 | alkyl hydroperoxide reductase, subunit F (ahpF) |
| 4516 | alkyl hydroperoxide reductase, subunit C (ahpC) |
| 4520 | ribosomal protein S2 (rpsB) |
| 4524 | translation elongation factor Ts (tsf) |
| 4532 | transcriptional regulator CtsR (ctsR) |
| 4536 | ATP-dependent Clp protease, ATP-binding subunit (clpC) |
| 4540 | deoxynucleoside kinase |
| 4544 | NifR3/Smm1 family protein |
| 4548 | chaperonin, 33 kDa (hslO) |

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|---|---|
| 4558 | glutamate--cysteine ligase (gshA) |
| 4562 | Helix-turn-helix domain, fis-type protein |
| 4566 | perfringolysin O regulator protein (pfoR) |
| 4570 | adenylosuccinate synthetase (purA) |
| 4578 | SgaT protein (sgaT) |
| 4582 | PTS system, IIB component (sgaT) |
| 4586 | PTS system, IIA component (mtlA) |
| 4590 | hexulose-6-phosphate synthase |
| 4594 | hexulose-6-phosphate isomerase |
| 4598 | L-ribulose-5-phosphate 4-epimerase (araD) |
| 4606 | sugar binding transcriptional regulator RegR |
| 4610 | D-isomer specific 2-hydroxyacid dehydrogenase family protein (serA) |
| 4622 | transcriptional regulator, BglG family |
| 4632 | glycine betaine/L-proline transport ATP binding subunit (proV) |
| 4636 | amino acid ABC transporter, permease protein |
| 4644 | Na+/H+ exchanger family protein (kefB) |
| 4648 | glyoxylase family protein |
| 4652 | LPXTG-site transpeptidase family protein |
| 4656 | DNA gyrase, A subunit (gyrA) |
| 4660 | L-lactate dehydrogenase (ldh) |
| 4664 | NADH oxidase (nox) |
| 4680 | lipoprotein (bmpD) |
| 4690 | pantothenate kinase (coaA) |
| 4694 | ribosomal protein S20 (rpsT) |
| 4698 | amino acid ABC transporter, amino acid-binding protein (aatB) |
| 4702 | amino acid ABC transporter, ATP-binding protein |
| 4726 | ribosomal large subunit pseudouridine synthase B (rluB) |
| 4734 | Uncharacterized ACR, COG1354 |
| 4738 | integrase/recombinase, phage integrase family (xerD) |
| 4742 | CBS domain protein |
| 4746 | phosphoesterase |
| 4750 | HAM1 protein |
| 4768 | transcriptional regulator, biotin repressor family |
| 4792 | amino acid ABC transproter, permease protein |
| 4796 | amino acid ABC transporter, substrate-binding protein |
| 4798 | 6-aminohexanoate-cyclic-dimer hydrolase |
| 4800 | transcription elongation factor GreA (greA) |
| 4804 | Uncharacterized BCR, YceG family COG1559 |
| 4812 | UDP-N-acetylmuramate--alanine ligase (murC) |
| 4822 | Snf2 family protein |
| 4828 | GTP-binding protein (b2511) |
| 4832 | primosomal protein DnaI (dnaI) |
| 4844 | sensor histidine kinase (arlS) |
| 4846 | DNA-binding response regulator (arlR) |
| 4852 | heat shock protein HtpX (htpX) |
| 4870 | potassium uptake protein, Trk family |
| 4874 | ABC transporter, ATP-binding protein |
| 4888 | phosphoglycerate kinase (pgk) |
| 4896 | transcriptional regulator, MerR family |
| 4900 | glutamine synthetase, type I (glnA) |
| 4904 | secreted 45 kd protein (usp45) |
| 4908 | metallo-beta-lactamase superfamily protein |
| 4916 | glycoprotease family protein |
| 4926 | glycoprotease family protein (gcp) |
| 4938 | ribosomal protein S14p/S29e (rpsN) |
| 4952 | exonuclease (dnaQ) |
| 4956 | transcriptional regulator, merR family |
| 4958 | cyclopropane-fatty-acyl-phospholipid synthase (cfa) |
| 4970 | 1,4-dihydroxy-2-naphthoate octaprenyltransferase (menA) |

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|---|---|
| 4972 | pyridine nucleotide-disulphide oxidoreductase (ndh) |
| 4974 | cytochrome d oxidase, subunit I (cydA) |
| 4976 | cytochrome d ubiquinol oxidase, subunit II (cydB) |
| 4980 | transport ATP-binding protein CydD |
| 4988 | polyprenyl synthetase (ispB) |
| 4990 | X-pro dipeptidyl-peptidase (pepX) |
| 4998 | drug transporter |
| 5002 | universal stress protein family |
| 5004 | glycerol uptake facilitator protein (glpF) |
| 5012 | cppA protein (cppA) |
| 5034 | exodeoxyribonuclease V, alpha subunit (recD) |
| 5038 | Signal peptidase I |
| 5042 | ribonuclease HIII (rnhC) |
| 5062 | transcriptional regulator |
| 5068 | maltose ABC transporter, permease protein (malD) |
| 5072 | maltose ABC transporter, permease protein (malC) |
| 5088 | ABC transporter, ATP-binding protein |
| 5092 | ABC transporter, permease protein |
| 5106 | spspoJ protein (spo0J) |
| 5114 | DNA polymerase III, beta subunit (dnaN) |
| 5118 | Diacylglycerol kinase catalytic domain (presumed) protein |
| 5138 | transcription-repair coupling factor (mfd) |
| 5142 | S4 domain protein |
| 5156 | MesJ/Ycf62 family protein |
| 5160 | hypoxanthine phosphoribosyltransferase (hpt) |
| 5164 | cell division protein FtsH (ftsH) |
| 5172 | hydrolase, haloacid dehalogenase-like family (b2690) |
| 5178 | transcriptional regulator, MarR family |
| 5182 | 3-oxoacyl-(acyl-carrier-protein) synthase III (fabH) |
| 5190 | enoyl-(acyl-carrier-protein) reductase (fabK) |
| 5194 | malonyl CoA-acyl carrier protein transacylase (fabD) |
| 5198 | 3-oxoacyl-[acyl-carrier protein] reductase (fabG) |
| 5200 | 3-oxoacyl-(acyl-carrier-protein) synthase II (fabF) |
| 5202 | acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB) |
| 5206 | (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ) |
| 5210 | acetyl-CoA carboxylase, biotin carboxylase (accC) |
| 5214 | acetyl-CoA carboxylase, carboxyl transferase, beta subunit (accD) |
| 5218 | acetyl-CoA carboxylase, carboxyl transferase, alpha subunit (accA) |
| 5224 | seryl-tRNA synthetase (serS) |
| 5234 | PTS system, mannose-specific IID component |
| 5246 | ribosomal large subunit pseudouridine synthase, RluD subfamily (rluD) |
| 5254 | GTP pyrophosphokinase (relA) |
| 5266 | ribose-phosphate pyrophosphokinase (prsA) |
| 5270 | aminotransferase, class-V |
| 5274 | DNA-binding protein |
| 5282 | Domain of unknown function |
| 5290 | platelet activating factor |
| 5296 | transcriptional regulator, AraC family |
| 5302 | voltage-gated chloride channel family protein |
| 5318 | spermidine/putrescine ABC transporter, ATP-binding protein (potA) |
| 5320 | UDP-N-acetylenolpyruvoylglucosamine reductase (murB) |
| 5324 | bifunctional folate synthesis protein (folK) |
| 5328 | dihydroneopterin aldolase (folB) |
| 5332 | dihydropteroate synthase (folP) |
| 5336 | GTP cyclohydrolase I (folE) |
| 5344 | rarD protein (rarD) |
| 5348 | homoserine kinase (thrB) |
| 5354 | Polysaccharide deacetylase family (icaB) |
| 5362 | osmoprotectant transporter, BCCT family (opuD) |

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|---|---|
| 5384 | thiol peroxidase (psaD) |
| 5388 | hydrolase |
| 5390 | transcriptional regulator, GntR family |
| 5402 | gls24 protein |
| 5424 | uncharacterized domain 1 |
| 5440 | cation efflux family protein |
| 5454 | dihydroorotate dehydrogenase A (pyrDa) |
| 5458 | beta-lactam resistance factor (fibB) |
| 5462 | beta-lactam resistance factor (fibA) |
| 5474 | HD domain protein |
| 5482 | cation-transporting ATPase, E1-E2 family |
| 5486 | fructose-1,6-bisphosphatase (fbp) |
| 5488 | iron-sulfur cluster-binding protein |
| 5492 | peptide chain release factor 2 (prfB) |
| 5496 | cell division ABC transporter, ATP-binding protein FtsE (ftsE) |
| 5504 | carboxymethylenebutenolidase-related protein |
| 5506 | metallo-beta-lactamase superfamily protein |
| 5514 | DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG |
| 5520 | asparaginyl-tRNA synthetase (asnS) |
| 5526 | inosine-uridine preferring nucleoside hydrolase (iunH) |
| 5528 | general stress protein 170 |
| 5534 | Uncharacterised protein family superfamily |
| 5538 | Uncharacterized BCR, COG1481 |
| 5546 | zinc ABC transporter, zinc-binding adhesion liprotein (adcA) |
| 5560 | isochorismatase family protein (entB) |
| 5566 | 3-hydroxybutyryl-CoA dehydrogenase |
| 5572 | pyruvate phosphate dikinase (ppdK) |
| 5574 | glutamyl-tRNA(Gln) amidotransferase, C subunit (gatC) |
| 5580 | glutamyl-tRNA(Gln) amidotransferase, A subunit (gatA) |
| 5594 | GTP-binding protein |
| 5612 | iojap-related protein |
| 5626 | transcriptional regulator SkgA (skgA) |
| 5630 | glycerol uptake facilitator protein (glpF) |
| 5634 | dihydroxyacetone kinase family protein |
| 5638 | dihydroxyacetone kinase family protein |
| 5640 | transcriptional regulator, tetR family |
| 5646 | dihydroxyacetone kinase family protein |
| 5654 | glutamine amidotransferase, class I |
| 5666 | peptidase, M20/M25/M40 family |
| 5668 | ABC transporter, ATP-binding protein |
| 5686 | pur operon repressor (purR) |
| 5690 | cmp-binding-factor 1 (cbf1) |
| 5694 | competence-induced protein Ccs50 (ccs50) |
| 5702 | ribulose-phosphate 3-epimerase (rpe) |
| 5710 | rRNA (guanine-N1-)-methyltransferase (rrmA) |
| 5712 | dimethyladenosine transferase (ksgA) |
| 5718 | primase-related protein |
| 5726 | endosome-associated protein |
| 5728 | CG17785 gene product |
| 5734 | dltD protein (dltD) |
| 5738 | D-alanyl carrier protein-related protein |
| 5742 | dltB protein (dltB) |
| 5754 | DNA-binding response regulator (arlR) |
| 5756 | ribosomal protein L34 (rpmH) |
| 5766 | penicillin-binding protein 4 (pbp4) |
| 5770 | intein-containing protein |
| 5774 | NifU family protein |
| 5778 | aminotransferase, class-V |
| 5782 | Uncharacterized protein family (UPF0051) family |

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| 5786 | ABC transporter, ATP-binding protein |
| 5790 | glycosyl transferase domain protein (llm) |
| 5794 | transcriptional regulator MecA (mecA) |
| 5798 | undecaprenol kinase |
| 5806 | amino acid ABC transporter, amino acid-binding protein/permease protein |
| 5808 | amino acid ABC transporter, ATP-binding protein |
| 5834 | riboflavin biosynthesis protein RibF (ribF) |
| 5850 | type I restriction-modification system, S subunit |
| 5860 | lipoprotein |
| 5862 | aggregation substance |
| 5866 | ID479 |
| 5896 | type II DNA modification methyltransferase Spn5252IP (spn5252IMP) |
| 5916 | ribosomal protein L10 (rplJ) |
| 5922 | ATP-dependent Clp protease, ATP-binding subunit ClpC (clpC) |
| 5926 | homocysteine S-methyltransferase (mmuM) |
| 5932 | transcriptional regulator, TetR family |
| 5938 | GTP-binding protein (cgpA) |
| 5952 | thymidylate synthase (thyA) |
| 5956 | condensing enzyme, FabH-related |
| 5960 | hydroxymethylglutaryl-CoA reductase, degradative |
| 5974 | gene_idK21C13.21~pir\|\|T04769~strong similarity to unknown protein, put |
| 5976 | FMN-dependent dehydrogenase family protein |
| 5980 | phosphomevalonate kinase |
| 5986 | diphosphomevalonate decarboxylase (mvaD) |
| 5990 | mevalonate kinase (mvk) |
| 5994 | Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family (PhoR1 |
| 6002 | GTP pyrophosphokinase (relA) |
| 6006 | transposase for insertion sequence element is904 |
| 6016 | 5'-nucleotidase family |
| 6018 | polypeptide deformylase (def) |
| 6022 | NADP-specific glutamate dehydrogenase (gdhA) |
| 6026 | ABC transporter, ATP-binding/permease protein |
| 6028 | ABC transporter, ATP-binding/permease protein |
| 6030 | acetyltransferase, GNAT family family |
| 6032 | ABC transporter, ATP-binding protein |
| 6040 | degV family protein (degV) |
| 6056 | carbohydrate kinase, PfkB family (fruB) |
| 6064 | beta-lactam resistance factor (fibB) |
| 6070 | 2-dehydropantoate 2-reductase |
| 6076 | PTS system component |
| 6078 | pyridine nucleotide-disulphide oxidoreductase family protein (trxB) |
| 6082 | tRNA (guanine-N1)-methyltransferase (trmD) |
| 6092 | c5a peptidase precursor |
| 6100 | ParA |
| 6102 | transposase family protein (orfA) |
| 6116 | Tn5252, relaxase |
| 6120 | Tn5252, Orf 10 protein |
| 6124 | mercuric reductase |
| 6126 | transcriptional regulator, MerR family |
| 6132 | cation transport ATPase, E1-E2 family |
| 6138 | cation-transporting ATPase, E1-E2 family |
| 6140 | cation-transporting ATPase, E1-E2 family |
| 6144 | cation-transporting ATPase, E1-E2 family |
| 6146 | transcriptional repressor, CopY (copY) |
| 6150 | cadmium resistance transporter |
| 6158 | membrane protein |
| 6162 | flavoprotein (dfp) |
| 6170 | lipoate-protein ligase A |
| 6174 | FMN oxidoreductase (nemA) |

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|---|---|
| 6178 | Bacterial luciferase superfamily |
| 6182 | glycine cleavage system H protein (gcvH) |
| 6186 | Domain of unknown function |
| 6194 | lipoate-protein ligase A (lplA) |
| 6198 | formate--tetrahydrofolate ligase (fhs) |
| 6202 | cardiolipin synthetase (cls) |
| 6220 | aminotransferase, class II (aspB) |
| 6222 | RNA methyltransferase, TrmH family, group 2 |
| 6232 | 60 kda chaperonin |
| 6242 | purine nucleoside phosphorylase (deoD) |
| 6248 | deoxyribose-phosphate aldolase (deoC) |
| 6254 | Lyme disease proteins of unknown function |
| 6258 | ribosomal large subunit pseudouridine synthase, RluD subfamily (rluD) |
| 6262 | penicillin-binding protein 2A (pbp2A) |
| 6266 | pathenogenicity protein |
| 6268 | transcription antitermination protein NusG (nusG) |
| 6272 | glycosyl transferase, family 8 |
| 6276 | glycosyl transferase, family 8 |
| 6284 | sugar transporter family protein |
| 6292 | sensory box histidine kinase |
| 6306 | homocysteine S-methyltransferase (metH) |
| 6310 | glycerol dehydrogenase |
| 6312 | DNA topology modulation protein FlaR |
| 6316 | translation initiation factor IF-1 (infA) |
| 6320 | adenylate kinase (adk) |
| 6326 | ribosomal protein L15 (rplO) |
| 6330 | ribosomal protein L30 (rpmD) |
| 6336 | ribosomal protein S5 (rpsE) |
| 6344 | ribosomal protein L6 (rplF) |
| 6348 | ribosomal protein S8 (rpsH) |
| 6352 | ribosomal protein S14 (rpsN) |
| 6356 | ribosomal protein L5 (rplE) |
| 6360 | ribosomal protein L24 (rplX) |
| 6366 | ribosomal protein L14 (rplN) |
| 6368 | ribosomal protein S17 (rpsQ) |
| 6372 | ribosomal protein L29 (rpmC) |
| 6374 | ribosomal protein L16 (rplP) |
| 6378 | ribosomal protein S3 (rpsC) |
| 6382 | ribosomal protein L22 (rplV) |
| 6386 | ribosomal protein S19 (rpsS) |
| 6390 | ribosomal protein L2 (rplB) |
| 6394 | ribosomal protein L23 (rplW) |
| 6398 | ribosomal protein L4/L1 family (rplD) |
| 6402 | ribosomal protein L3 (rplC) |
| 6408 | ribosomal protein S10 (rpsJ) |
| 6414 | MATE efflux family protein |
| 6418 | threonine synthase (thrC) |
| 6428 | Uncharacterized BCR, COG1636 superfamily |
| 6436 | 4-alpha-glucanotransferase (malQ) |
| 6440 | glycogen phosphorylase family protein (malP) |
| 6444 | glycerol-3-phosphate transporter (glpT) |
| 6452 | rhodanese family protein |
| 6458 | ammonium transporter |
| 6464 | DNA repair protein RadA (radA) |
| 6472 | oxidoreductase, pyridine nucleotide-disulfide, class I |
| 6478 | ribose ABC transporter, periplasmic D-ribose-binding protein (rbsB) |
| 6484 | ribose ABC transporter, ATP-binding protein (rbsA) |
| 6486 | ribose ABC transporter protein (rbsD) |
| 6488 | ribokinase (rbsK) |

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| 6498 | ABC transporter, ATP-binding protein |
| 6502 | DNA-binding response regulator (vicR) |
| 6506 | argininosuccinate synthase (argG) |
| 6508 | argininosuccinate lyase (argH) |
| 6514 | bacteriophage L54a, repressor protein |
| 6528 | soluble transducer HtrXIII |
| 6542 | probable transposase (insertion sequence IS861) |
| 6544 | ABC transporter, ATP-binding/permease protein |
| 6550 | ABC transporter, ATP-binding/permease protein |
| 6560 | Serine hydroxymethyltransferase |
| 6568 | HemK protein (hemK) |
| 6572 | peptide chain release factor 1 (prfA) |
| 6576 | thymidine kinases |
| 6580 | 4-oxalocrotonate tautomerase (dmpI) |
| 6588 | oxidoreductase |
| 6594 | oxidoreductase |
| 6600 | formate/nitrite transporter family protein |
| 6608 | xanthine permease (pbuX) |
| 6612 | xanthine phosphoribosyltransferase (xpt) |
| 6616 | guanosine monophosphate reductase (guaC) |
| 6620 | drug resistance transporter, EmrB/QacA subfamily |
| 6622 | oxidoreductase |
| 6624 | Kup system potassium uptake protein (kup) |
| 6636 | O-methyltransferase |
| 6642 | oligoendopeptidase F (pepF) |
| 6646 | competence protein CoiA (coiA) |
| 6650 | major facilitator superfamily protein superfamily |
| 6652 | ribosomal small subunit pseudouridine synthase A (rsuA) |
| 6658 | glucosamine-6-phosphate isomerase (nagB) |
| 6662 | nodulin-related protein, truncation |
| 6664 | S-adenosylmethioninetRNA ribosyltransferase-isomerase (queA) |
| 6674 | permease, GntP family |
| 6684 | 6-phospho-beta-glucosidase (bglA) |
| 6686 | PTS system, beta-glucosides-specific IIABC components |
| 6688 | transcription antiterminator Lict (licT) |
| 6704 | esterase |
| 6706 | sugar-binding transcriptional repressor, LacI family |
| 6708 | hydrolase, haloacid dehalogenase-like family |
| 6712 | DNA internalization-related competence protein ComEC/Rec2 |
| 6716 | competence protein CelA (celA) |
| 6720 | acyltransferase family protein |
| 6732 | ATP-dependent RNA helicase DeaD (deaD) |
| 6736 | lipoprotein, YaeC family |
| 6738 | ABC transporter, permease protein |
| 6752 | diacylglycerol kinase (dgkA) |
| 6768 | formamidopyrimidine-DNA glycosylase (mutM) |
| 6776 | epidermin immunity protein F |
| 6788 | glycyl-tRNA synthetase, beta subunit (glyS) |
| 6790 | acyl carrier protein phosphodiesterase |
| 6800 | SsrA-binding protein (smpB) |
| 6822 | D-alanine--D-alanine ligase |
| 6824 | recombination protein RecR (recR) |
| 6830 | penicillin-binding protein 2b |
| 6832 | phosphoglycerate mutase (gpmA) |
| 6836 | triosephosphate isomerase (tpiA) |
| 6856 | phosphoglycerate mutase family protein |
| 6860 | D-alanyl-D-alanine carboxypeptidase family |
| 6864 | autolysin |
| 6868 | heat-inducible transcription repressor HrcA (hrcA) |

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| 6872 | heat shock protein GrpE (grpE) |
| 6876 | chaperone protein dnak |
| 6880 | dnaJ protein (dnaJ) |
| 6884 | transcriptional regulator, gntR family domain protein |
| 6888 | tRNA pseudouridine synthase A (truA) |
| 6892 | phosphomethylpyrimidine kinase (thiD) |
| 6910 | galactose-6-phosphate isomerase, LacA subunit (lacA) |
| 6922 | tagatose 1,6-diphosphate aldolase (lacD) |
| 6932 | sugar ABC transporter, ATP-binding protein (msmK) |
| 6936 | glucan 1,6-alpha-glucosidase (dexB) |
| 6940 | UDP-glucose 4-epimerase (galE) |
| 6942 | response regulator (citB) |
| 6950 | citrate carrier protein (citS) |
| 6954 | malate oxidoreductase (tme) |
| 6958 | bacterocin transport accessory protein |
| 6976 | transposase family protein (orfA) |
| 6980 | pXO1-128 |
| 6986 | adhesion lipoprotein (lmb) |
| 6994 | DNA-directed RNA polymerase, alpha subunit (rpoA) |
| 6998 | ribosomal protein L17 (rplQ) |
| 7040 | probable dna-directed rna polymerase delta subunit |
| 7044 | CTP synthase (pyrG) |
| 7058 | bacteriocin transport accessory protein |
| 7074 | translation initiation factor IF-3 (infC) |
| 7100 | adenosine deaminase |
| 8468 | preprotein translocase, SecE subunit |
| 8476 | antigen, 67 kDa |
| 8486 | Lipase/Acylhydrolase |
| 8492 | peptide ABC transporter, permease protein (oppB) |
| 8494 | competence protein CglB (cglB) |
| 8502 | peptide ABC transporter, peptide-binding protein |
| 8504 | oxidoreductase |
| 8510 | amino acid ABC transporter, permease protein (opuBB) |
| 8522 | abc transporter atp-binding protein ybhf |
| 8530 | glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA) |
| 8538 | sugar ABC transporter, sugar-binding protein |
| 8544 | secreted 45 kd protein (usp45) |
| 8556 | phosphoglycerate mutase family protein |
| 8566 | glycosyl hydrolase, family 3 |
| 8576 | N-acetylmuramoyl-L-alanine amidase |
| 8596 | sensory box histidine kinase (withHAMPandPASd) |
| 8608 | aminoglycoside 6-adenylyltransferase |
| 8622 | iron compound ABC transporter, permease protein (sirB) |
| 8636 | phosphate ABC transporter, permease protein (pstC-2) |
| 8650 | branched-chain amino acid transport system II carrier protein (brnQ) |
| 8658 | PTS system, IID component |
| 8662 | replisome organiser-related protein |
| 8674 | alkaline amylopullulanase |
| 8676 | exfoliative toxin A |
| 8690 | glycerol uptake facilitator protein (glpF) |
| 8698 | ABC transporter, ATP-binding protein |
| 8706 | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (pgs |
| 8708 | cobalt transport protein |
| 8730 | integral membrane protein |
| 8734 | yadS protein |
| 8736 | cell wall surface anchor family protein |
| 8748 | polysaccharide biosynthesis protein |
| 8752 | glycosyl transferase domain protein |
| 8764 | endopeptidase O |

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| 8770 | beta-ketoacyl-acyl carrier protein synthase II |
| 8772 | ABC transporter, ATP-binding protein |
| 8776 | penicillin-binding protein |
| 8778 | cell wall surface anchor family protein |
| 8780 | cell wall surface anchor family protein |
| 8786 | LPXTG-motif cell wall anchor domain protein |
| 8788 | 6-aminohexanoate-cyclic-dimer hydrolase |
| 8796 | NLP/P60 family protein |
| 8802 | DNA/RNA non-specific endonuclease |
| 8806 | hydroxyethylthiazole kinase (thiM) |
| 8826 | PTS system component |
| 8832 | sugar ABC transporter, permease protein |
| 8836 | potassium uptake protein, Trk family (trkA) |
| 8850 | lemA protein (lemA) |
| 8856 | cobalt transport protein |
| 8882 | spermidine/putrescine ABC transporter, spermidine/putrescine-binding pr |
| 8884 | spermidine/putrescine ABC transporter, permease protein (potC) |
| 8906 | ABC transporter, substrate-binding protein |
| 8908 | lipoprotein |
| 8916 | sensor histidine kinase |
| 8930 | TrsK-like protein (traK) |
| 8936 | R5 protein |
| 8962 | chromosome assembly protein homolog |
| 8978 | ribose ABC transporter, permease protein (rbsC) |
| 8980 | permease |
| 8982 | sensor histidine kinase (arlS) |
| 8986 | hydrolase, haloacid dehalogenase-like family (gph) |
| 8994 | dephospho-CoA kinase |
| 8996 | oxalateformate antiporter |
| 9004 | sensory box protein |
| 9006 | host cell surface-exposed lipoprotein |
| 9012 | PAP2 family protein |
| 9034 | GtrA family protein |
| 9050 | lipoprotein signal peptidase (lspA) |
| 9280 | alcohol dehydrogenase, zinc-containing (adh) |
| 9284 | trigger factor (tig) |
| 9290 | fructose-bisphosphate aldolase (fba) |
| 9292 | DAK2 domain protein |
| 9296 | oligopeptide ABC transporter, permease protein |
| 9298 | N-acetylglucosamine-6-phosphate deacetylase (nagA) |
| 9300 | transcriptional regulator, DeoR family (lacR) |
| 9302 | PTS system, mannose-specific IIC component (manM) |
| 9306 | Phosphoglucose isomerase |
| 9310 | aspartate--ammonia ligase (asnA) |
| 9312 | amino acid ABC transporter, ATP-binding protein |
| 9314 | DNA-binding protein HU (hup) |
| 9316 | DHH subfamily 1 protein |
| 9318 | chloride channel |
| 9320 | integrase (int) |
| 9324 | DNA/RNA non-specific endonuclease |
| 9326 | PTS system component |
| 9328 | cell division protein, FtsW/RodA/SpoVE family (ftsW) |
| 9330 | LPXTG-motif cell wall anchor domain protein |
| 9332 | peptide chain release factor 3 (prfC) |
| 9334 | ABC transporter, ATP-binding protein |
| 9336 | superoxide dismutase [mn-fe] |
| 9340 | phenylalanyl-tRNA synthetase, alpha subunit (pheS) |
| 9342 | amino acid ABC transporter, permease protein |
| 9344 | phosphate ABC transporter, phosphate-binding protein (pstS) |

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| 9346 | NOL1/NOP2/sun family protein (sun) |
| 9348 | Abortive infection protein family |
| 9350 | permease |
| 9352 | N-acetylmuramoyl-L-alanine amidase domain protein (usp45) |
| 9354 | ABC transporter, ATP-binding protein |
| 9356 | phosphoglucomutase (pgm) |
| 9358 | oxidoreductase, short chain dehydrogenase/reductase family |
| 9360 | phosphate acetyltransferase |
| 9362 | gls24 protein |
| 9364 | ribosomal protein S1 (rpsA) |
| 9368 | dTDP-glucose 4,6-dehydratase (rfbB) |
| 9370 | excinuclease ABC, C subunit (uvrC) |
| 9372 | MATE efflux family protein |
| 9378 | amino acid permease (rocE) |
| 9380 | DNA-binding response regulator TrcR (trcR) |
| 9382 | 16S rRNA processing protein RimM (rimM) |
| 9384 | transcriptional regulator |
| 9388 | ribosomal protein L20 (rplT) |
| 9394 | sugar-binding transcriptional repressor, LacI family (malR) |
| 9396 | proton/peptide symporter family protein |
| 9398 | amino acid permease |
| 9400 | exoribonuclease, VacB/Rnb family (vacB) |
| 9402 | multi-drug resistance efflux pump (pmrA) |
| 9404 | adhesion lipoprotein (psaA) |
| 9406 | iron-dependent transcriptional regulator (sirR) |
| 9410 | branched-chain amino acid ABC transporter, amino acid-binding protein ( |
| 9412 | amino acid permease |
| 9414 | SpoU rRNA Methylase family protein |
| 9416 | sodium/dicarboxylate symporter (gltP-2) |
| 9418 | branched-chain amino acid transport system II carrier protein (brnQ) |
| 9420 | alcohol dehydrogenase, zinc-containing |
| 9422 | aminotransferase, class I (aspB) |
| 9424 | ribosomal protein S6 (rpsF) |
| 9426 | A/G-specific adenine glycosylase (mutY) |
| 9428 | acid phosphatase (olpA) |
| 9430 | ribosomal protein S12 (rpsL) |
| 9434 | microcin immunity protein MccF (mccF-1) |
| 9436 | undecaprenyl diphosphate synthase (uppS) |
| 9438 | preprotein translocase, YajC subunit (yajC) |
| 9440 | chaperonin, 10 kDa (groES) |
| 9444 | YitT family protein |
| 9446 | serine protease (htrA) |
| 9448 | ribose-phosphate pyrophosphokinase (prsA) |
| 9450 | aromatic amino acid aminotransferase (araT) |
| 9452 | Recombination protein O (recO) |
| 9454 | Abortive infection protein family |
| 9456 | fatty acid/phospholipid synthesis protein PlsX (plsX) |
| 9458 | acyl carrier protein (acpP) |
| 9462 | phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK) |
| 9464 | alcohol dehydrogenase, iron-containing |
| 9466 | ribosomal protein L18 (rplR) |
| 9468 | preprotein translocase, SecY subunit |
| 9470 | transcriptional regulator ComX1 (comX1) |
| 9472 | deoxyuridine 5`-triphosphate nucleotidohydrolase (dut) |
| 9478 | sugar-binding transcriptional regulator, LacI family (rbsR) |
| 9480 | SPFH domain/Band 7 family |
| 9488 | zinc ABC transporter, permease protein (adcB) |
| 9492 | abortive infection protein |
| 9494 | hydrolase, haloacid dehalogenase-like family |

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|---|---|
| 9496 | response regulator (lytT) |
| 9500 | transketolase, C-terminal subunit |
| 9502 | polyribonucleotide nucleotidyltransferase (pnp) |
| 9504 | serine O-acetyltransferase (cysE) |
| 9508 | ribosomal protein L13 (rplM) |
| 9510 | replication initiation protein |
| 9518 | amino acid ABC transporter, amino acid-binding protein |
| 9522 | glycyl-tRNA synthetase, alpha subunit (glyQ) |
| 9524 | NADH oxidase |
| 9528 | transketolase (tkt) |
| 9534 | penicillin-binding protein 1A (pbp1A) |
| 9536 | cell division protein DivIVA (divIVA) |
| 9538 | sensor histidine kinase |
| 9540 | serine/threonine protein kinase (pknB) |
| 9542 | transcriptional regulator |
| 9544 | PTS system, IIA component (lacF) |
| 9546 | glycerol dehydrogenase (gldA) |
| 9548 | aspartate kinase (thrA) |
| 9550 | enoyl-CoA hydratase/isomerase family protein |
| 9552 | acyl carrier protein (acpP) |
| 9564 | ABC transporter, ATP-binding protein |
| 9566 | N utilization substance protein A (nusA) |
| 9568 | ribosome-binding factor A (rbfA) |
| 9570 | Cof family protein |
| 9572 | CoA binding domain protein (b0965) |
| 9574 | transcriptional regulator, Fur family |
| 9578 | queuine tRNA-ribosyltransferase (tgt) |
| 9580 | ribonuclease P protein component (rnpA) |
| 9582 | serine protease, subtilase family |
| 9584 | glycosyl transferase domain protein |
| 9586 | transcriptional activator, AraC family |
| 9588 | transcriptional regulator, TetR family |
| 9590 | transcriptional regulator, AraC family |
| 9594 | surface protein Rib |
| 9596 | transposase, mutator family |
| 9600 | acetyltransferase, GNAT family |
| 9602 | Transposase, Mutator family |
| 9606 | UDP-sugar hydrolase |
| 9610 | anthranilate synthase component II (trpG) |
| 9612 | biotin synthetase (bioB) |
| 9616 | UDP-N-acetylmuramoylalanine--D-glutamate ligase (murD) |
| 9618 | ylmF protein (ylmF) |
| 9620 | amino acid ABC transporter, permease protein |
| 9622 | phosphoglucomutase (pgm) |
| 9624 | YjeF-related protein, C-terminus |
| 9626 | FemAB family protein (fibA) |
| 9628 | Cof family protein |
| 9630 | cell division ABC transporter, permease protein FtsX (ftsX) |
| 9632 | oxidoreductase, short-chain dehydrogenase/reductase family (fabG) |
| 9634 | aspartate aminotransferase (aspC) |
| 9638 | ribosomal protein L31 (rpmE) |
| 9640 | nrdI protein (nrdI) |
| 9642 | ribosomal protein L19 (rplS) |
| 9644 | bacteriophage L54a, repressor protein |
| 9646 | bacteriophage L54a, antirepressor |
| 9652 | single-strand binding protein (ssb) |
| 9660 | pneumococcal surface protein A |
| 9666 | DNA-binding response regulator (vncR) |
| 9668 | transposase OrfAB, subunit B |

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|---|---|
| 9670 | cell division protein, FtsW/RodA/SpoVE family (rodA) |
| 9672 | DNA gyrase, B subunit (gyrB) |
| 9674 | 3-phosphoshikimate 1-carboxyvinyltransferase (aroA) |
| 9676 | RNA methyltransferase, TrmA family |
| 9680 | transcriptional regulator, AraC family |
| 9682 | ABC transporter, ATP-binding protein |
| 9690 | CylJ |
| 9696 | permease |
| 9698 | regulatory protein |
| 9700 | carbohydrate kinase, pfkB family |
| 9702 | beta-glucuronidase |
| 9704 | 2-deydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldo |
| 9706 | 3-oxoacyl-(acyl-carrier-protein) reductase |
| 9708 | catabolite control protein A (ccpA) |
| 9712 | ribonuclease III (rnc) |
| 9714 | SMC family, C-terminal domain family |
| 9718 | S1 RNA binding domain protein |
| 9722 | prolipoprotein diacylglyceryl transferase (lgt) |
| 9724 | riboflavin synthase, alpha subunit (ribE) |
| 9726 | 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (ri |
| 9728 | lysyl-tRNA synthetase (lysS) |
| 9734 | Transposase subfamily |
| 9738 | translation elongation factor Tu (tuf) |
| 9740 | UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-a |
| 9746 | Glutathione S-transferases domain protein |
| 9754 | Ribonucleotide reductases |
| 9756 | biotin--acetyl-CoA-carboxylase ligase |
| 9760 | Uncharacterized protein family SNZ family |
| 9762 | methionine aminopeptidase, type I (map) |
| 9764 | DNA ligase, NAD-dependent (ligA) |
| 9766 | glucose-1-phosphate adenylyltransferase (glgC) |
| 9768 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA) |
| 9770 | acetyltransferase, GNAT family |
| 9772 | exonuclease RexA (rexA) |
| 9774 | tRNA modification GTPase TrmE (trmE) |
| 9776 | ABC transporter, ATP-binding protein |
| 9778 | pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase al |
| 9782 | Mur ligase family protein |
| 9786 | HD domain protein |
| 9788 | translation elongation factor G (fusA) |
| 9796 | pyruvate kinase (pyk) |
| 9798 | Signal peptidase I |
| 9802 | cytidine deaminase (cdd) |
| 9804 | sugar ABC transporter, ATP-binding protein |
| 9806 | sugar ABC transporter, permease protein |
| 9808 | acetyltransferase, GNAT family |
| 9810 | ABC transporter, permease protein |
| 9812 | SatD |
| 9814 | Helix-turn-helix domain, fis-type protein |
| 9816 | phosphate ABC transporter, ATP-binding protein (pstB-1) |
| 9818 | tRNA pseudouridine synthase B (truB) |
| 9820 | Acetyltransferase (GNAT) family |
| 9822 | DNA topoisomerase I (topA) |
| 9824 | ribonuclease HII (rnhB) |
| 9830 | orotidine 5'-phosphate decarboxylase (pyrF) |
| 9832 | aspartate-semialdehyde dehydrogenase (asd) |
| 9836 | pantothenate metabolism flavoprotein (dfp) |
| 9840 | Sua5/YciO/YrdC/YwlC family protein |
| 9844 | thiamine biosynthesis protein ApbE |

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|---|---|
| 9846 | Domain of unknown function |
| 9848 | DNA repair protein RadC (radC) |
| 9850 | glycosyl hydrolase, family 1 (bglA) |
| 9852 | Cof family protein (b0844) |
| 9854 | spermidine/putrescine ABC transporter, permease protein (potH) |
| 9856 | folylpolyglutamate synthase (folC) |
| 9858 | homoserine dehydrogenase (hom) |
| 9860 | succinate-semialdehyde dehydrogenase (gabD-1) |
| 9862 | membrane protein |
| 9864 | ATP-dependent DNA helicase PcrA (pcrA) |
| 9866 | uracil permease (uraA) |
| 9868 | sodiumalanine symporter family protein |
| 9878 | capsular polysaccharide biosynthesis protein Cps4B (cps4B) |
| 9880 | transcriptional regulator, LysR family |
| 9882 | CpslaS |
| 9884 | chloride channel protein |
| 9886 | tributyrin esterase (estA) |
| 9888 | ABC transporter, ATP-binding protein (potA) |
| 9890 | alpha-acetolactate decarboxylase (budA) |
| 9892 | TPR domain protein |
| 9896 | metallo-beta-lactamase superfamily protein |
| 9898 | tRNA delta(2)-isopentenylpyrophosphate transferase (miaA) |
| 9902 | glycerophosphoryl diester phosphodiesterase |
| 9904 | transposase OrfAB, subunit B |
| 9906 | IS3-Spn1, transposase |
| 9908 | transposase OrfAB, subunit B (orfB) |
| 9910 | reverse transcriptase |
| 9916 | transposase OrfAB, subunit B |
| 9918 | integrase, phage family (int) |
| 9920 | transcription regulator |
| 9922 | TnpA |
| 9926 | structural gene for ultraviolet resistance (uvra) |
| 9930 | Helicases conserved C-terminal domain protein |
| 9932 | abortive infection bacteriophage resistance protein (abiEi) |
| 9944 | ribosomal protein L7/L12 (rplL) |
| 9948 | ATP-dependent Clp protease, ATP-binding subunit ClpX (clpX) |
| 9950 | dihydrofolate reductase (folA) |
| 9952 | hemolysin |
| 9954 | transcriptional regulator, MarR family |
| 9958 | polyA polymerase family protein |
| 9960 | PTS system, fructose specific IIABC components (fruA-1) |
| 9962 | lactose phosphotransferase system repressor (lacR) |
| 9964 | choline binding protein D (cbpD) |
| 9968 | pyrimidine operon regulatory protein (pyrR) |
| 9970 | ribosomal large subunit pseudouridine synthase D (rluD) |
| 9972 | thiamine biosynthesis protein ThiI (thiI) |
| 9974 | 3-dehydroquinate dehydratase, type I (aroD) |
| 9976 | iron compound ABC transporter, ATP-binding protein (fepC) |
| 9980 | transcriptional regulator |
| 9982 | glycosyl transferase domain protein |
| 9984 | Cps9H |
| 9988 | 4-diphosphocytidyl-2C-methyl-D-erythritol synthase (ispD) |
| 9990 | licD1 protein (licD1) |
| 9996 | large conductance mechanosensitive channel protein (mscL) |
| 10000 | maltose ABC transporter, maltose-binding protein |
| 10004 | nucleotide sugar synthetase-like protein |
| 10006 | transcriptional regulator |
| 10008 | oxidoreductase, aldo/keto reductase family |
| 10010 | NAD(P)H-flavin oxidoreductase |

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|---|---|
| 10016 | transcriptional regulator MutR |
| 10018 | GTP-binding protein Era (era) |
| 10022 | peptide methionine sulfoxide reductase (msrA) |
| 10026 | peptide ABC transporter, ATP-binding protein |
| 10028 | peptide ABC transporter, ATP-binding protein (amiE) |
| 10030 | peptide ABC transporter, peptide-binding protein |
| 10032 | transposase, IS30 family |
| 10034 | transcriptional regulator, LysR family |
| 10036 | spoE family protein (ftsK) |
| 10044 | methionyl-tRNA synthetase (metG) |
| 10046 | D-isomer specific 2-hydroxyacid dehydrogenase family protein (serA) |
| 10048 | acetyltransferase, GNAT family |
| 10050 | phosphoserine aminotransferase (serC) |
| 10054 | thymidylate kinase (tmk) |
| 10060 | branched-chain amino acid ABC transporter, permease protein (livH) |
| 10062 | ATP-dependent Clp protease, proteolytic subunit ClpP (clpP) |
| 10064 | uracil phosphoribosyltransferase (upp) |
| 10066 | potassium uptake protein, Trk family (trkH) |
| 10068 | glutamate racemase (murI) |
| 10070 | membrane protein |
| 10072 | HD domain protein |
| 10074 | Acylphosphatase |
| 10076 | spoIIIJ family protein |
| 10078 | acetyltransferase, GNAT family |
| 10080 | glucose-inhibited division protein B (gidB) |
| 10082 | potassium uptake protein, Trk family |
| 10084 | ABC transporter, permease protein |
| 10088 | isochorismatase family protein |
| 10092 | haloacid dehalogenase-like hydrolase superfamily |
| 10094 | membrane protein |
| 10096 | glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB) |
| 10098 | CBS domain protein protein |
| 10100 | transcriptional regulator (codY) |
| 10102 | universal stress protein family |
| 10104 | L-asparaginase (ansA) |
| 10106 | oxidoreductase, aldo/keto reductase 2 family |
| 10108 | preprotein translocase, SecA subunit (secA) |
| 10112 | excinuclease ABC, A subunit (uvrA) |
| 10114 | magnesium transporter, CorA family (corA) |
| 10116 | thioredoxin (trx) |
| 10118 | MutS2 family protein (mutS2) |
| 10122 | DNA-damage inducible protein P (dinP) |
| 10124 | formate acetyltransferase (pfl) |
| 10126 | transcriptional regulator, Crp family |
| 10128 | transport ATP-binding protein CydC |
| 10138 | ribosomal-protein-alanine acetyltransferase (rimI) |
| 10140 | hydrolase |
| 10144 | D-alanine-activating enzyme (dltA) |
| 10148 | carbohydrate kinase, FGGY family |
| 10150 | transaldolase |
| 10160 | Helix-turn-helix domain protein |
| 10164 | single-strand binding protein (ssb) |
| 10166 | type II DNA modification methyltransferase Spn5252IP (spn5252IMP) |
| 10174 | integrase, phage family |
| 10178 | Cyclic nucleotide-binding domain protein |
| 10180 | transcriptional regulator, MarR family |
| 10182 | prolyl-tRNA synthetase (proS) |
| 10184 | leucine-rich protein |
| 10186 | lacX protein, truncation (lacX) |

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|---|---|
| 10188 | tagatose-6-phosphate kinase (lacC) |
| 10190 | galactose-6-phosphate isomerase, LacB subunit (lacB) |
| 10192 | neuraminidase |
| 10198 | Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase domain protei |
| 10200 | ABC transporter, ATP-binding protein |
| 10202 | PTS system, IIABC components (ptsG) |
| 10204 | phosphate regulon response regulator PhoB (phoB) |
| 10212 | Uncharacterized ACR, COG2161 subfamily |
| 10216 | abortive phage resistance protein |
| 10222 | TnpA |
| 10226 | acetyltransferase, GNAT family |
| 10230 | ABC transporter domain protein |
| 10234 | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase ( |
| 10236 | branched-chain amino acid transport protein AzlC (azlC) |
| 10240 | DNA-binding response regulator (srrA) |
| 10242 | leucyl-tRNA synthetase (leuS) |
| 10246 | NupC family protein |
| 10248 | transcriptional regulator, GntR family |
| 10252 | glyoxalase family protein |
| 10254 | anaerobic ribonucleoside-triphosphate reductase (nrdD) |
| 10256 | competence-induced protein Ccs4 |
| 10262 | competence/damage-inducible protein CinA (cinA) |
| 10264 | DNA-3-methyladenine glycosylase I (tag) |
| 10268 | DNA mismatch repair protein HexB (hexB) |
| 10270 | arginine repressor (argR) |
| 10272 | arginyl-tRNA synthetase (argS) |
| 10274 | aspartyl-tRNA synthetase (aspS) |
| 10276 | histidyl-tRNA synthetase (hisS) |
| 10280 | AGR_pAT_51p |
| 10286 | hydrolase, alpha/beta hydrolase fold family |
| 10288 | phage infection protein |
| 10290 | Glucose inhibited division protein A (gidA) |
| 10292 | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (trmU) |
| 10296 | arginine/ornithine antiporter (arcD) |
| 10298 | chromosomal replication initiator protein DnaA (dnaA) |
| 10302 | peptidyl-tRNA hydrolase (pth) |
| 10310 | phosphotyrosine protein phosphatase |
| 10316 | ribosomal protein L36 (rpmJ) |
| 10318 | ribosomal protein S13/S18 (rpsM) |
| 10328 | L-lactate dehydrogenase (ldh) |
| 10330 | ribosomal protein L28 (rpmB) |
| 10362 | RNA polymerase sigma-70 factor, ECF subfamily |
| 10384 | BioY family protein |
| 10386 | AtsA/ElaC family protein |
| 10388 | cytidine/deoxycytidylate deaminase family protein |
| 10394 | phosphorylase, Pnp/Udp family |
| 10396 | transcriptional regulator, MerR family |
| 10402 | methyltransferase (ubiE) |
| 10412 | type IV prepilin peptidase |
| 10416 | ylmG protein (ylmG) |
| 10444 | transposase OrfAB, subunit B |
| 10446 | IS150-like transposase |
| 10452 | Bacterial regulatory proteins, tetR family domain protein |
| 10454 | cell wall surface anchor family protein, authentic frameshift (clfB) |
| 10456 | transposase OrfAB, subunit A (orfA) |
| 10460 | chaperonin, 33 kDa (hslO) |
| 10472 | (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ) |
| 10482 | sprT protein |
| 10490 | transcriptional regulator, MarR family |

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|---|---|
| 10498 | transcriptional regulator |
| 10504 | glycogen biosynthesis protein GlgD (glgD) |
| 10536 | ribonucleoside-diphosphate reductase, alpha subunit, truncation (nrdD) |
| 10538 | LPXTG-motif cell wall anchor domain |
| 10550 | membrane protein |
| 10554 | arsenate reductase (arsC) |
| 10564 | transposase, authentic frameshift |
| 10570 | transposase OrfAB, subunit A (orfA) |
| 10574 | Tn5252, Orf 9 protein |
| 10580 | IS3-Spn1, transposase |
| 10584 | transcriptional regulator, ArsR family |
| 10628 | ribosomal protein L35 (rpmI) |
| 10630 | cytidylate kinase (cmk) |
| 10636 | MutT/nudix family protein |
| 10644 | preprotein translocase, SecG subunit |
| 10680 | ribosomal protein S18 (rpsR) |
| 10682 | single-strand binding protein (ssb) |
| 10692 | glyceraldehyde 3-phosphate dehydrogenase (gap) |
| 10694 | translation elongation factor G (fusA) |
| 10696 | ribosomal protein S7 (rpsG) |
| 10704 | phosphinothricin N-acetyltransferase (pat) |
| 10730 | nrdI protein (nrdI) |
| 10732 | accessory gene regulator protein C (blpH) |
| 10744 | rhodanese family protein (pspE) |
| 10746 | cAMP factor |
| 10758 | competence/damage-inducible protein CinA (cinA) |
| 10770 | transcriptional regulator, ArgR family (argR) |
| 10772 | FliP family family |
| 10794 | peptide ABC transporter, peptide-binding protein |
| 10800 | ribosomal protein S21 (rpsU) |
| 10802 | transposase, IS30 family |
| 10816 | mucin 2 precursor, intestinal |
| 10854 | SV40-transformed marker protein pG1-related protein |
| 10856 | SV40-transformed marker protein pG1-related protein |
| 10858 | SV40-transformed marker protein pG1-related protein |
| 10860 | SV40-transformed marker protein pG1-related protein |
| 10862 | SV40-transformed marker protein pG1-related protein |
| 10864 | SV40-transformed marker protein pG1-related protein |
| 10866 | SV40-transformed marker protein pG1-related protein |
| 10910 | transcriptional regulator |
| 10920 | ribosomal protein S11 (rpsK) |
| 10922 | elaA protein |
| 10926 | 5-formyltetrahydrofolate cyclo-ligase family protein |
| 10938 | inositol monophosphatase family protein |
| 10940 | amino acid ABC transporter, amino acid-binding protein (artI) |
| 10944 | Holliday junction DNA helicase RuvB (ruvB) |
| 10946 | D-alanyl-D-alanine carboxypeptidase (dacA) |
| 10948 | lipoprotein (bmpD) |
| 10950 | peptidase, U32 family family |
| 10952 | protease maturation protein |
| 10954 | glutamyl-tRNA synthetase (gltX) |
| 10956 | GTP-binding protein LepA (lepA) |
| 10960 | translation initiation factor if-2 |
| 10962 | phosphoenolpyruvate carboxylase (ppc) |
| 10964 | calcium E1-E2-type ATPase |
| 10966 | serine protease, subtilase family |

## CLAIMS

1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1014, 1016, 1018, 1020, 1022, 1024, 1026, 1028, 1030, 1032, 1034, 1036, 1038, 1040, 1042, 1044, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1068, 1070, 1072, 1074, 1076, 1078, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1134, 1136, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408, 1410, 1412, 1414, 1416, 1418, 1420, 1422, 1424, 1426, 1428, 1430, 1432, 1434, 1436, 1438, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1454, 1456, 1458, 1460, 1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490, 1492, 1494, 1496, 1498, 1500, 1502, 1504, 1506, 1508, 1510, 1512, 1514, 1516, 1518, 1520, 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550, 1552, 1554, 1556, 1558, 1560, 1562, 1564, 1566, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1586, 1588, 1590, 1592, 1594, 1596, 1598, 1600, 1602, 1604, 1606, 1608, 1610, 1612, 1614, 1616, 1618, 1620, 1622, 1624, 1626, 1628, 1630, 1632, 1634, 1636, 1638, 1640, 1642, 1644, 1646, 1648, 1650, 1652, 1654, 1656, 1658, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1678, 1680, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1706, 1708, 1710, 1712, 1714, 1716, 1718, 1720,

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2. A protein having 50% or greater sequence identity to a protein according to claim 1.

3. A protein comprising a fragment of 7 or more consecutive amino acids from an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1014, 1016, 1018, 1020, 1022, 1024, 1026, 1028, 1030, 1032, 1034, 1036, 1038, 1040, 1042, 1044, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1068, 1070, 1072, 1074, 1076, 1078, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1134, 1136, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408, 1410, 1412, 1414, 1416, 1418, 1420, 1422, 1424, 1426, 1428, 1430, 1432, 1434, 1436, 1438, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1454, 1456, 1458, 1460, 1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490, 1492, 1494, 1496, 1498, 1500, 1502, 1504, 1506, 1508, 1510, 1512, 1514, 1516, 1518, 1520, 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550, 1552, 1554, 1556, 1558, 1560, 1562, 1564, 1566, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1586, 1588, 1590,

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4. An antibody which binds to a protein according to any one of claims 1 to 3.

5. The antibody of claim 4, wherein said antibody is a monoclonal antibody, a chimeric antibody, a humanised antibody, or a fully human antibody.

6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.

7. A nucleic acid molecule according to claim 6, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, 687, 689, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729, 731, 733, 735, 737, 739, 741, 743, 745, 747, 749, 751, 753, 755, 757, 759, 761, 763, 765, 767, 769, 771, 773, 775, 777, 779, 781, 783, 785, 787, 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859, 861, 863, 865, 867, 869, 871, 873, 875, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 899, 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 965, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1015, 1017, 1019, 1021, 1023, 1025, 1027, 1029, 1031, 1033, 1035, 1037, 1039, 1041, 1043, 1045, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1069, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1115, 1117, 1119, 1121, 1123, 1125, 1127, 1129, 1131, 1133, 1135, 1137, 1139, 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1161, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1211, 1213, 1215, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329,

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8. A nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ IDs 10967, 10968, 10969, 10970, 10971, 10972, 10973, 10974, 10975, 10976, 10977, 10978, 10979, 10980, 10981, 10982, 10983, 10984, 10985, 10986, 10987, 10988, 10989, 10990, 10991, 10992, 10993, 10994, 10995, 10996, 10997, 10998, 10999, 11000, 11001, 11002, 11003, 11004, 11005, 11006, 11007, 11008, 11009, 11010, 11011, 11012, 11013, 11014, 11015, 11016, 11017, 11018, 11019, 11020, 11021, 11022, 11023, 11024, 11025, 11026, 11027, 11028, 11029, 11030, 11031, 11032, 11033, 11034, 11035, 11036, 11037, 11038, 11039, 11040, 11041, 11042, 11043, 11044, 11045, 11046, 11047, 11048, 11049, 11050, 11051, 11052, 11053, 11054, 11055, 11056, 11057, 11058, 11059, 11060, 11061, 11062, 11063, 11064, 11065, 11066, 11067, 11068, 11069, 11070, 11071, 11072, 11073, 11074, 11075, 11076, 11077, 11078, 11079, 11080, 11081, 11082, 11083, 11084, 11085, 11086, 11087, 11088, 11089, 11090, 11091, 11092, 11093, 11094, 11095, 11096, 11097, 11098, 11099, 11100, 11101, 11102, 11103, 11104, 11105, 11106, 11107, 11108, 11109, 11110, 11111, 11112, 11113, 11114, 11115, 11116, 11117, 11118, 11119, 11120, 11121, 11122, 11123, 11124, 11125, 11126, 11127, 11128, 11129, 11130, 11131, 11132, 11133, 11134, 11135, 11136, 11137, 11138, 11139, 11140, 11141, 11142, 11143, 11144, 11145, 11146, 11147, 11148, 11149, 11150, 11151, 11152, 11153, 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161, 11162, 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170, 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178, 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186, 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195, 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203, 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211, 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219, 11220, 11221, 11222, 11223, 11224, 11225, 11226, 11227, 11228, 11229, 11230, 11231, 11232, 11233, 11234, 11235, 11236, 11237, 11238, 11239, 11240, 11241, 11242, 11243, 11244, 11245, 11246, 11247, 11248, 11249, 11250, 11251, 11252, 11253, 11254, 11255, 11256, 11257, 11258, 11259, 11260, 11261, 11262, 11263, 11264, 11265, 11266, 11267, 11268, 11269, 11270, 11271, 11272, 11273, 11274, 11275, 11276, 11277, 11278, 11279, 11280, 11281, 11282, 11283, 11284, 11285, 11286, 11287, 11288, 11289, 11290, 11291, 11292, 11293, 11294, 11295, 11296, 11297, 11298, 11299, 11300, 11301, 11302, 11303, 11304, 11305, 11306, 11307, 11308, 11309, 11310, 11311, 11312, 11313, 11314, 11315, 11316, 11317, 11318, 11319, 11320, 11321, 11322, 11323, 11324, 11325, 11326, 11327, 11328, 11329, 11330, 11331, 11332, 11333, 11334, 11335, 11336, 11337, 11338, 11339, 11340, 11341, 11342, 11343, 11344, 11345, 11346, 11347, 11348, 11349, 11350, 11351, 11352, 11353, 11354, 11355, 11356, 11357, 11358, 11359, 11360, 11361, 11362, 11363, 11364, 11365, 11366, 11367, 11368, 11369, 11370, 11371, 11372, 11373, 11374, 11375, 11376, 11377, 11378, 11379, 11380, 11381, 11382, 11383, 11384,

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12009, 12010, 12011, 12012, 12013, 12014, 12015, 12016, 12017, 12018, 12019, 12020, 12021, 12022, 12023 and 12024.

9. A nucleic acid molecule comprising a fragment of 10 or more consecutive nucleotides from a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, 687, 689, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729, 731, 733, 735, 737, 739, 741, 743, 745, 747, 749, 751, 753, 755, 757, 759, 761, 763, 765, 767, 769, 771, 773, 775, 777, 779, 781, 783, 785, 787, 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859, 861, 863, 865, 867, 869, 871, 873, 875, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 899, 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 965, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1015, 1017, 1019, 1021, 1023, 1025, 1027, 1029, 1031, 1033, 1035, 1037, 1039, 1041, 1043, 1045, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1069, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1115, 1117, 1119, 1121, 1123, 1125, 1127, 1129, 1131, 1133, 1135, 1137, 1139, 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1161, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1211, 1213, 1215, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329, 1331, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1347, 1349, 1351, 1353, 1355, 1357, 1359, 1361, 1363, 1365, 1367, 1369, 1371, 1373, 1375, 1377, 1379, 1381, 1383, 1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1403, 1405, 1407, 1409, 1411, 1413, 1415, 1417, 1419, 1421, 1423, 1425, 1427, 1429, 1431, 1433, 1435, 1437, 1439, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1455, 1457, 1459, 1461, 1463, 1465, 1467, 1469, 1471, 1473, 1475, 1477, 1479, 1481, 1483, 1485, 1487, 1489, 1491, 1493, 1495, 1497, 1499, 1501, 1503, 1505, 1507, 1509, 1511, 1513, 1515, 1517, 1519, 1521, 1523, 1525, 1527, 1529, 1531, 1533, 1535, 1537, 1539, 1541, 1543, 1545, 1547, 1549, 1551, 1553, 1555, 1557, 1559, 1561, 1563, 1565, 1567, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1585, 1587, 1589, 1591, 1593, 1595, 1597, 1599, 1601, 1603, 1605, 1607, 1609, 1611, 1613, 1615, 1617, 1619, 1621, 1623,

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10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 6 to 9.

11. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 6 to 10.

12. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 6 to 11 under high stringency conditions.

13. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.

14. A composition according to claim 13, being an immunogenic composition, a vaccine composition or a diagnostic composition.

15. A composition according to claim 13 or claim 14 for use as a pharmaceutical.

16. The use of a composition according to claim 13 in the manufacture of a medicament for the treatment or prevention of infection or disease caused by streptococcus bacteria, particularly *S.agalactiae* and *S.pyogenes*.

17. A method of treating a patient, comprising administering to the patient a therapeutically effective amount of the composition of claim 13.

18. A hybrid protein represented by the formula $NH_2$-A-[-X-L-]$_n$-B-COOH, wherein X is an amino acid sequence as defined in claim 1, L is an optional linker amino acid sequence, A is an optional N-terminal amino acid sequence, B is an optional C-terminal amino acid sequence, and n is an integer greater than 1.

19. A kit comprising primers for amplifying a template sequence contained within a *Streptococcus* nucleic acid sequence, the kit comprising a first primer and a second primer, wherein the first primer is substantially complementary to said template sequence and the second primer is substantially complementary to a complement of said template sequence, wherein the parts of said primers which have substantial complementarity define the termini of the template sequence to be amplified.

20. A kit comprising first and second single-stranded oligonucleotides which allow amplification of a Streptococcus template nucleic acid sequence contained in a single- or double-stranded nucleic acid (or mixture thereof), wherein: (a) the first oligonucleotide comprises a primer sequence which is substantially complementary to said template nucleic acid sequence; (b) the second oligonucleotide comprises a primer sequence which is substantially complementary to the complement of said template nucleic acid sequence; (c) the first oligonucleotide and/or the second oligonucleotide comprise(s) sequence which is not compementary to said template nucleic acid; and (d) said primer sequences define the termini of the template sequence to be amplified.

21. The kit of claim 20, wherein the non-complementary sequence(s) of (c) comprise a restriction site and/or a promoter sequence.

22. A computer-readable medium containing one or more of SEQ IDs 1 to 12024.

23. A process for detecting Streptococcus in a biological sample, comprising the step of contacting nucleic acid according to any of claims 6 to 12 with the biological sample under hybridising conditions.

24. The process of claim 23, wherein the process involves nucleic acid amplification.

25. A process for determining whether a compound binds to a protein according to claim 1, claim 2 or claim 3, comprising the step of contacting a test compound with a protein according to claim 1, claim 2 or claim 3 and determining whether the test compound binds to said protein.

26. A compound identified by the process of claim 25.

27. A composition comprising a protein according to claim 1, claim 2 or claim 3 and one or more of the following antigens:
- a protein antigen from *Helicobacter pylori*;
- a protein antigen from *N.meningitidis* serogroup B;
- an outer-membrane vesicle (OMV) preparation from *N.meningitidis* serogroup B;
- a saccharide antigen from N.meningitidis serogroup A, C, W135 and/or Y;
- a saccharide antigen from *Streptococcus pneumoniae*;
- an antigen from hepatitis A virus;
- an antigen from hepatitis B virus;
- an antigen from hepatitis C virus;
- an antigen from *Bordetella pertussis*;
- a diphtheria antigen;
- a tetanus antigen;
- a saccharide antigen from *Haemophilus influenzae* B.
- an antigen from N.gonorrhoeae;
- an antigen from *Chlamydia pneumoniae*;
- an antigen from *Chlamydia trachomatis*;
- an antigen from *Porphyromonas gingivalis*;
- polio antigen(s);
- rabies antigen(s);
- measles, mumps and/or rubella antigens;
- influenza antigen(s);
- an antigen from *Moraxella catarrhalis*; and/or
- an antigen from *Staphylococcus aureus*.

28. A composition comprising two or more proteins, wherein each protein is a protein according to claim 1, claim 2 or claim 3.

**FIGURE 1**

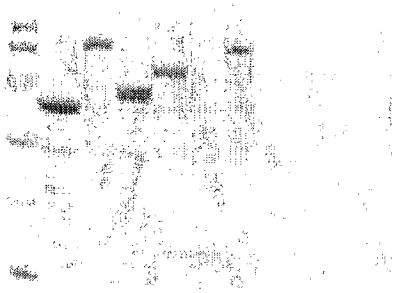


**FIGURE 2**

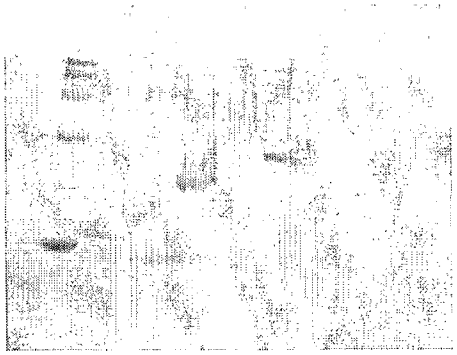
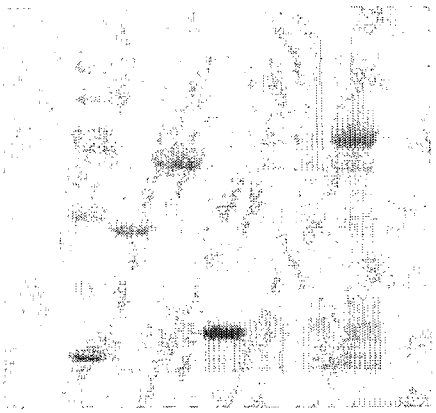


**FIGURE 3**



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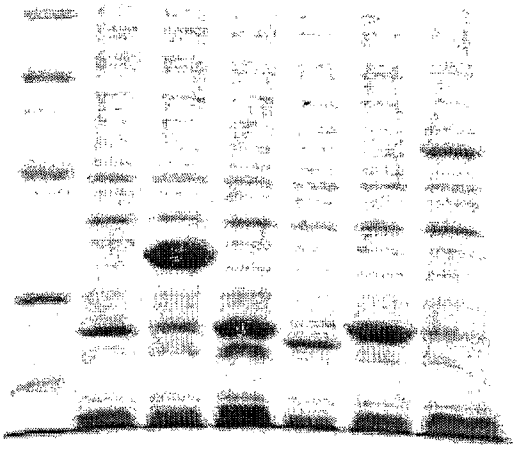
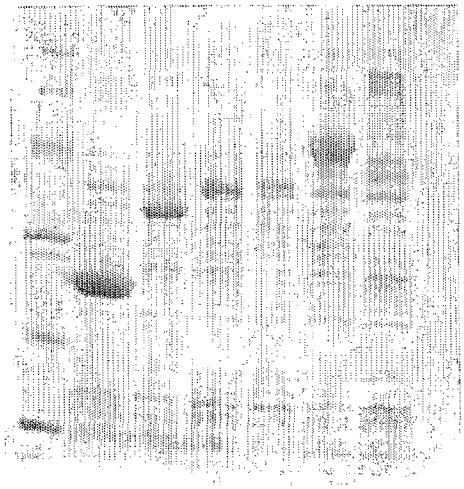


**FIGURE 5**



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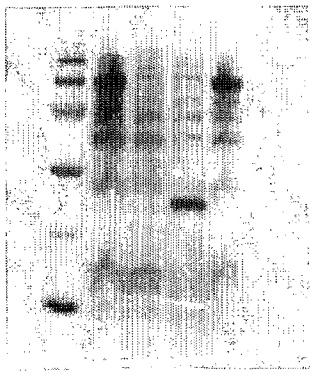

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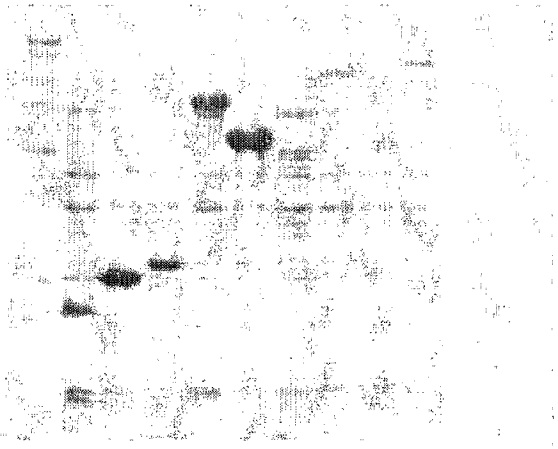

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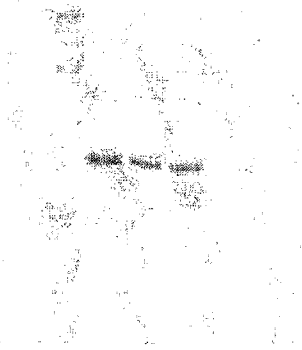

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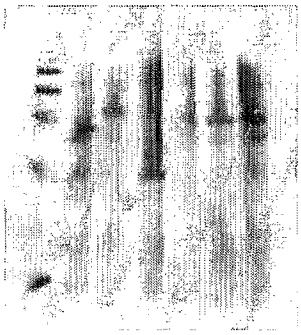

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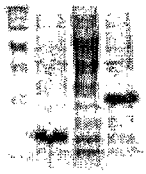

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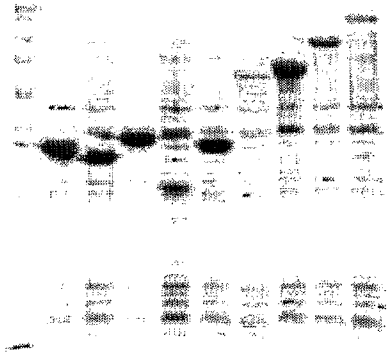

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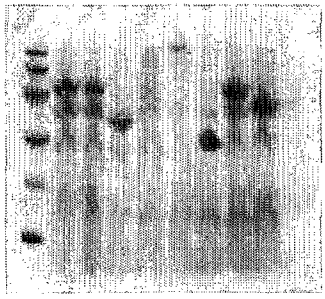

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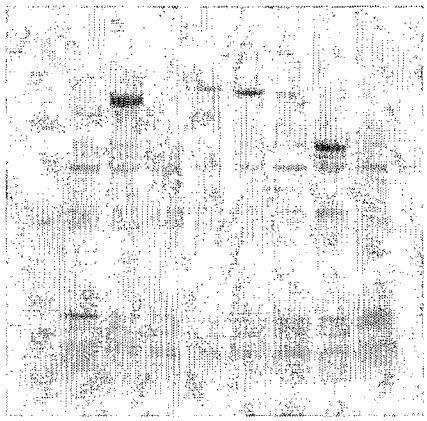

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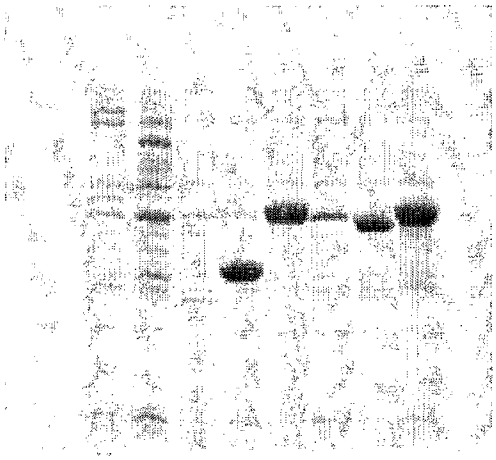

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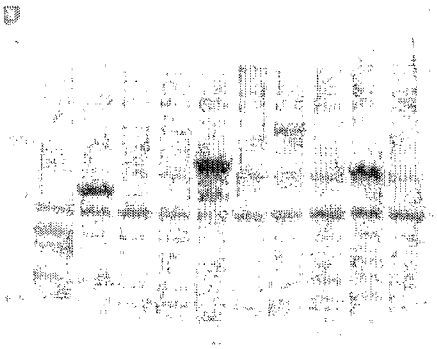

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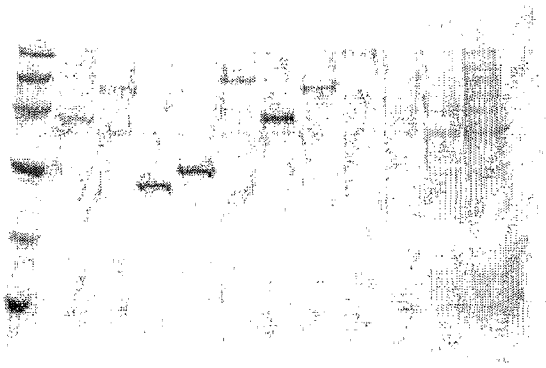

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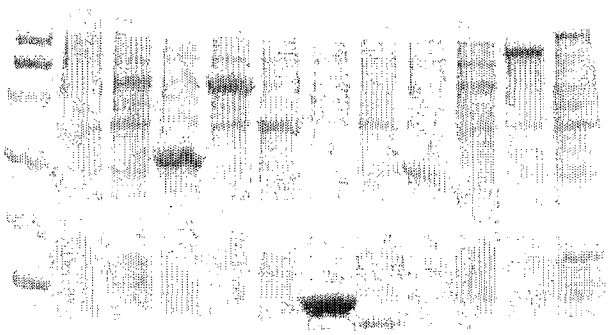

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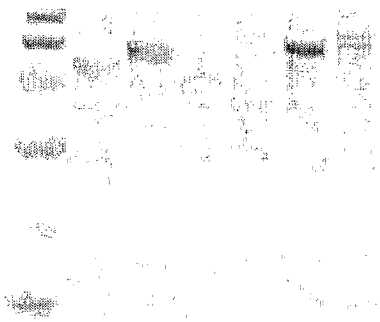

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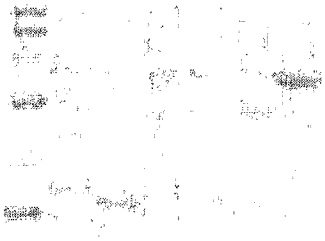

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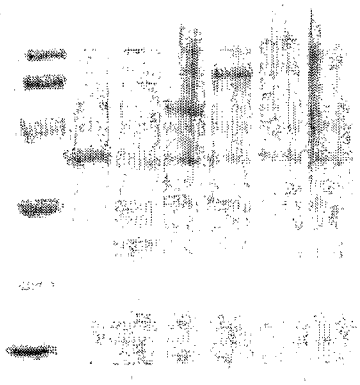

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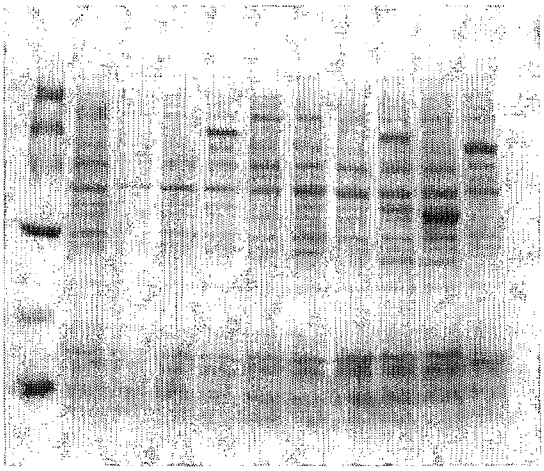

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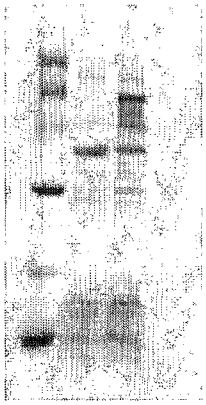

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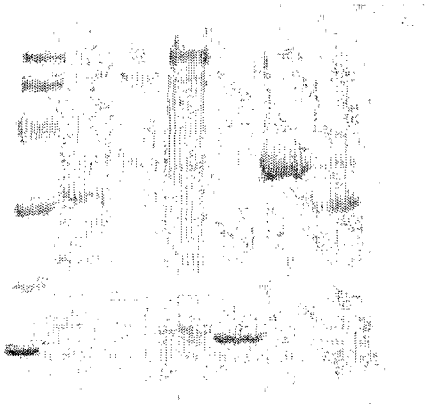

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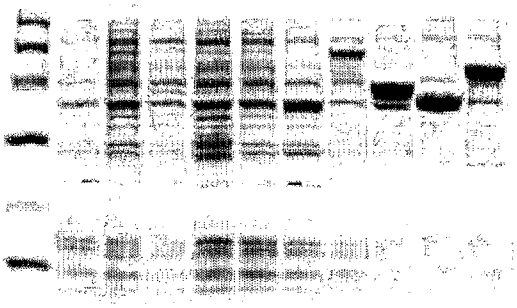

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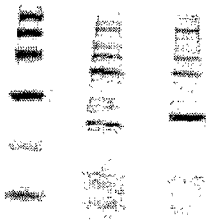

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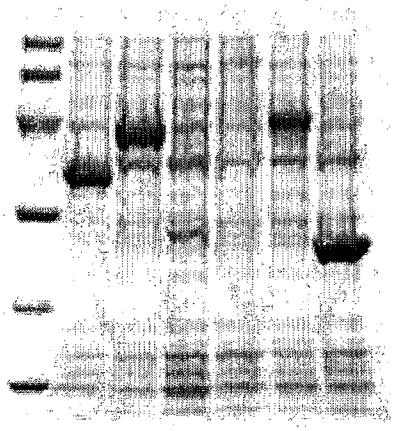

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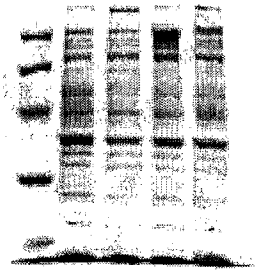


**FIGURE 28**

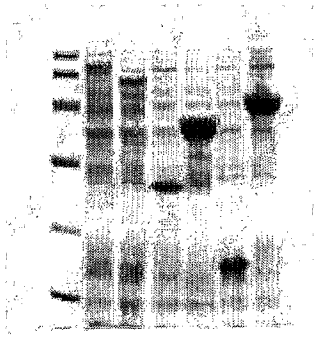


**FIGURE 29**

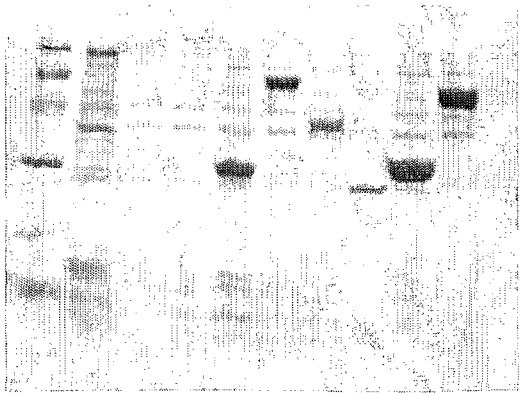


**FIGURE 30**

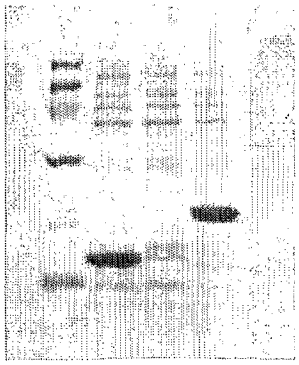


**FIGURE 31**

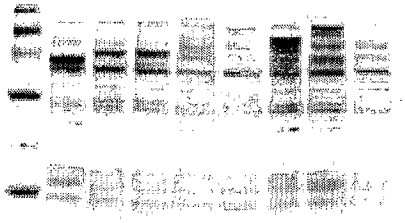
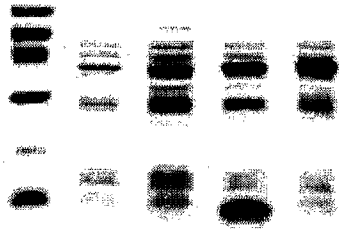


**FIGURE 32**



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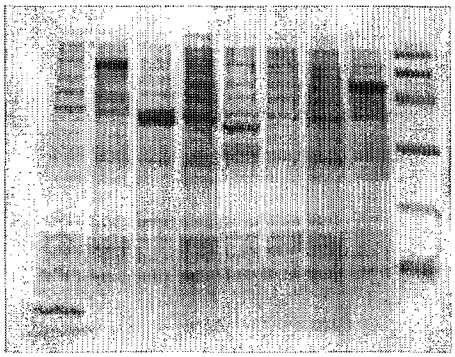

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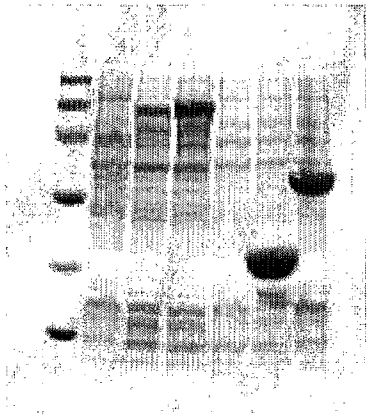

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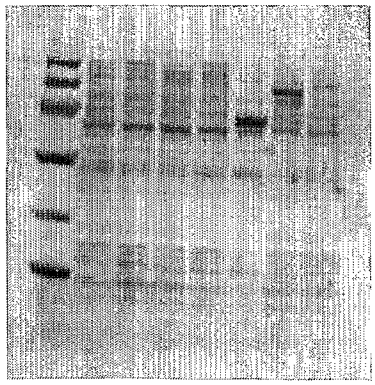

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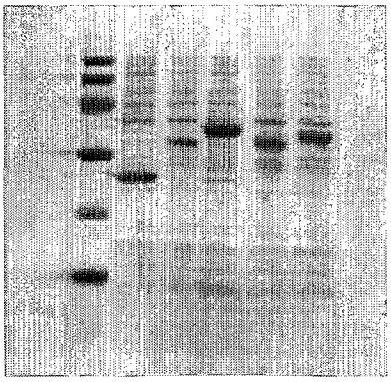
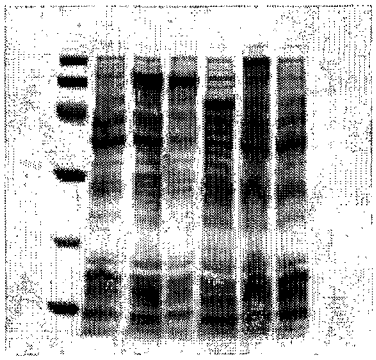


**FIGURE 37**



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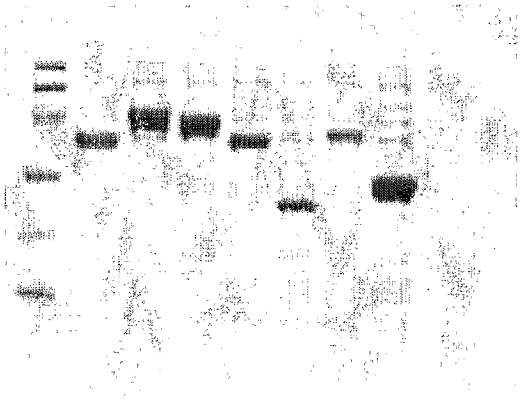

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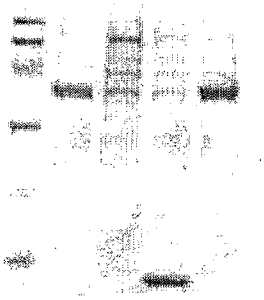

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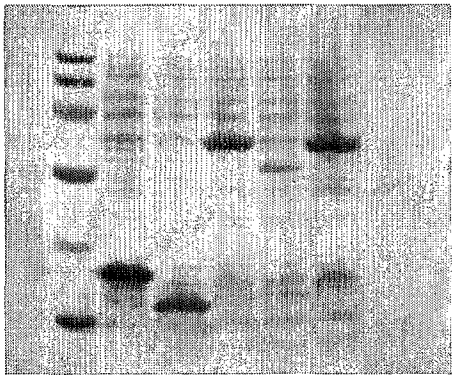


**FIGURE 41**

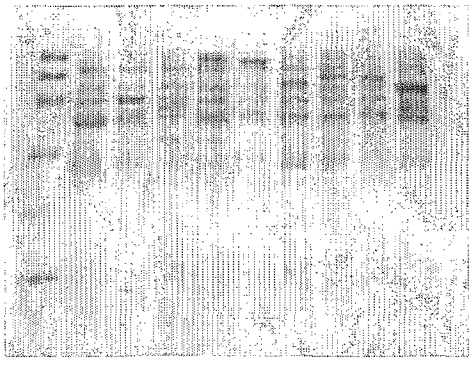
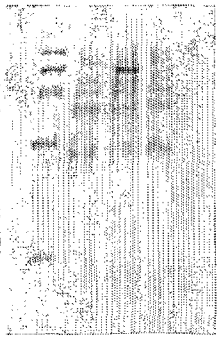


**FIGURE 42**



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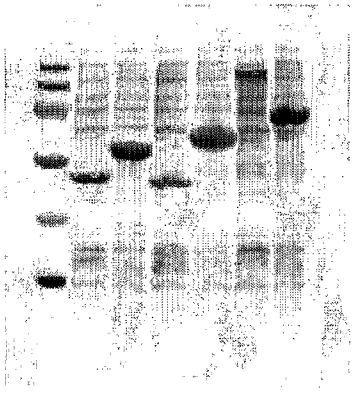


**FIGURE 44**

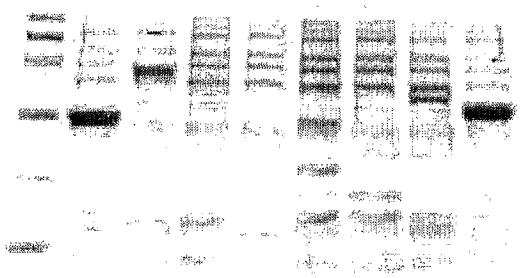
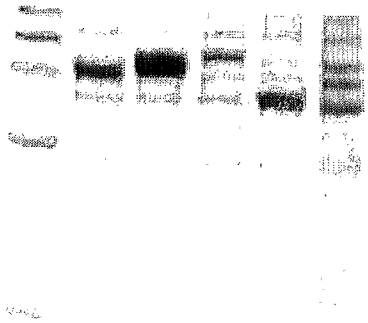


**FIGURE 45**



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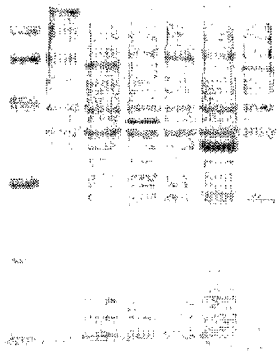


**FIGURE 47**

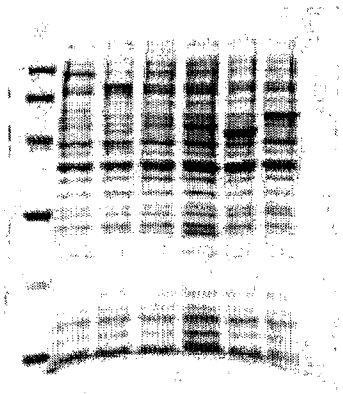


**FIGURE 48**

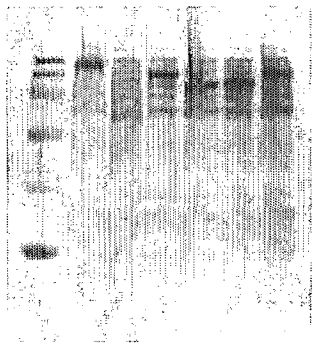


**FIGURE 49**

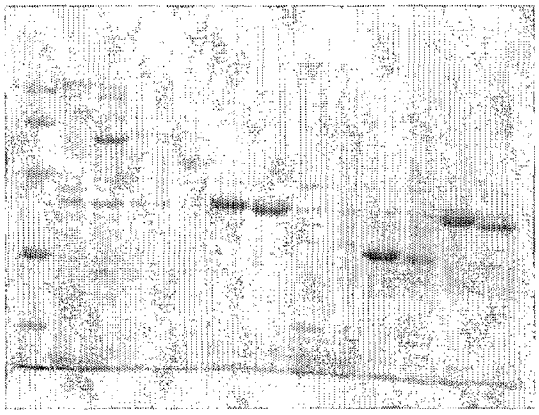
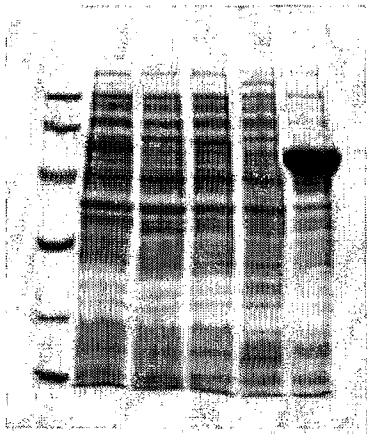


**FIGURE 50**



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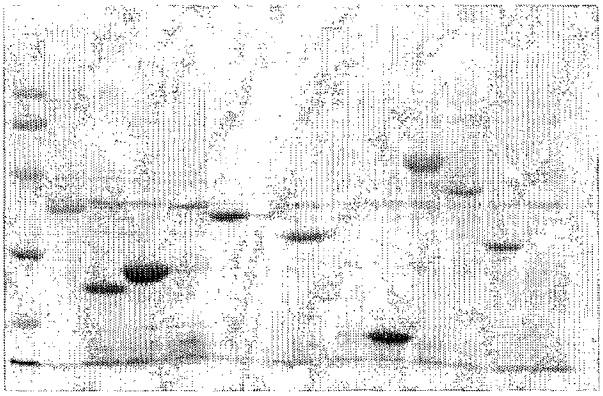

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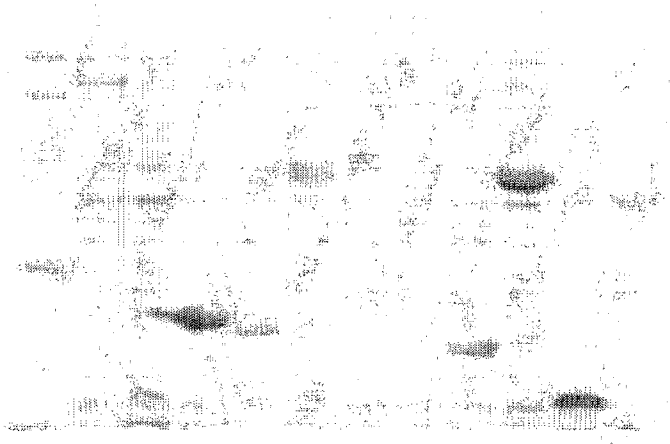

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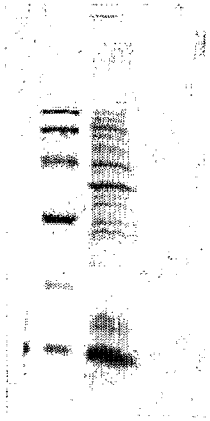


**FIGURE 54**

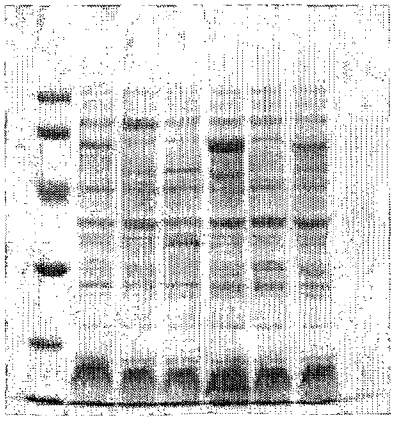


**FIGURE 55**

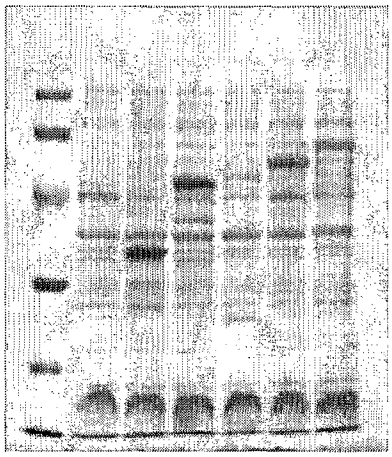


**FIGURE 56**

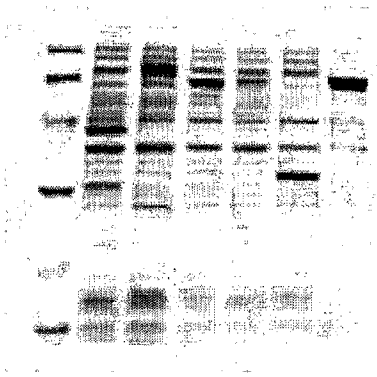


**FIGURE 57**

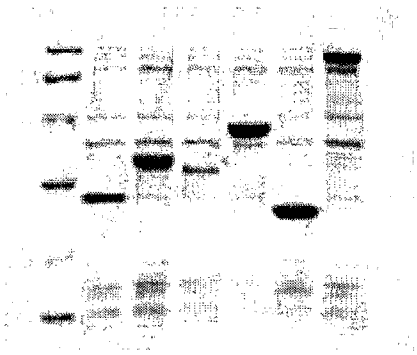


**FIGURE 58**

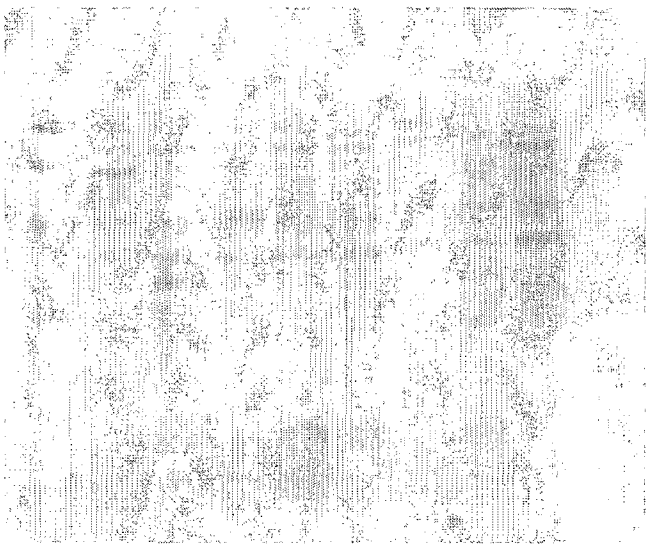


**FIGURE 59**

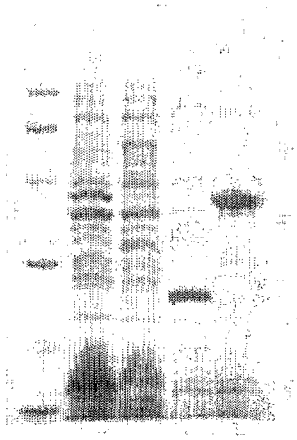


**FIGURE 60**

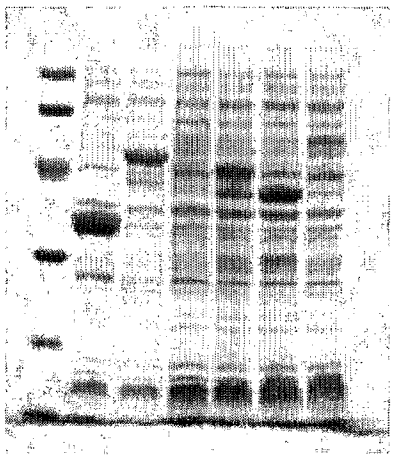


**FIGURE 61**

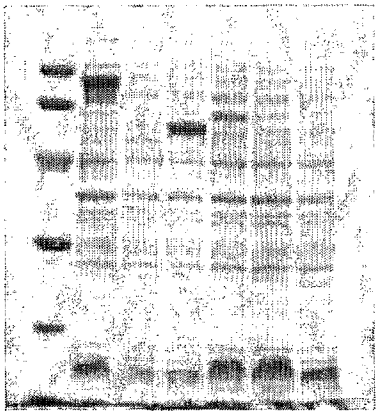


**FIGURE 62**

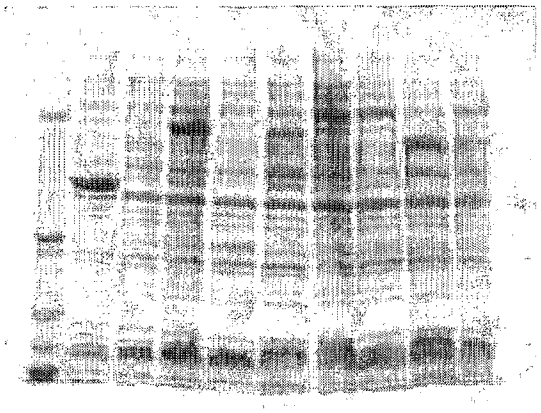


**FIGURE 63**

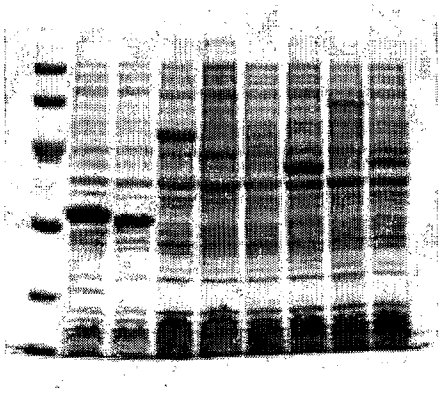


**FIGURE 64**

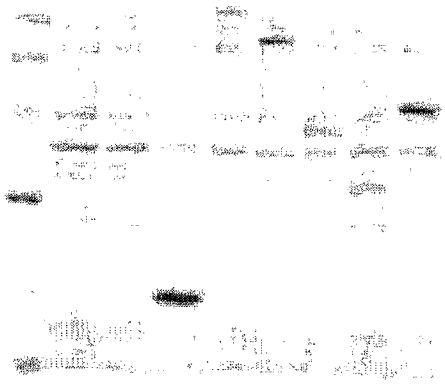


**FIGURE 65**

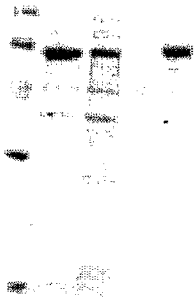


**FIGURE 66**

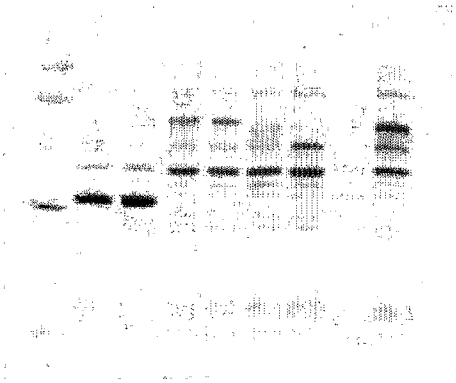


**FIGURE 67**

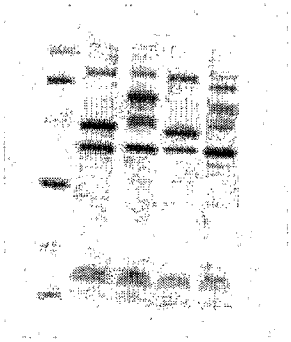


**FIGURE 68**

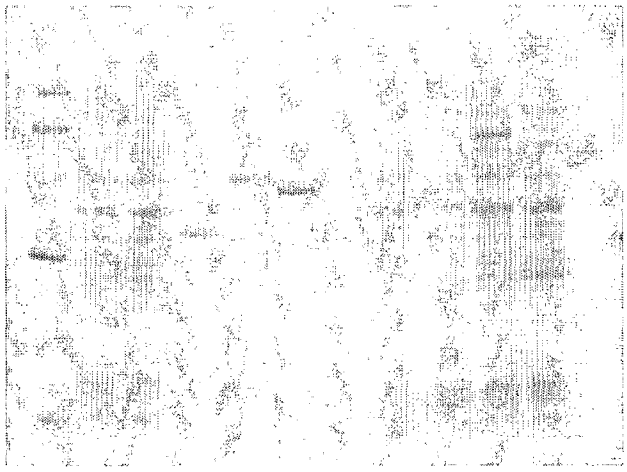


**FIGURE 69**

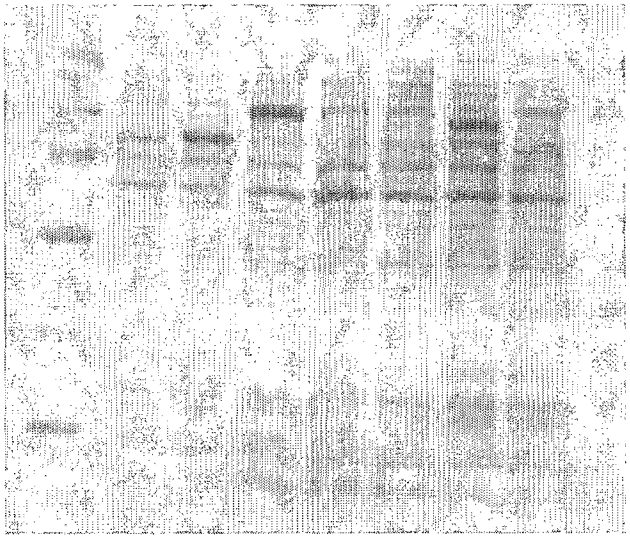


**FIGURE 70**

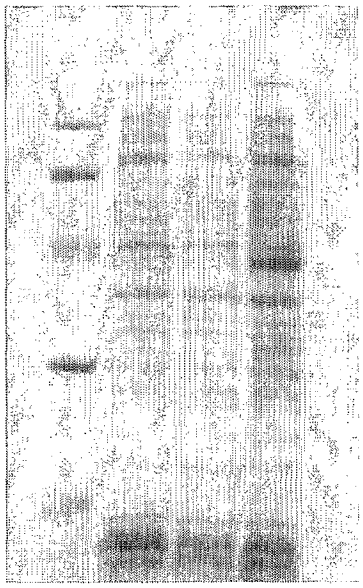


**FIGURE 71**

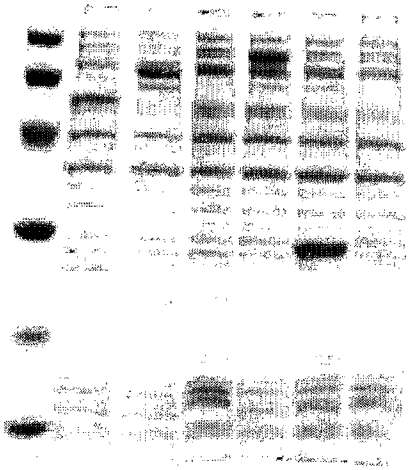


**FIGURE 72**

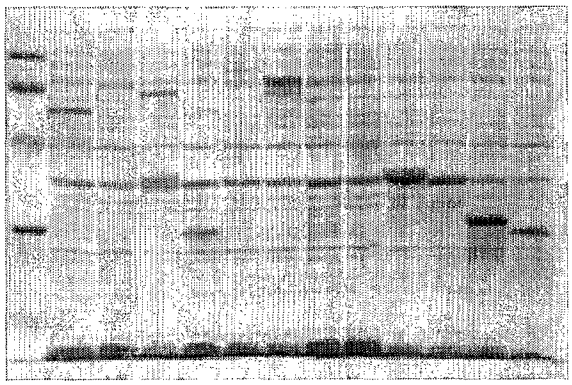


**FIGURE 73**

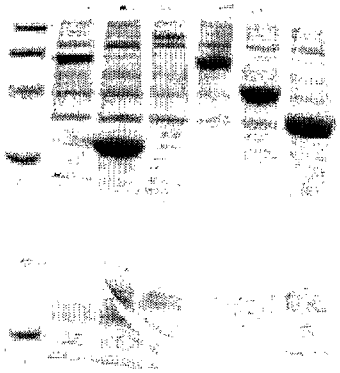


**FIGURE 74**

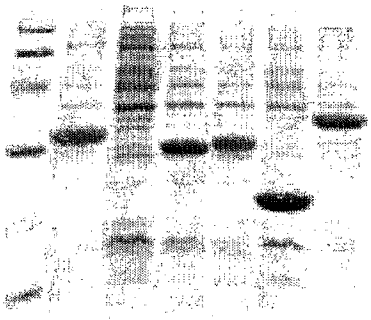


**FIGURE 75**

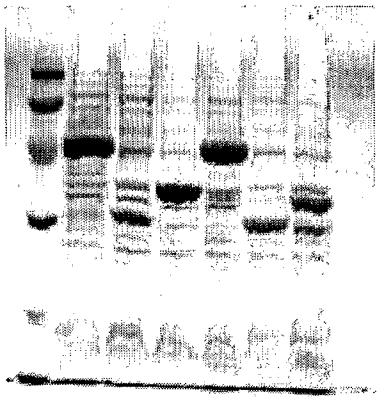


**FIGURE 76**

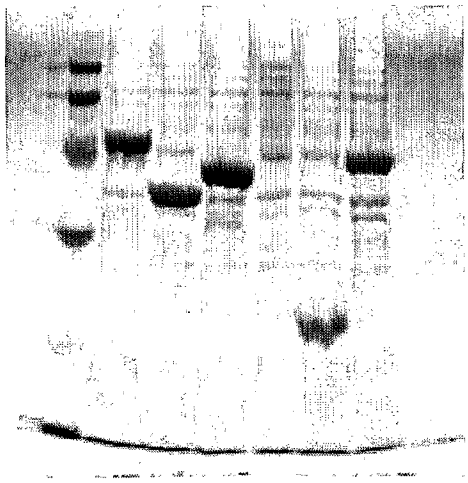


**FIGURE 77**

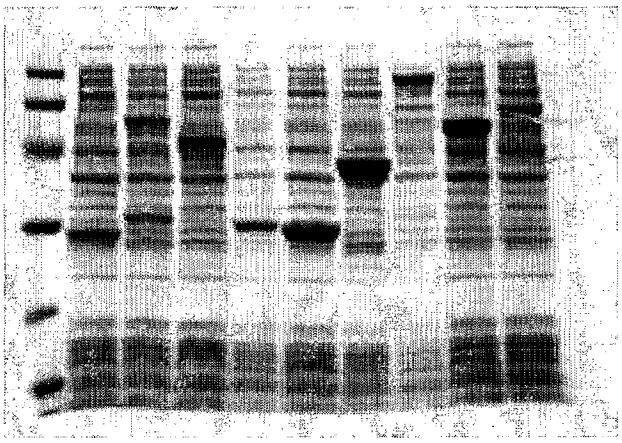


**FIGURE 78**

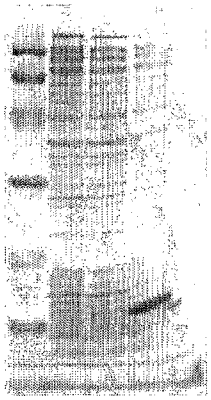


**FIGURE 79**

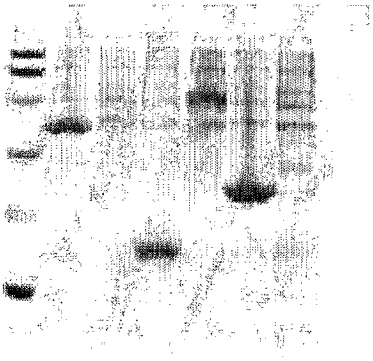


**FIGURE 80**

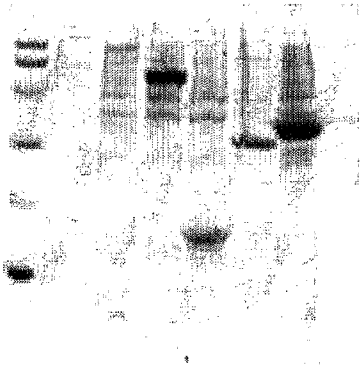


**FIGURE 81**

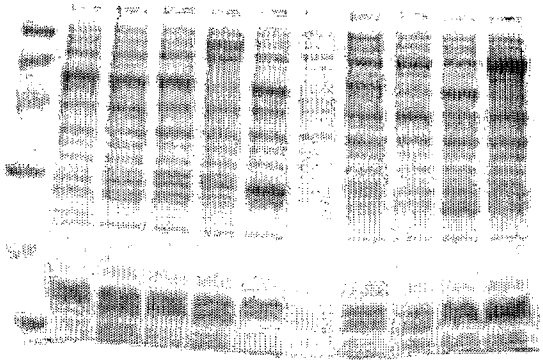


**FIGURE 82**

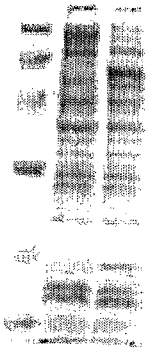


**FIGURE 83**

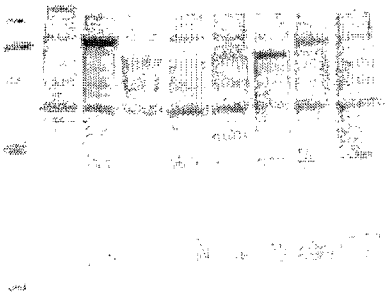


**FIGURE 84**

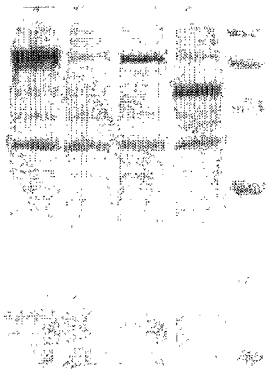
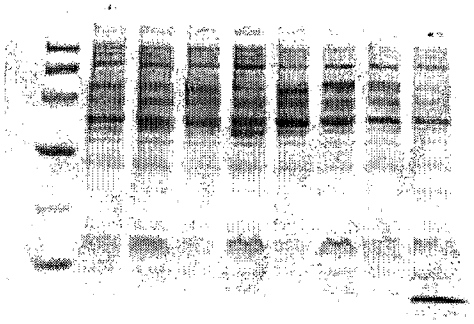
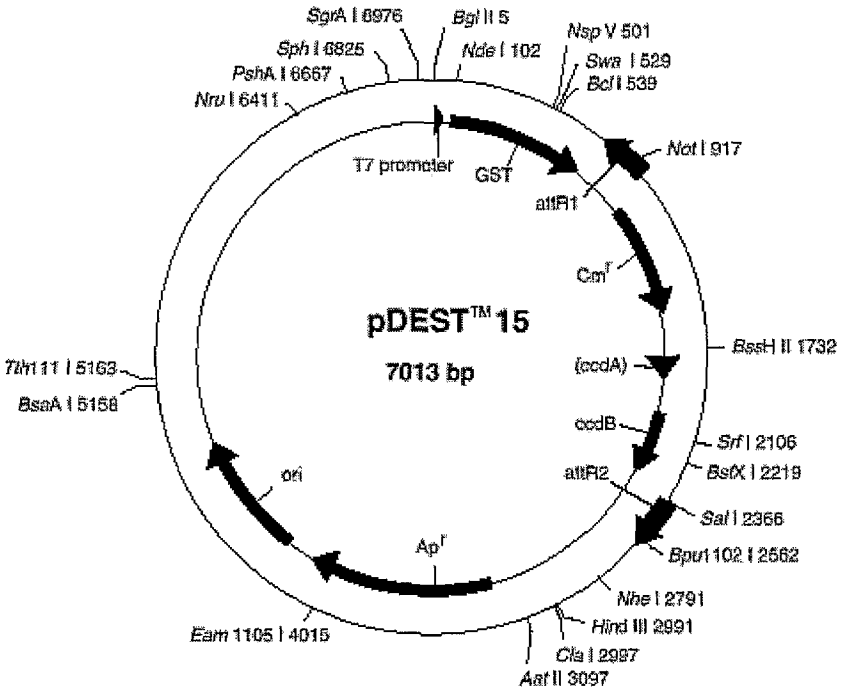


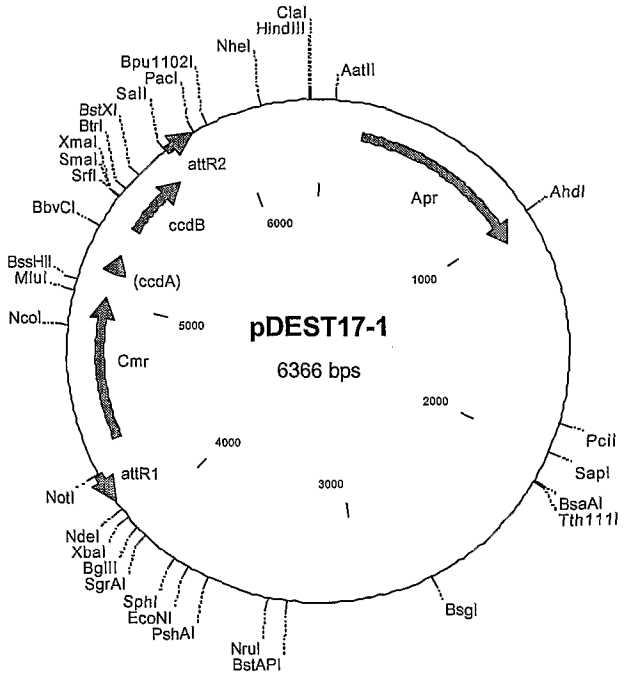
**FIGURE 85**



## FIGURE 86A

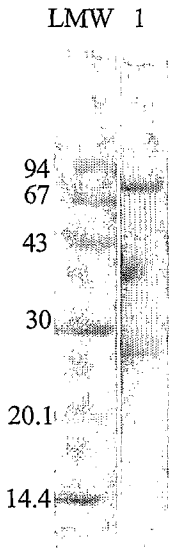



## FIGURE 86B

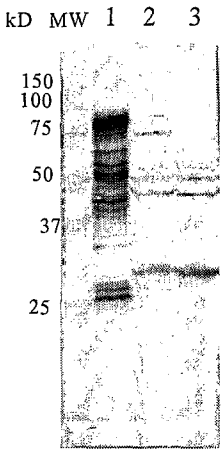


## FIGURE 87

## FIGURE 87A

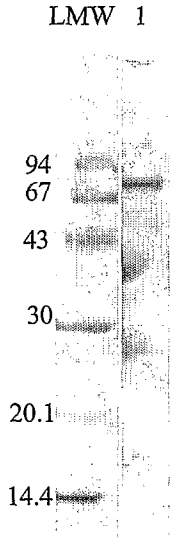



## FIGURE 87B

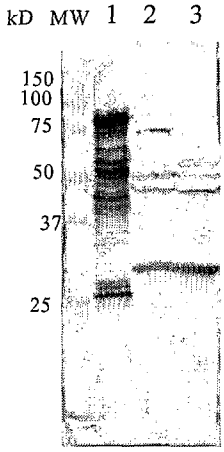



## FIGURE 88

## FIGURE 88A

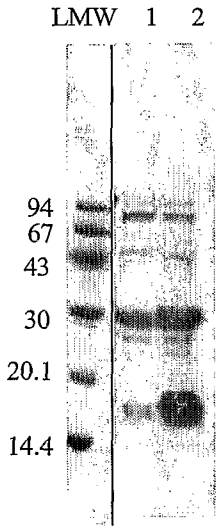



## FIGURE 88B

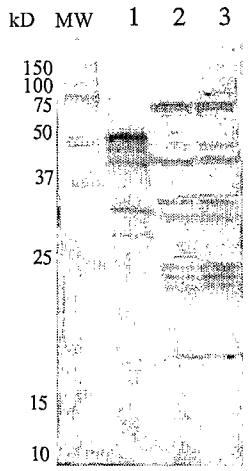


# FIGURE 89

## FIGURE 89A

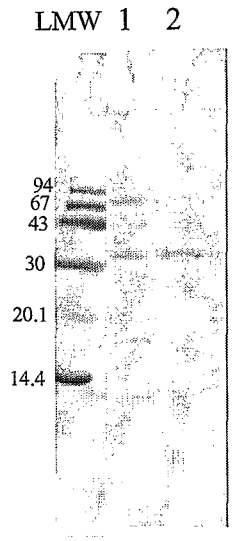



## FIGURE 89B

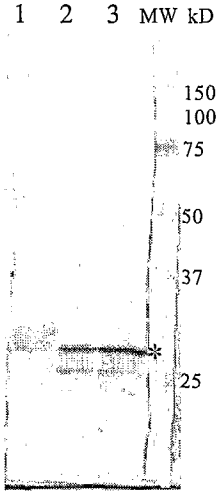


# FIGURE 90

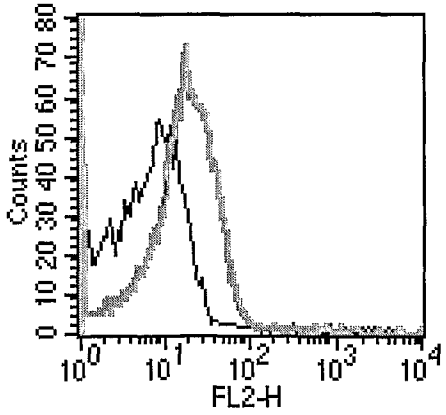
## FIGURE 90A




## FIGURE 90B

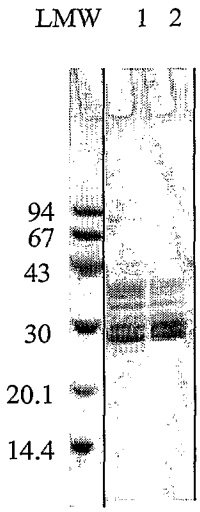



## FIGURE 90C

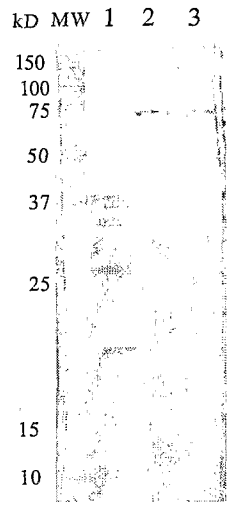


# FIGURE 91

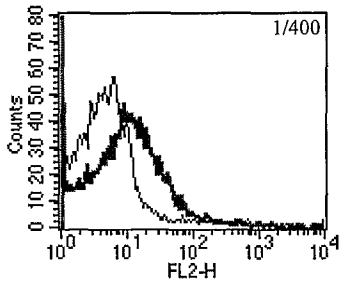
## FIGURE 91A




## FIGURE 91B

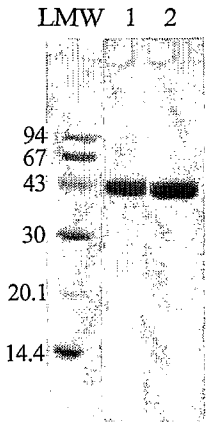



## FIGURE 91C

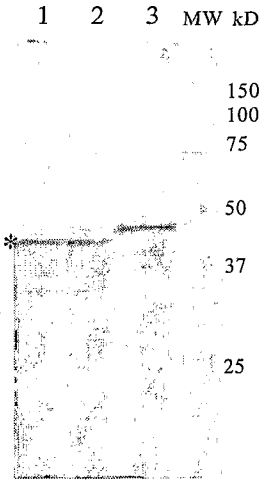


# FIGURE 92

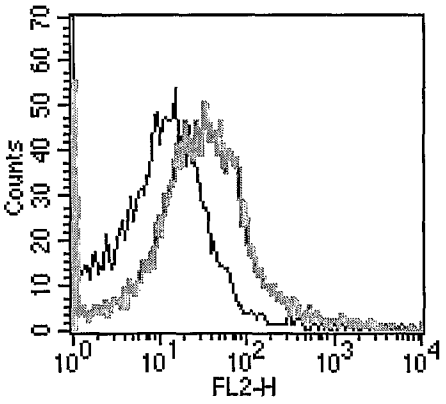
## FIGURE 92A




## FIGURE 92B

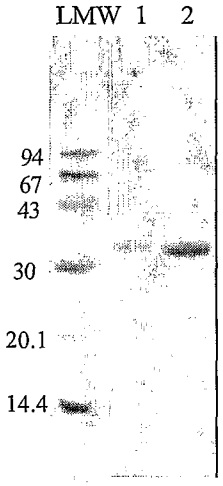



## FIGURE 92C

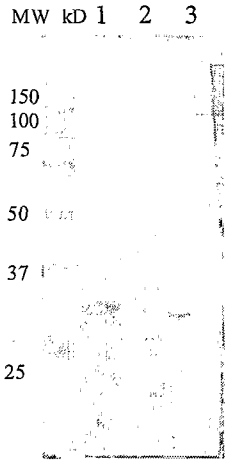


# FIGURE 93

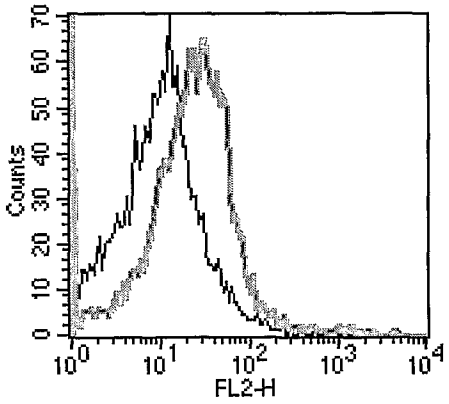
## FIGURE 93A




## FIGURE 93B

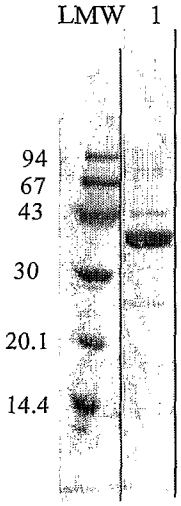



## FIGURE 93C

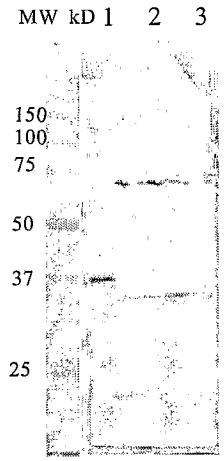


# FIGURE 94

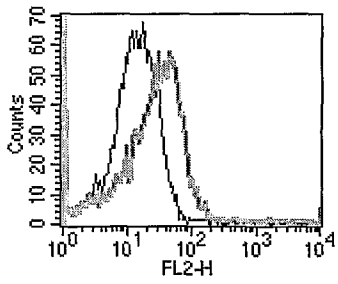
## FIGURE 94A




## FIGURE 94B

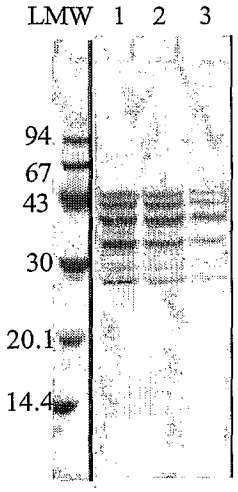



## FIGURE 94C

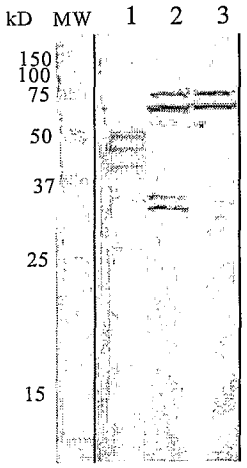


# FIGURE 95

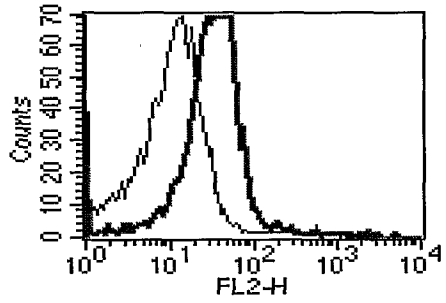
## FIGURE 95A




## FIGURE 95B

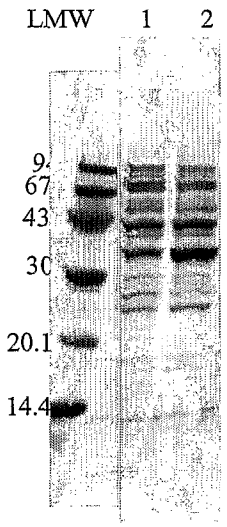



## FIGURE 95C

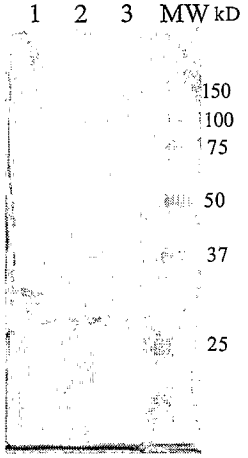


# FIGURE 96

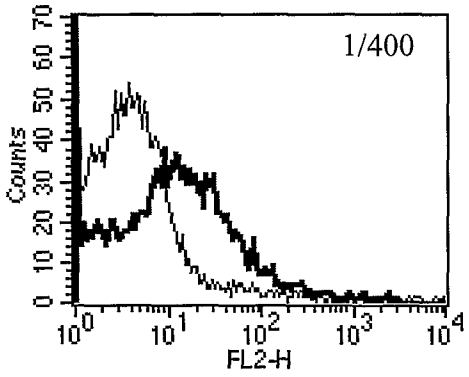
## FIGURE 96A




## FIGURE 96B

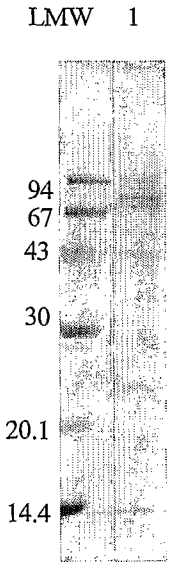



## FIGURE 96C

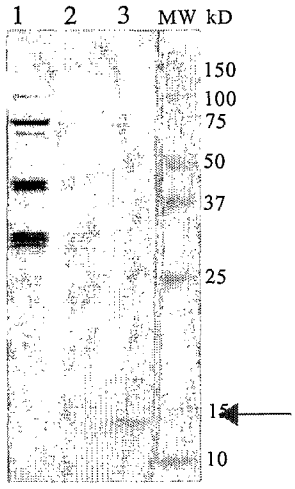


# FIGURE 97

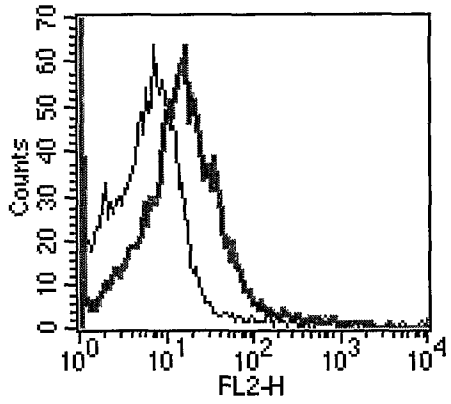
## FIGURE 97A




## FIGURE 97B

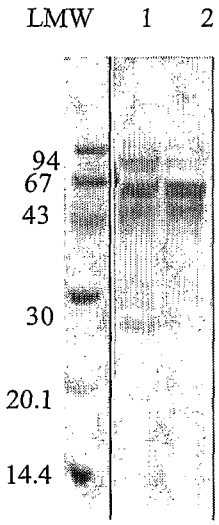



## FIGURE 97C

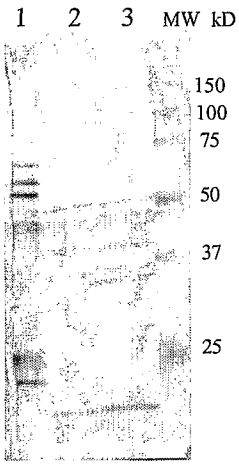


# FIGURE 98

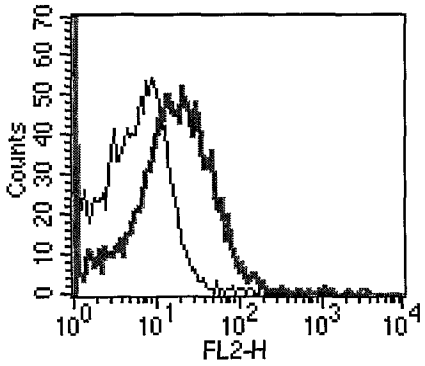
## FIGURE 98A




## FIGURE 98B

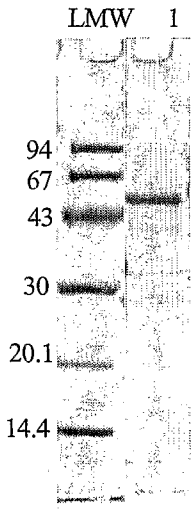



## FIGURE 98C

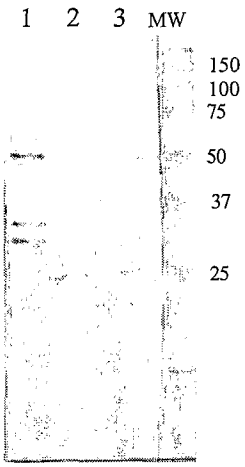


# FIGURE 99

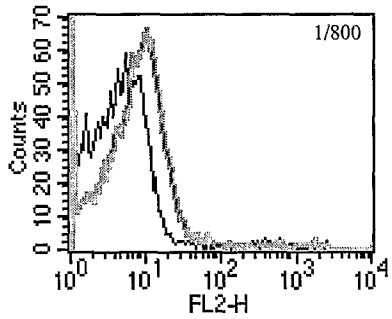
## FIGURE 99A




## FIGURE 99B

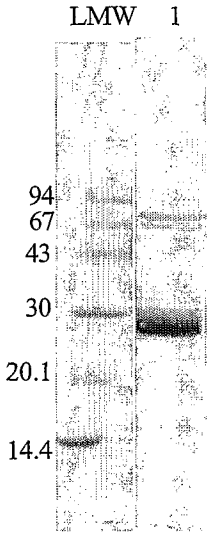



## FIGURE 99C

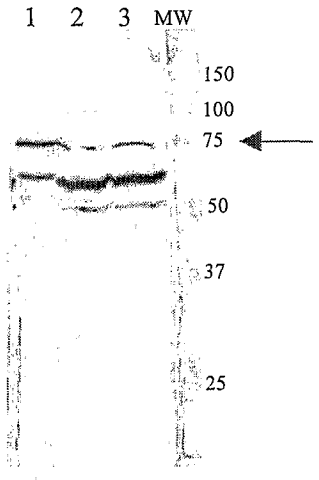


# FIGURE 100

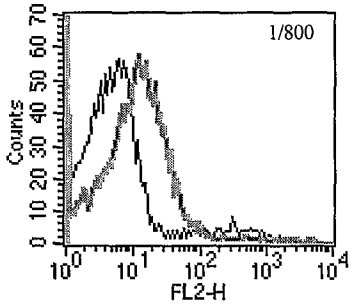
## FIGURE 100A




## FIGURE 100B

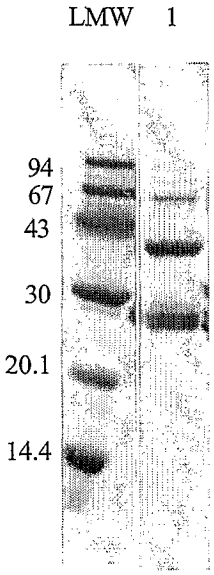



## FIGURE 100C

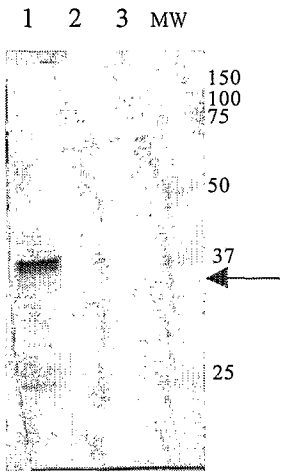


# FIGURE 101

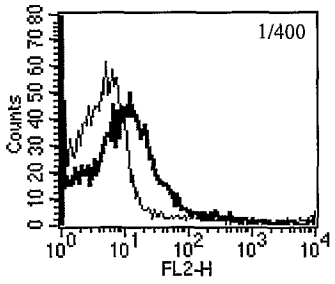
## FIGURE 101A




## FIGURE 101B

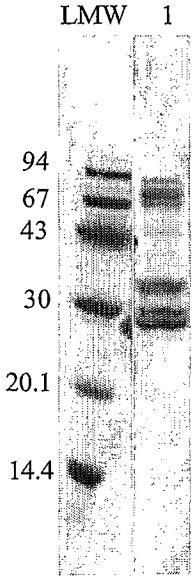



## FIGURE 101C

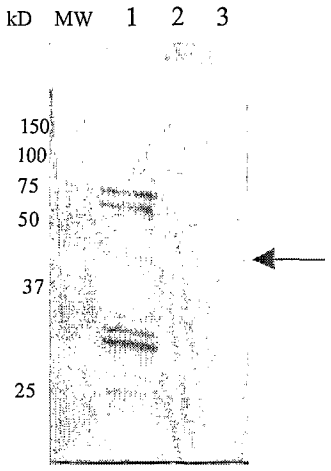


## FIGURE 102

### FIGURE 102A

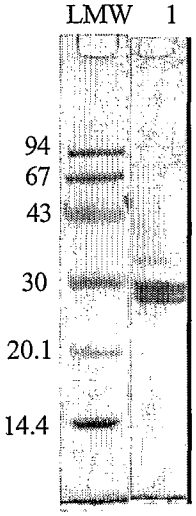



### FIGURE 102B

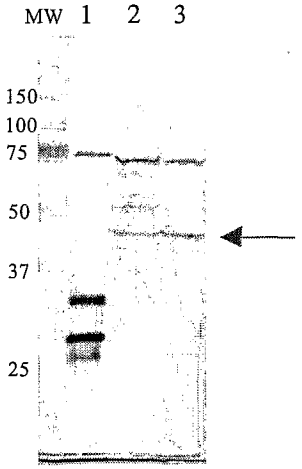



## FIGURE 103

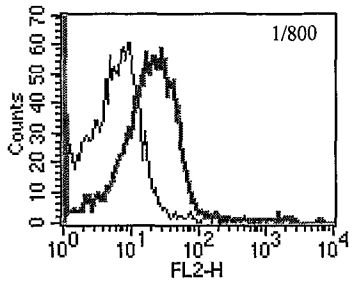
### FIGURE 103A




### FIGURE 103B

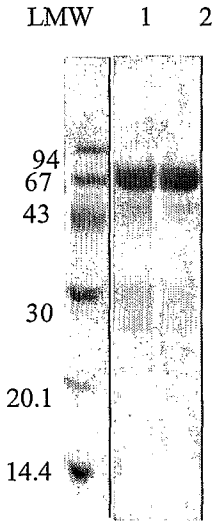


## FIGURE 103C

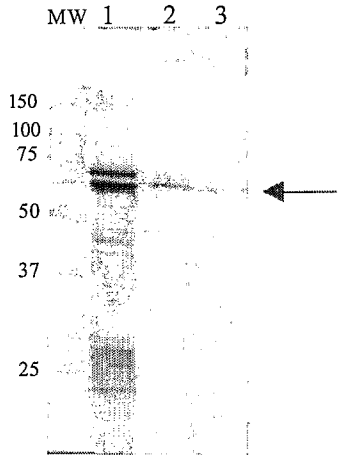



## FIGURE 104

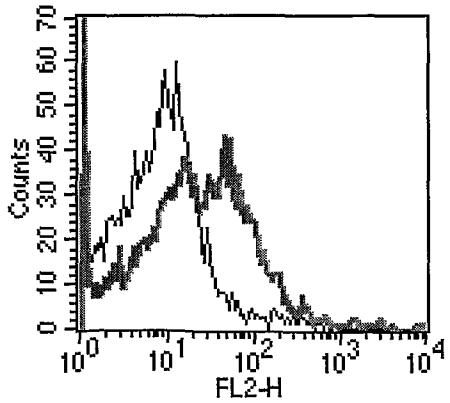
## FIGURE 104A




## FIGURE 104B

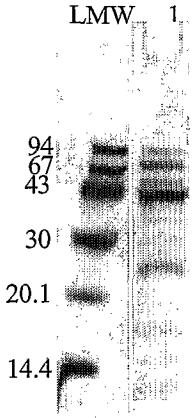



## FIGURE 104C

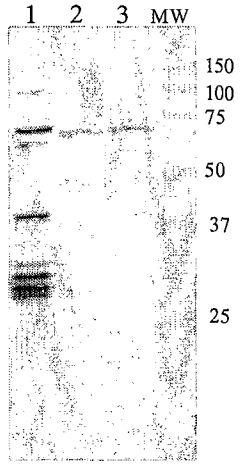


# FIGURE 105

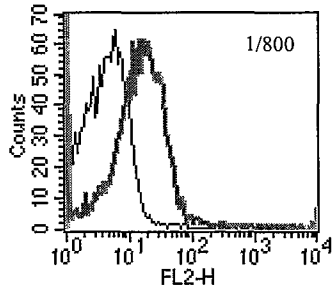
## FIGURE 105A




## FIGURE 105B

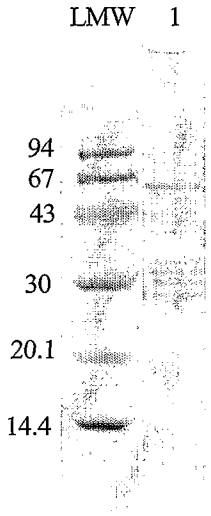



## FIGURE 105C

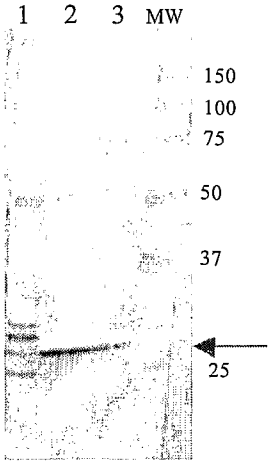


# FIGURE 106

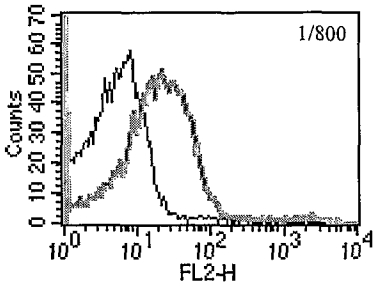
## FIGURE 106A




## FIGURE 106B

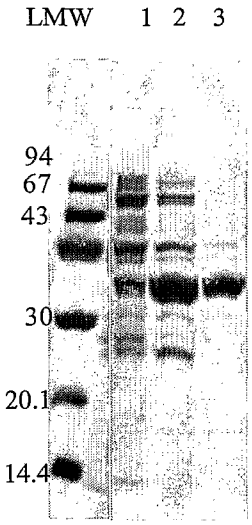



## FIGURE 106C

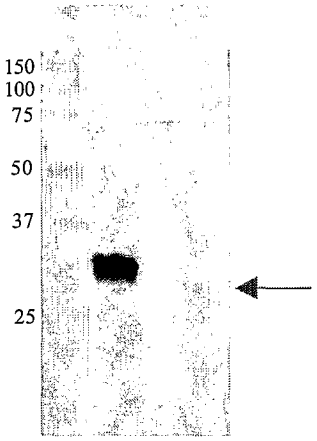


# FIGURE 107

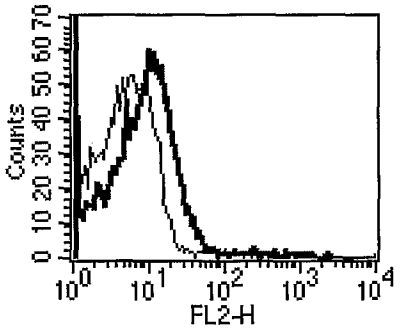
## FIGURE 107A




## FIGURE 107B

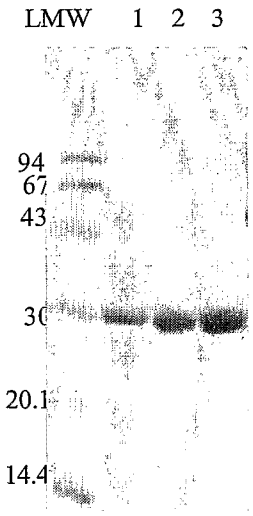



## FIGURE 107C

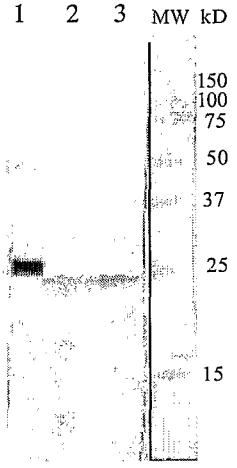


# FIGURE 108

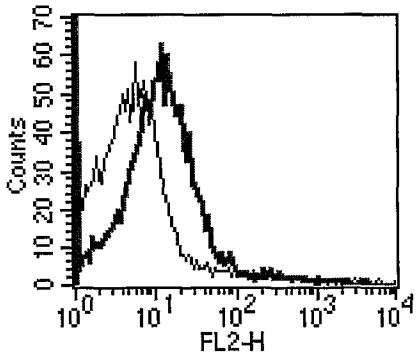
## FIGURE 108A




## FIGURE 108B

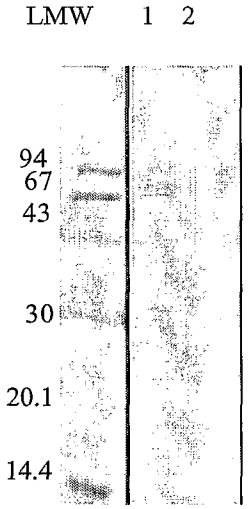



## FIGURE 108C

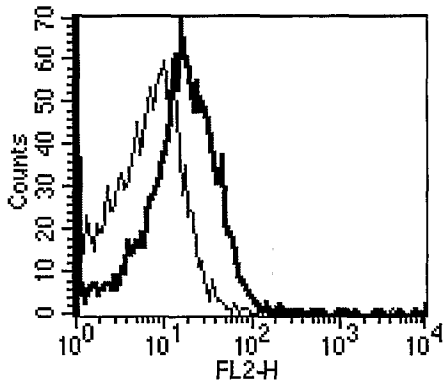


## FIGURE 109

### FIGURE 109A

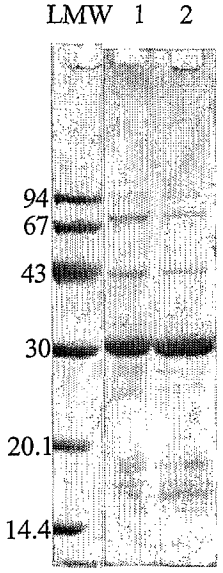



### FIGURE 109B

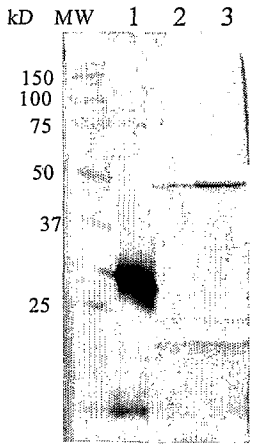



## FIGURE 110

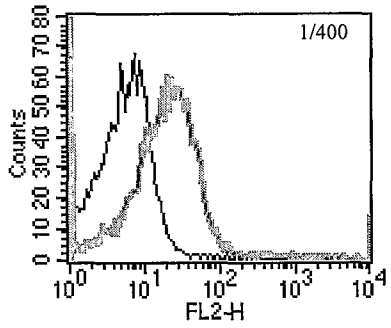
### FIGURE 110A



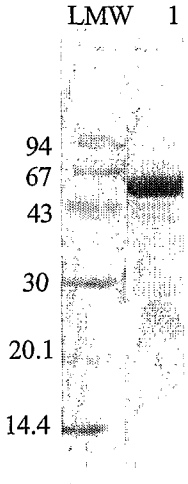

### FIGURE 110B



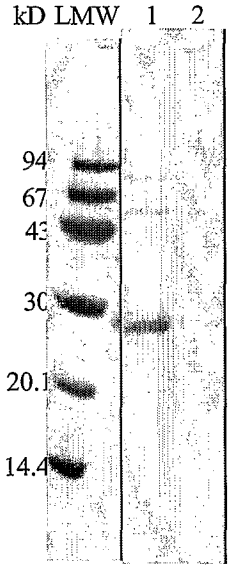
## FIGURE 110C




## FIGURE 111

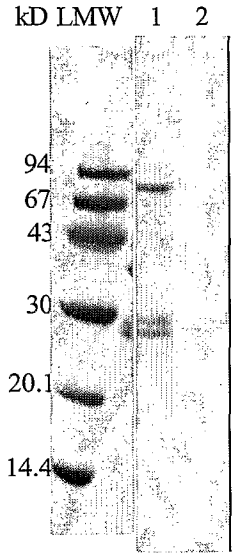



## FIGURE 113

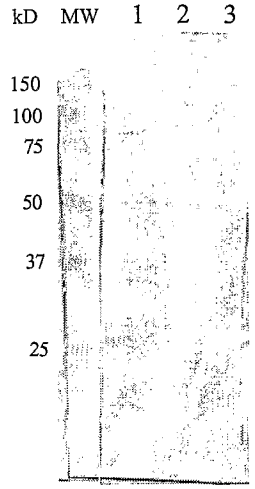


## FIGURE 112

### FIGURE 112A

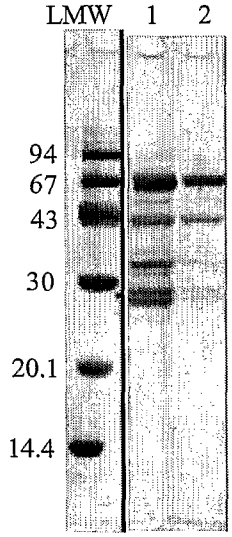



### FIGURE 112B

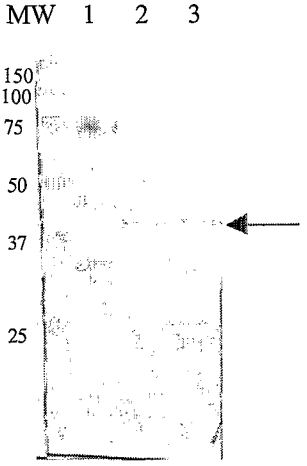



## FIGURE 114

### FIGURE 114A

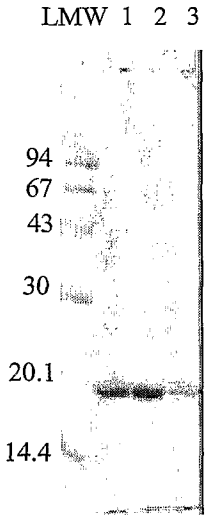



### FIGURE 114B

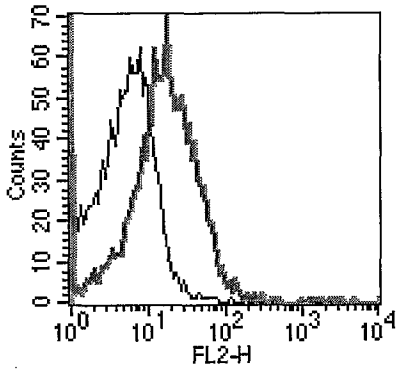


## FIGURE 115

### FIGURE 115A

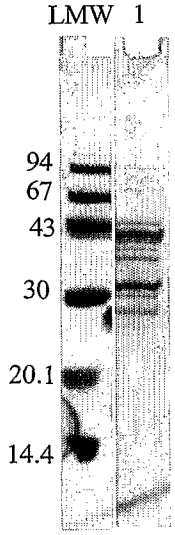



### FIGURE 115B



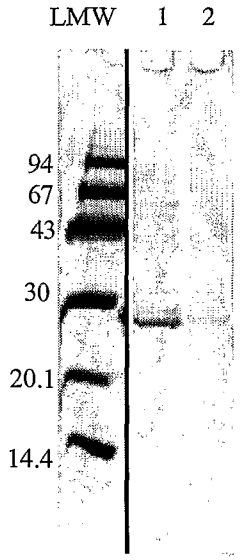

## FIGURE 116

### FIGURE 116A

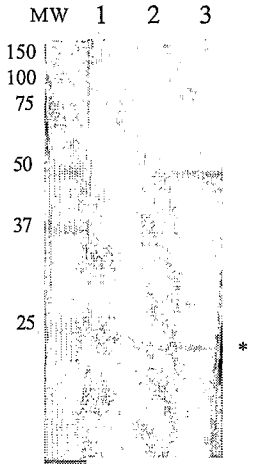


# FIGURE 117

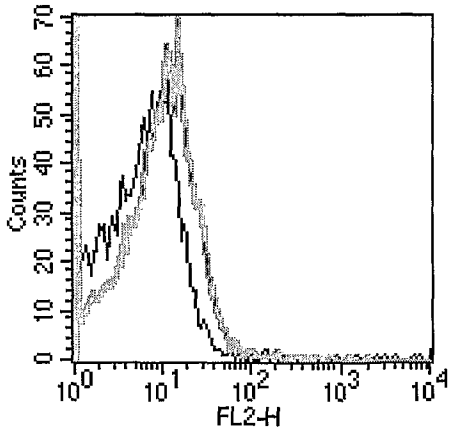
## FIGURE 117A



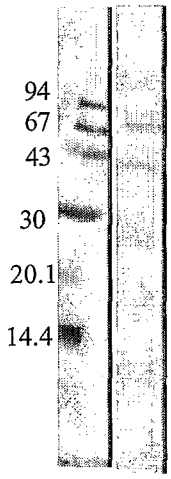

## FIGURE 117B



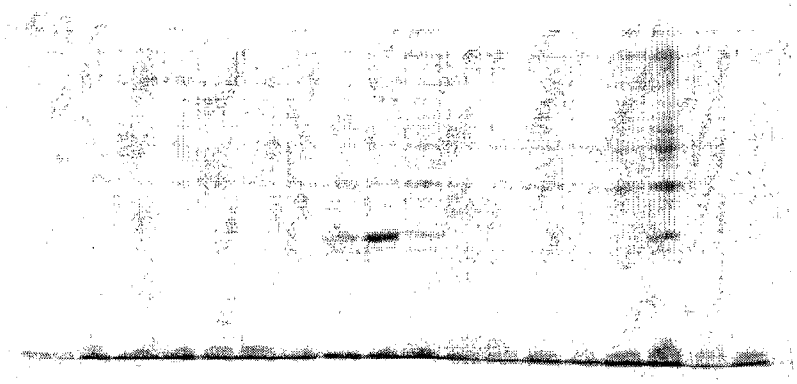

## FIGURE 117C



## FIGURE 118




## FIGURE 119



## FIGURE 120

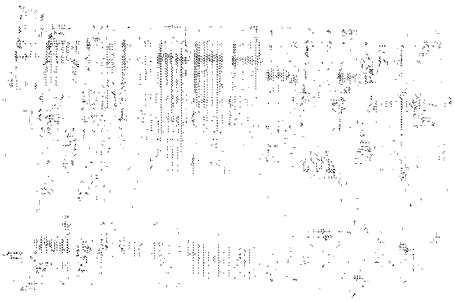


**FIGURE 121**

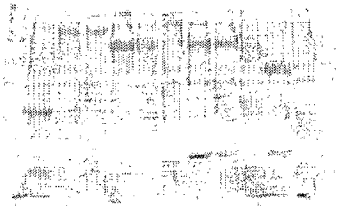


**FIGURE 122**

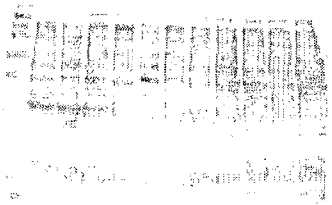


**FIGURE 123**

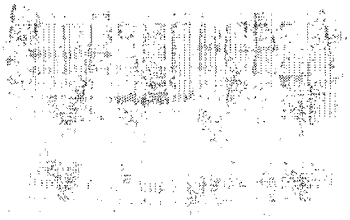


**FIGURE 124**

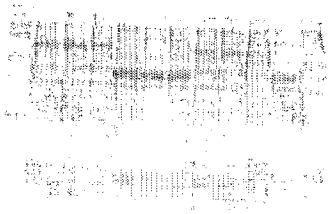


**FIGURE 125**

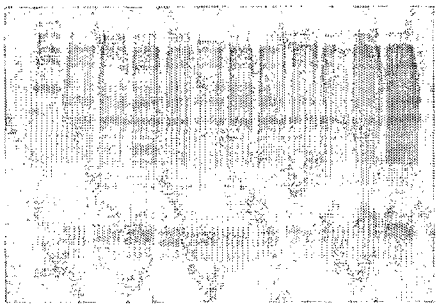


**FIGURE 126**

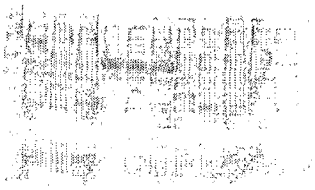


**FIGURE 127**

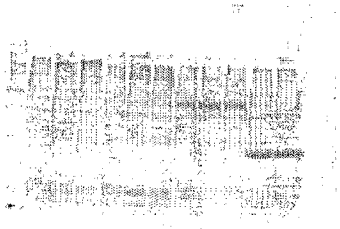


**FIGURE 128**

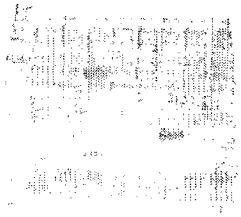


**FIGURE 129**

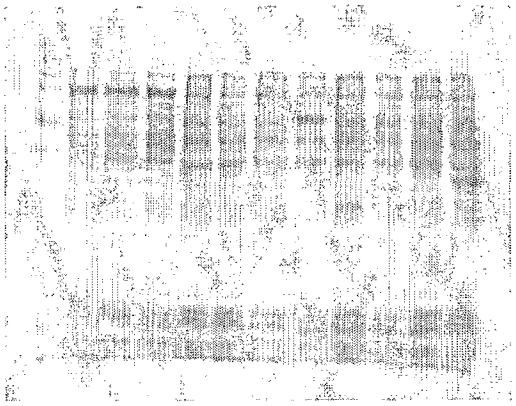


**FIGURE 130**

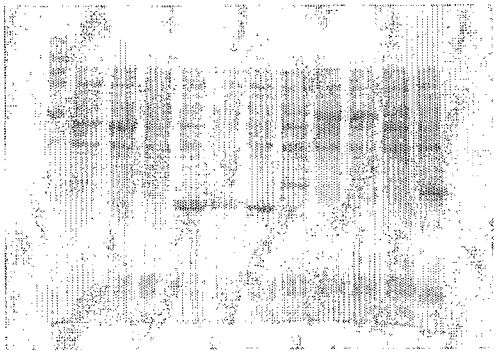
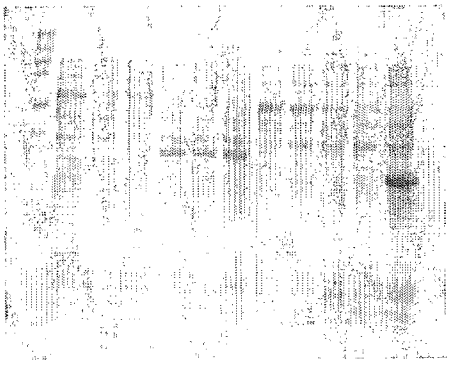


**FIGURE 131**



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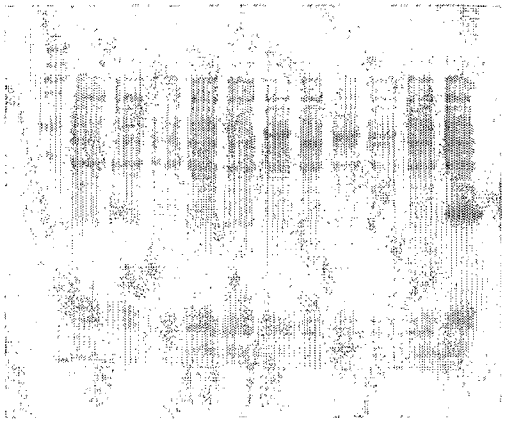


**FIGURE 133**

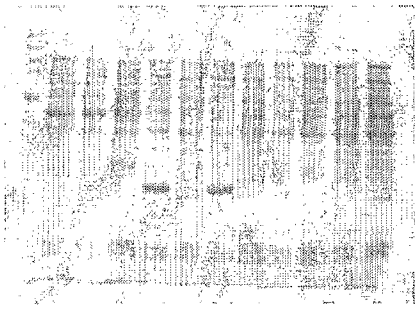


**FIGURE 134**

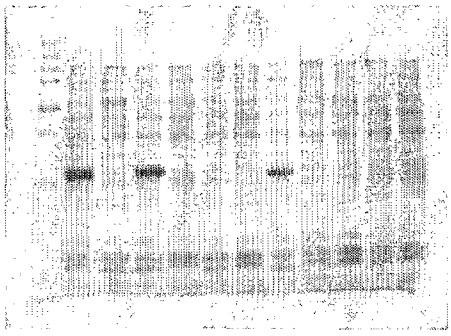
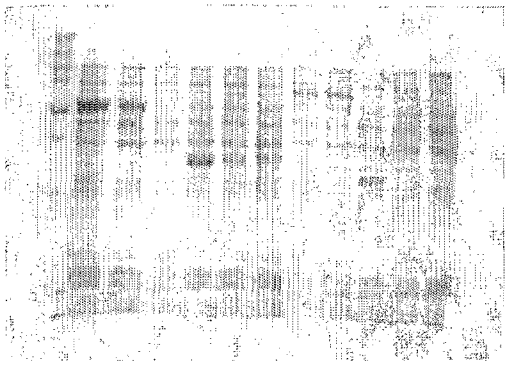


**FIGURE 135**



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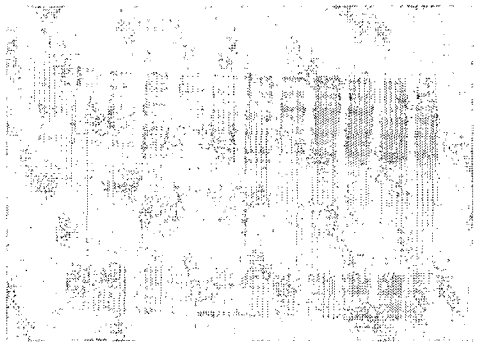
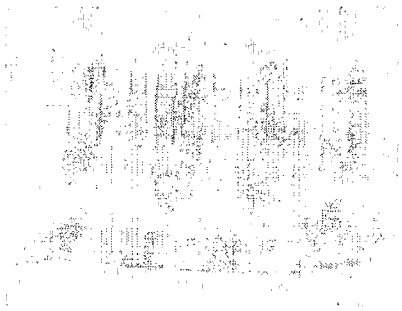


**FIGURE 137**



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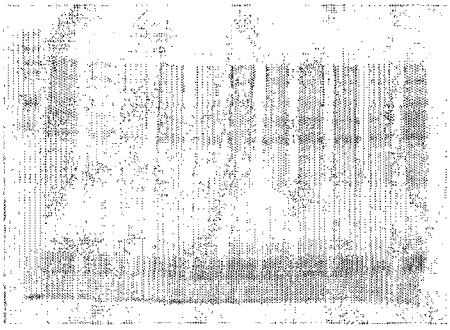


**FIGURE 139**

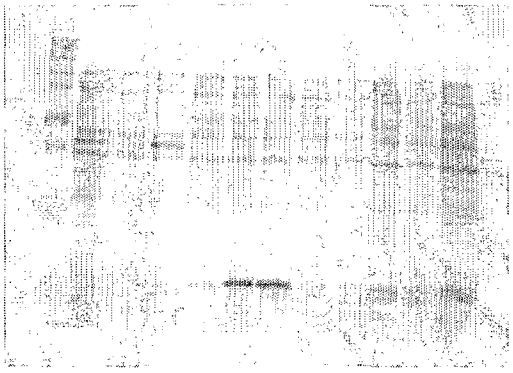


**FIGURE 140**

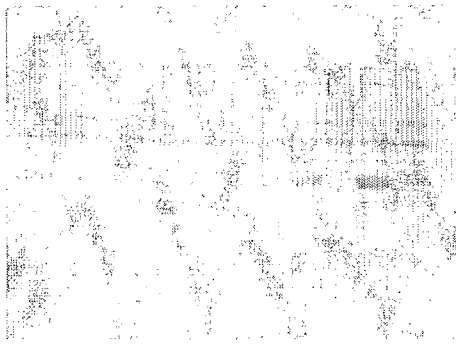


**FIGURE 141**

**FIGURE 142**

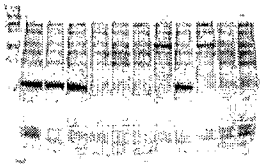


**FIGURE 143**

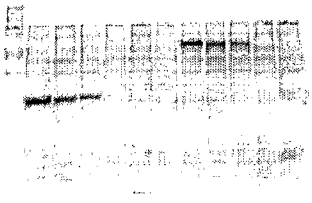


**FIGURE 144**

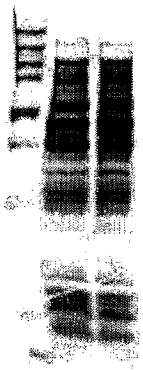
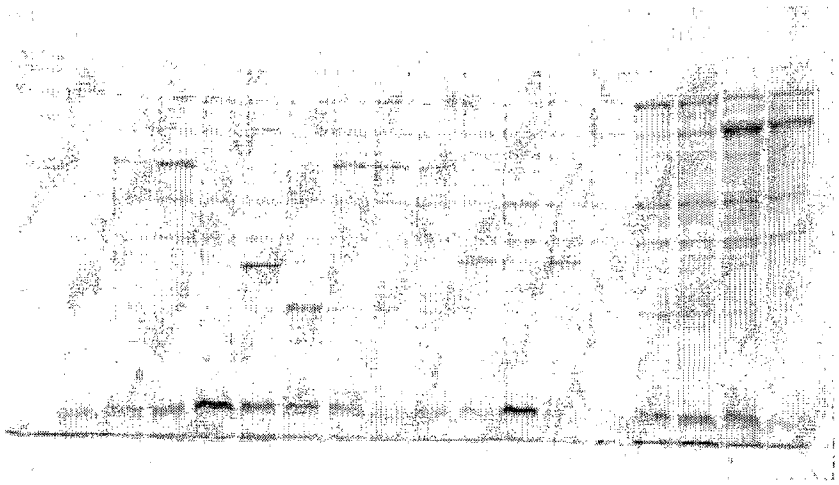


**FIGURE 145**



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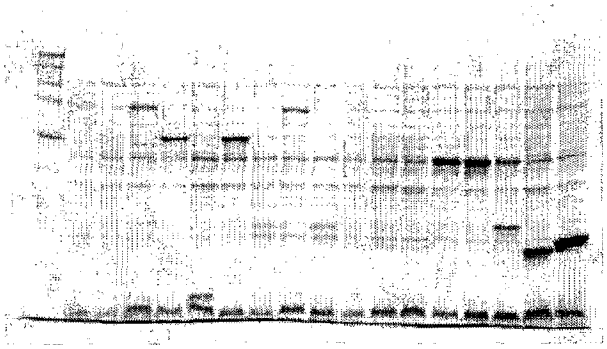


**FIGURE 147**

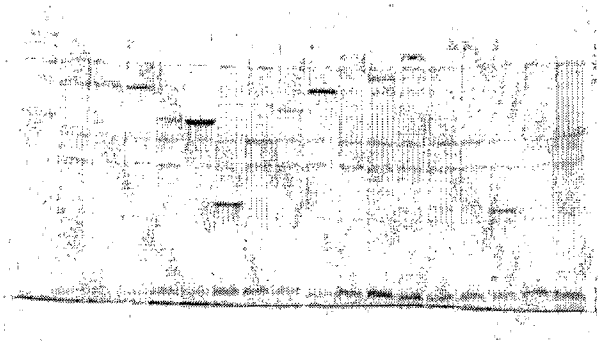


**FIGURE 148**

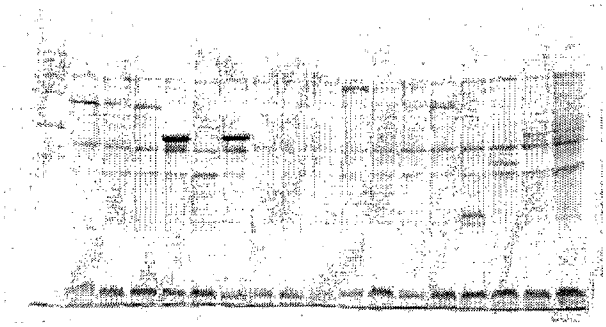


**FIGURE 149**

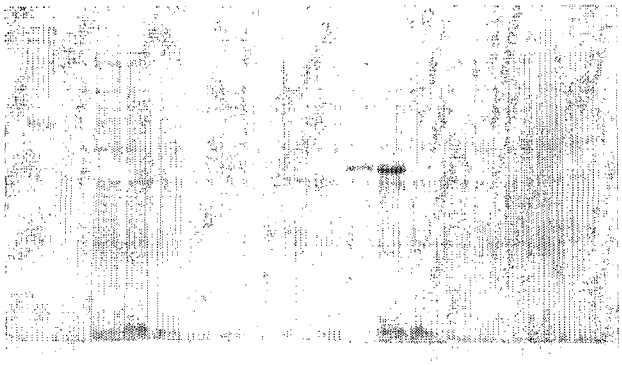


**FIGURE 150**

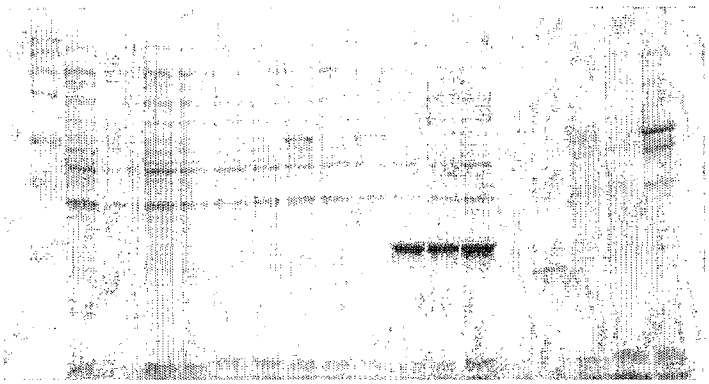


**FIGURE 151**

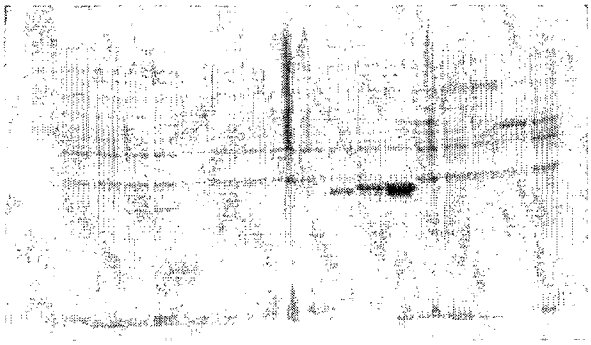


**FIGURE 152**

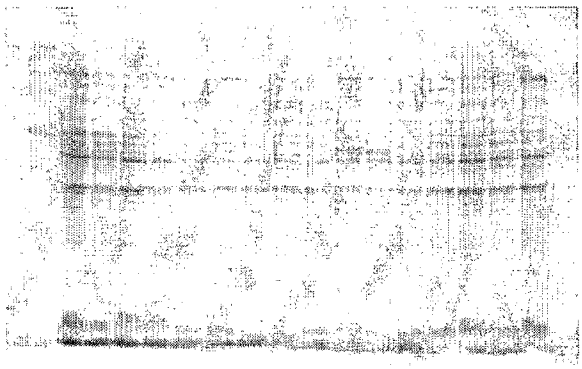


**FIGURE 153**

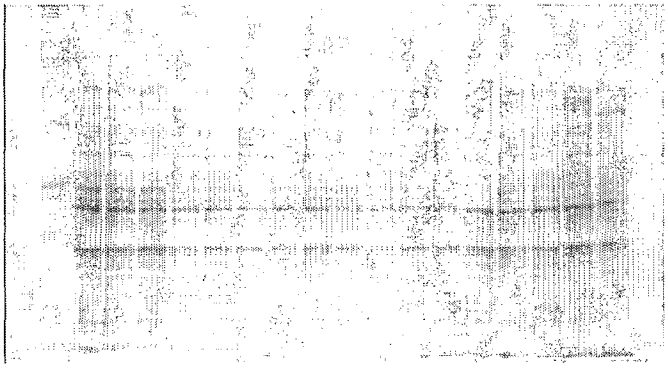


**FIGURE 154**

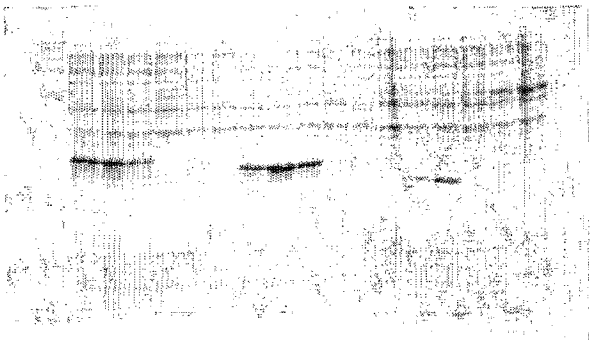


**FIGURE 155**

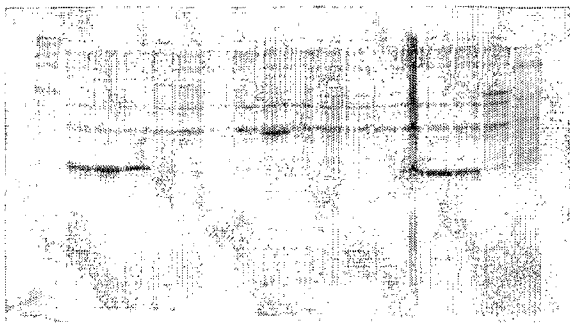
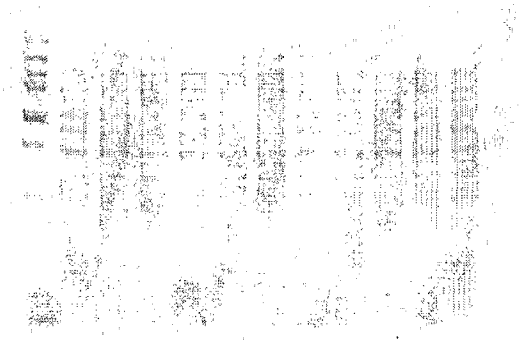


**FIGURE 156**



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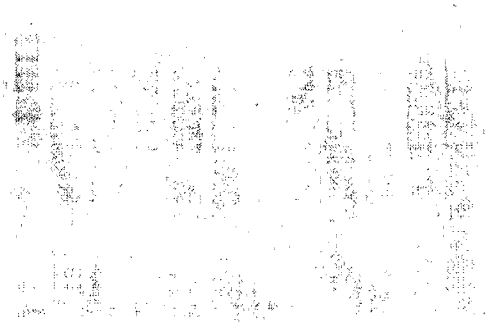


**FIGURE 158**

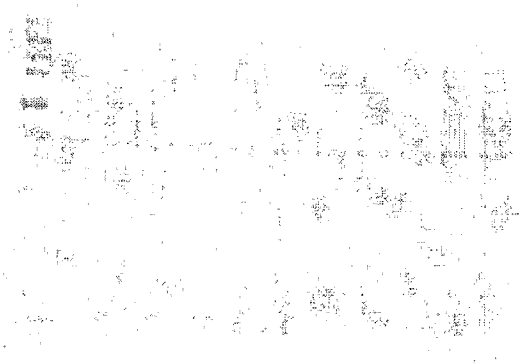


**FIGURE 159**

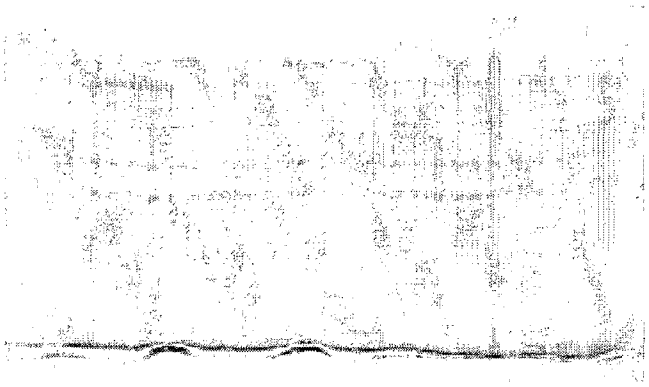


**FIGURE 160**

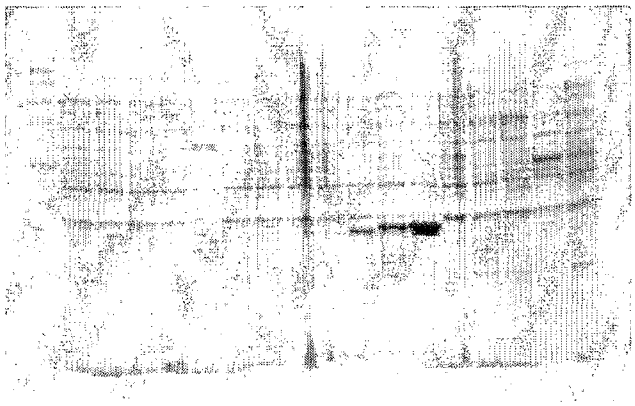


**FIGURE 161**

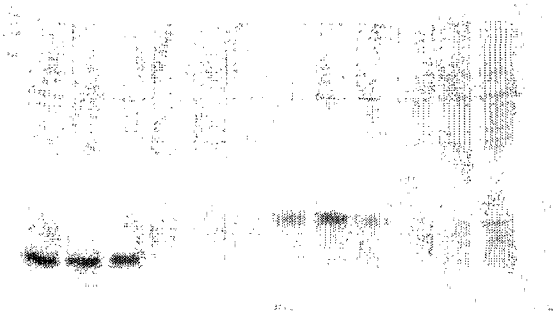


**FIGURE 162**

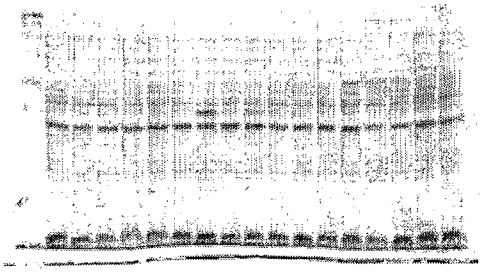


**FIGURE 163**

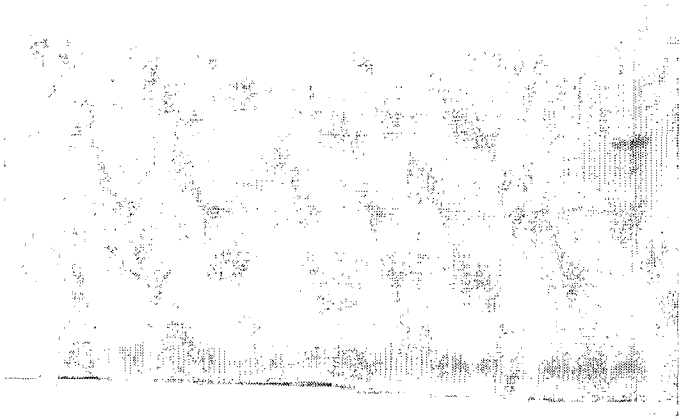


**FIGURE 164**

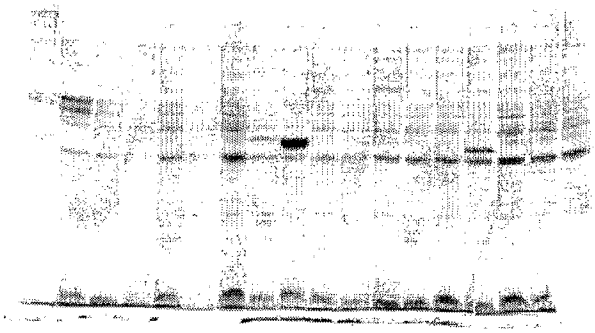


**FIGURE 165**

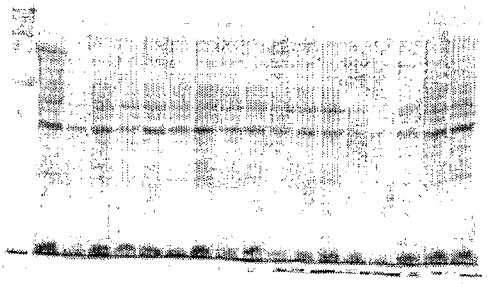


**FIGURE 166**

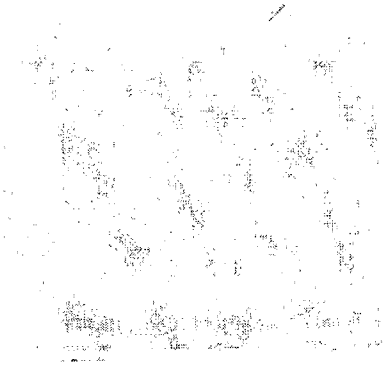


**FIGURE 167**

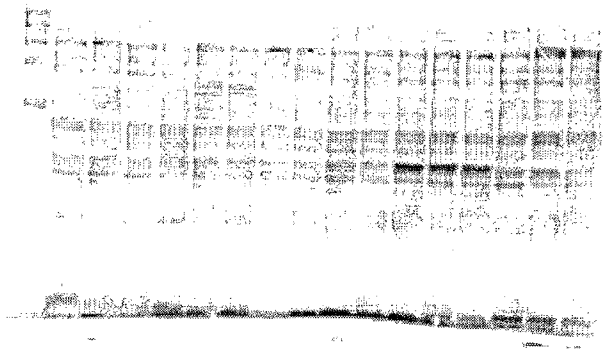


**FIGURE 168**

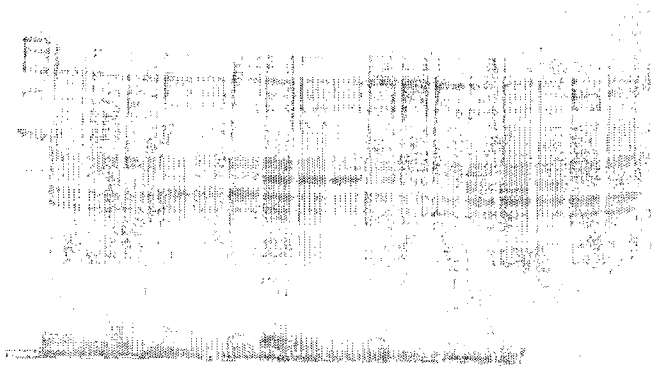


**FIGURE 169**

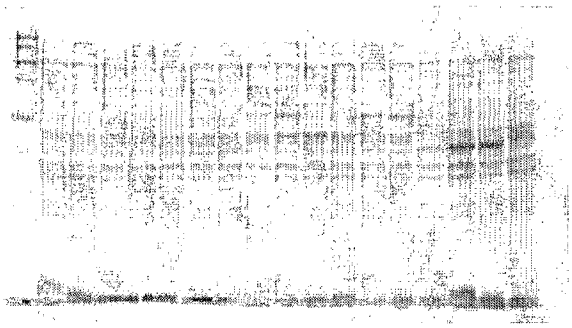


**FIGURE 170**

**FIGURE 171**

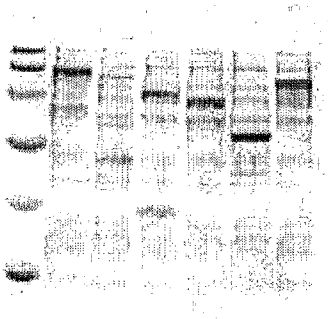


**FIGURE 172**

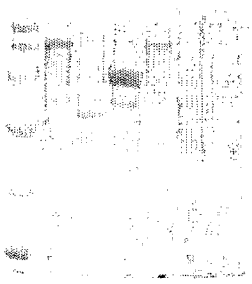


**FIGURE 173**

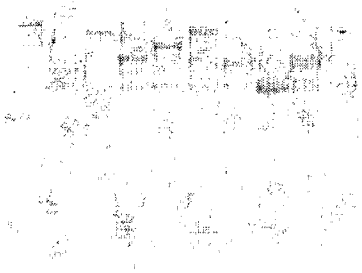


**FIGURE 174**

**FIGURE 175**

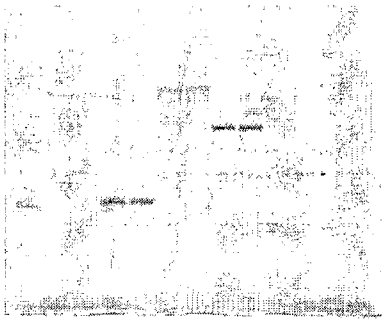


**FIGURE 176**

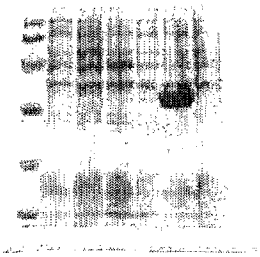


**FIGURE 177**

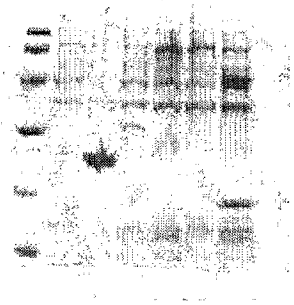


**FIGURE 178**

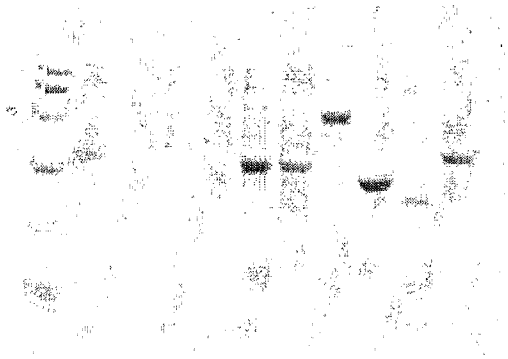


**FIGURE 179**

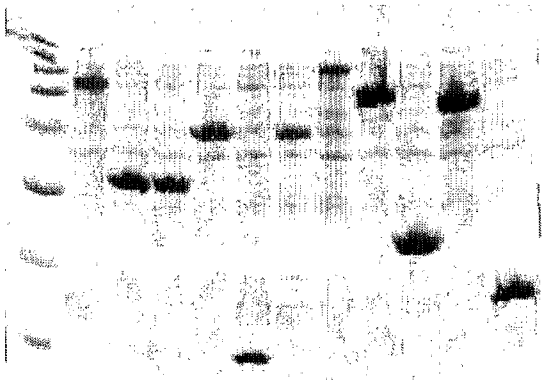


**FIGURE 180**

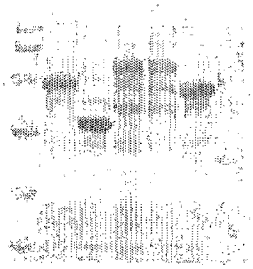


**FIGURE 181**

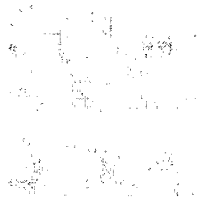


**FIGURE 182**

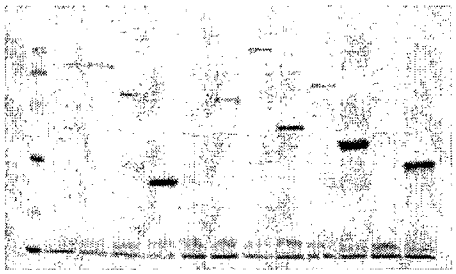


**FIGURE 183**

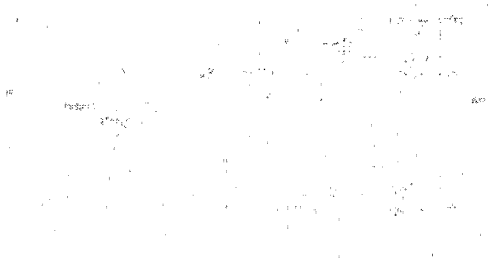


**FIGURE 184**

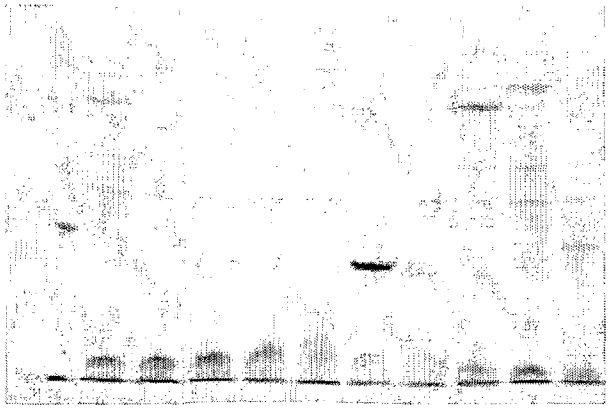


**FIGURE 185**

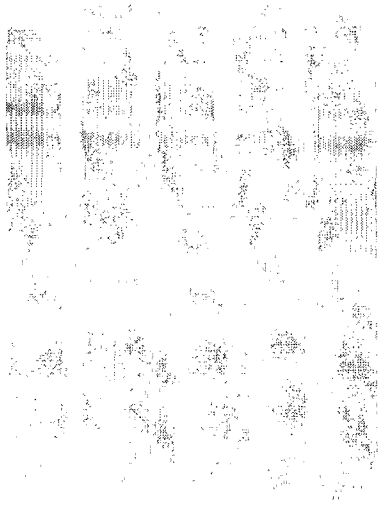
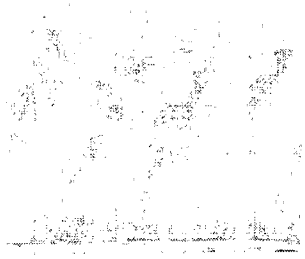


**FIGURE 186**



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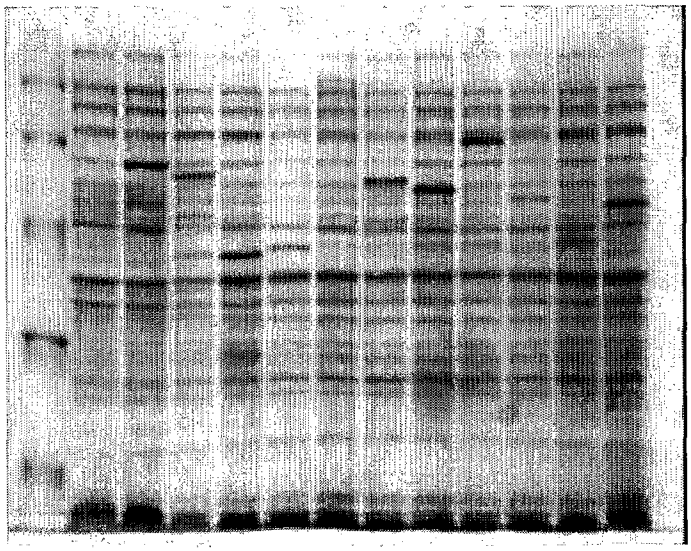

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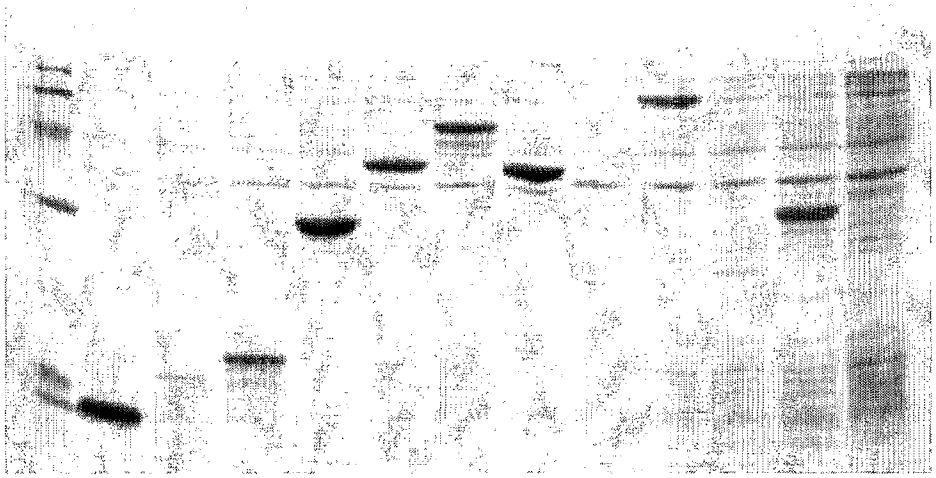

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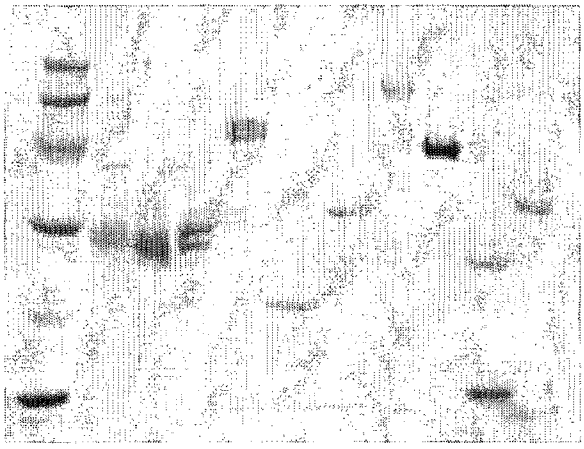
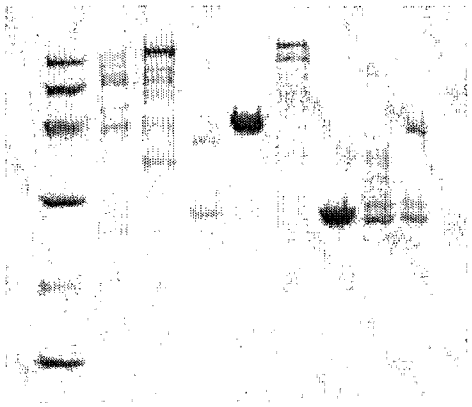


**FIGURE 190**



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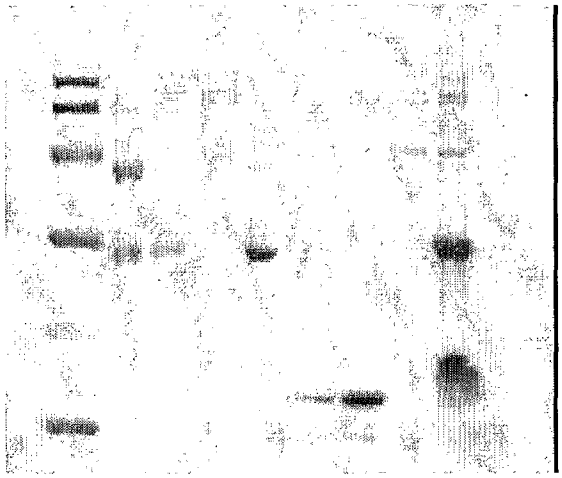

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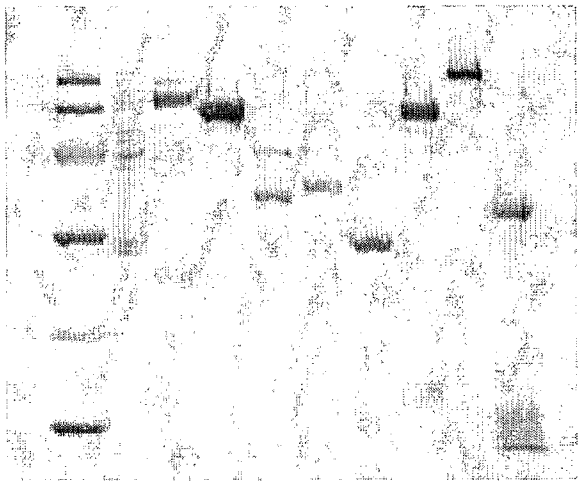

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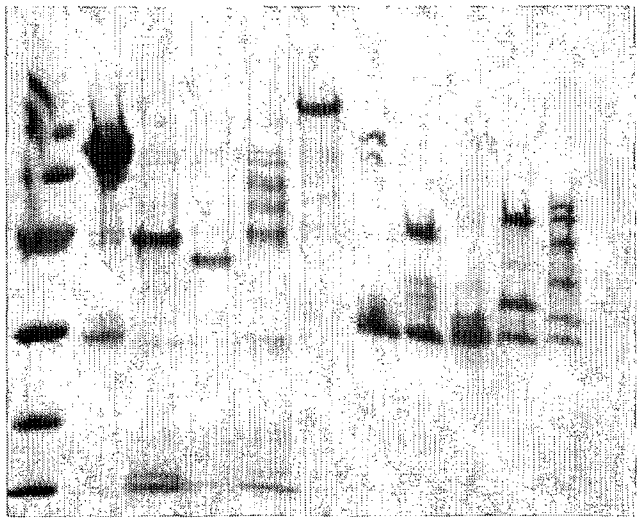

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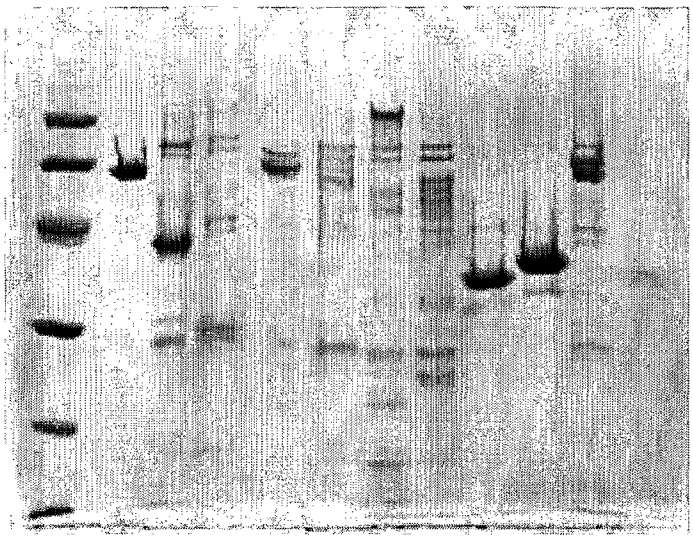

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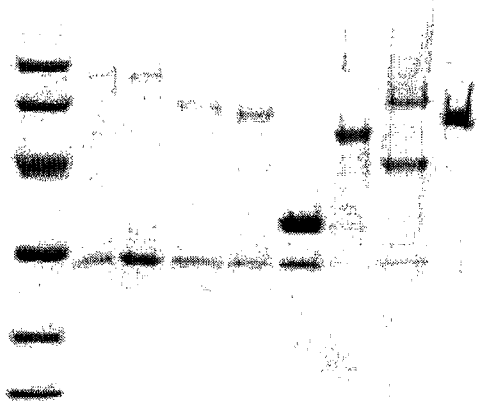

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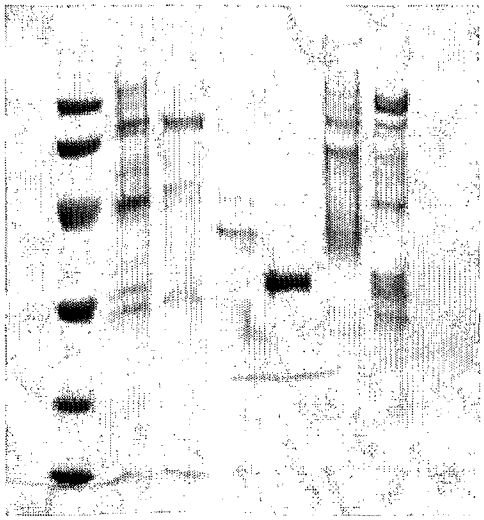

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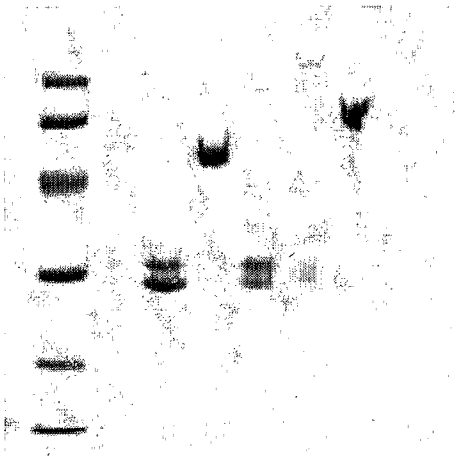

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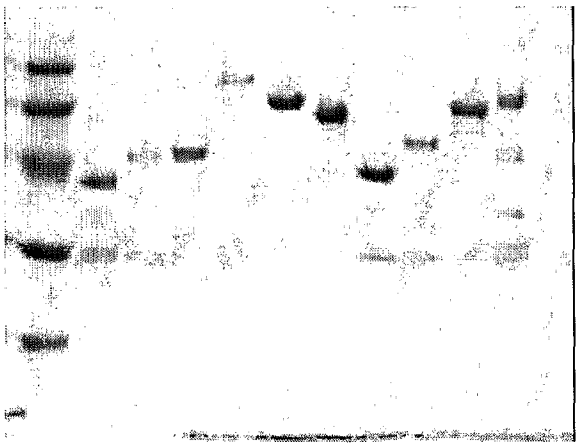

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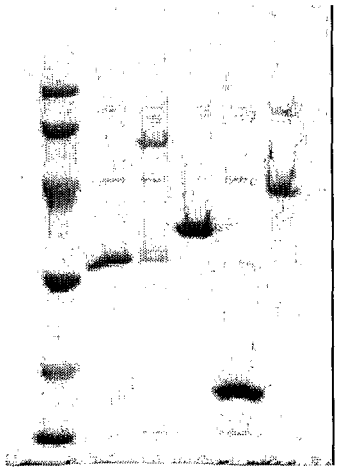

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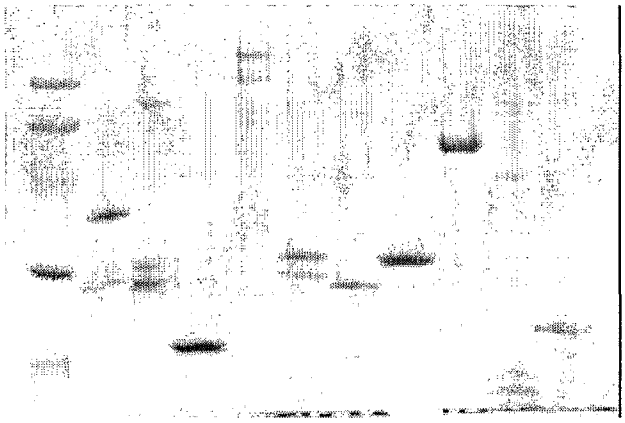

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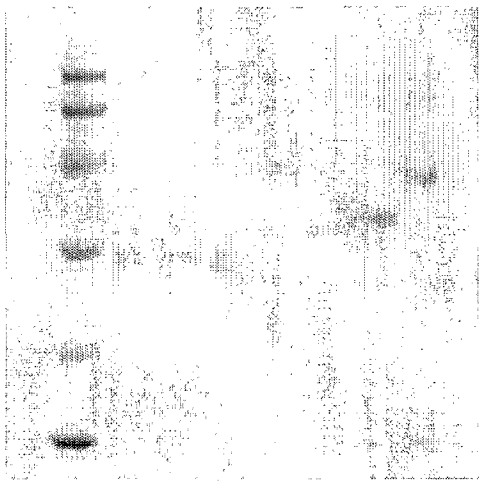

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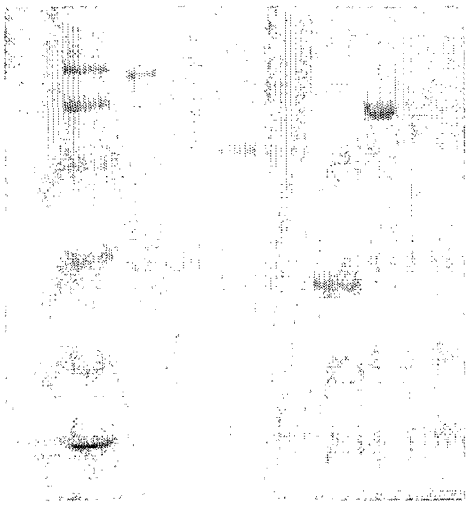
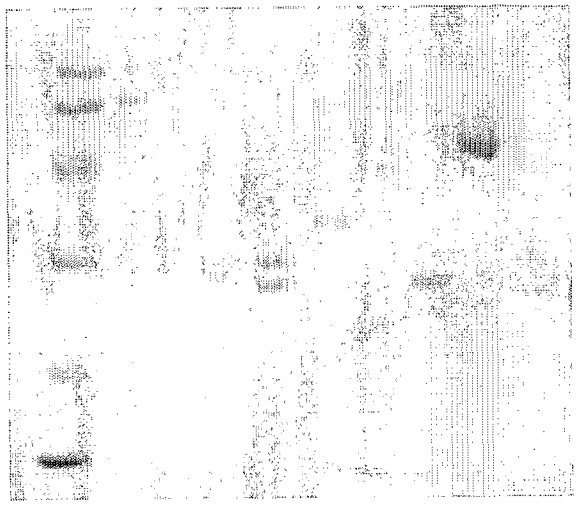


**FIGURE 203**



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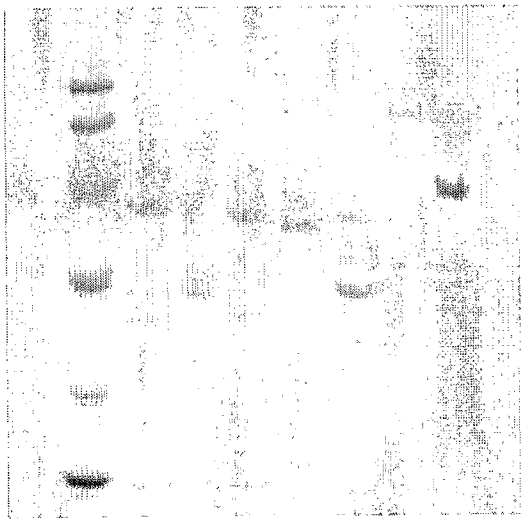

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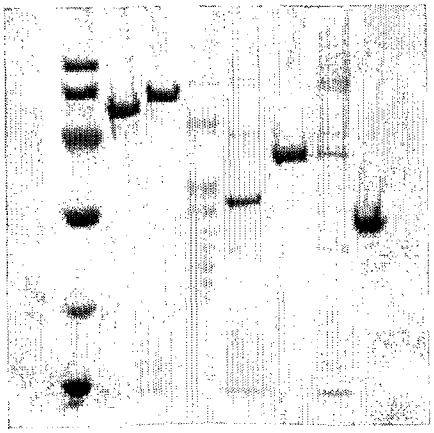

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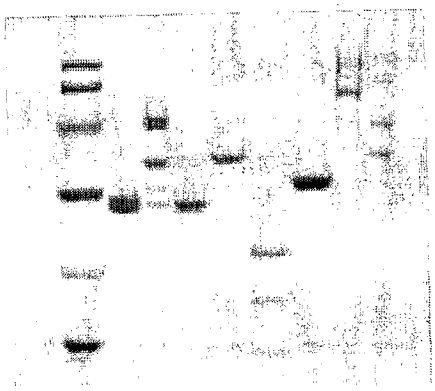

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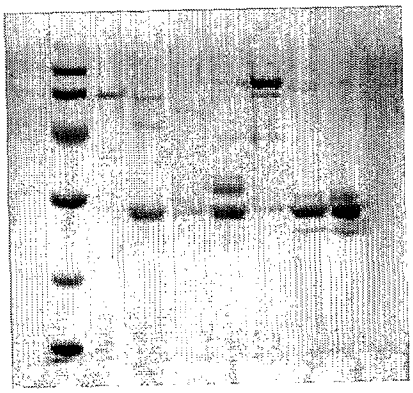

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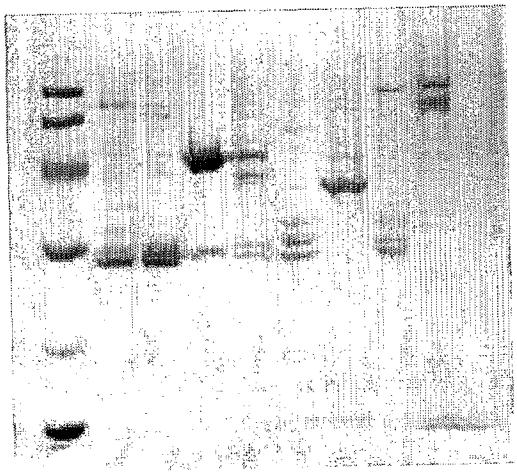

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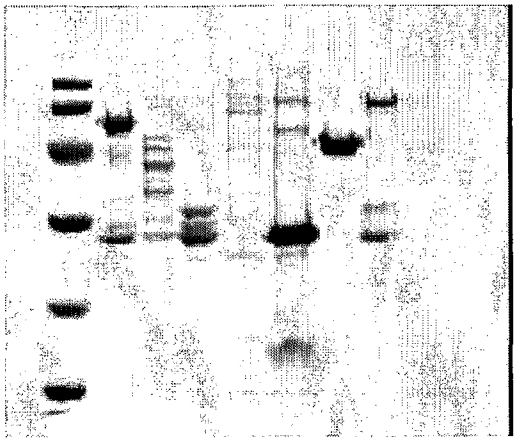

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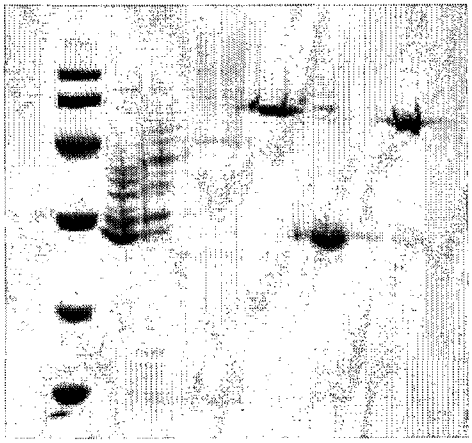

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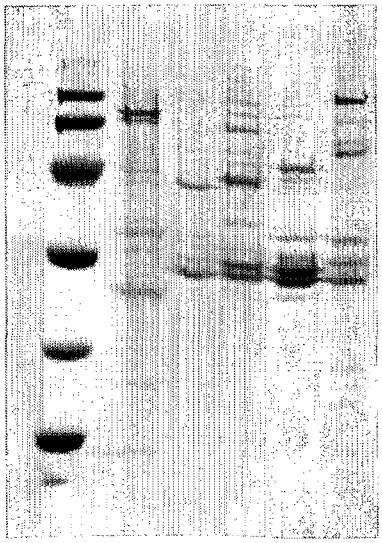

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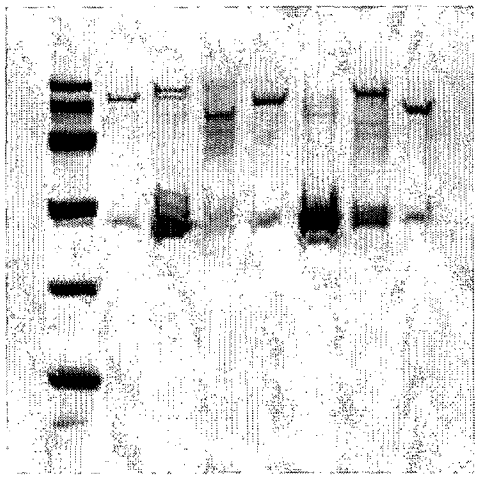

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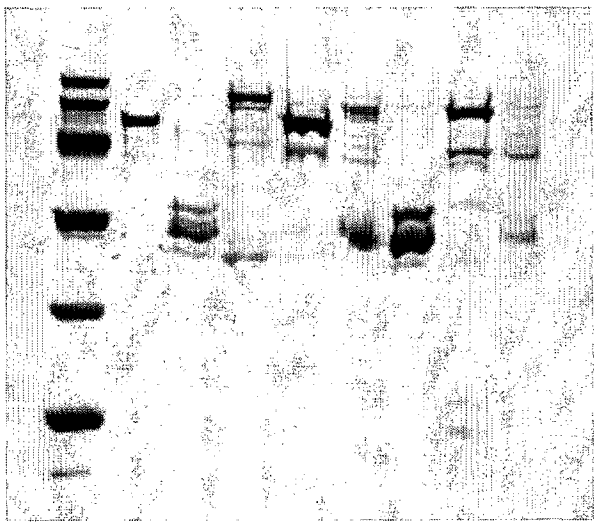

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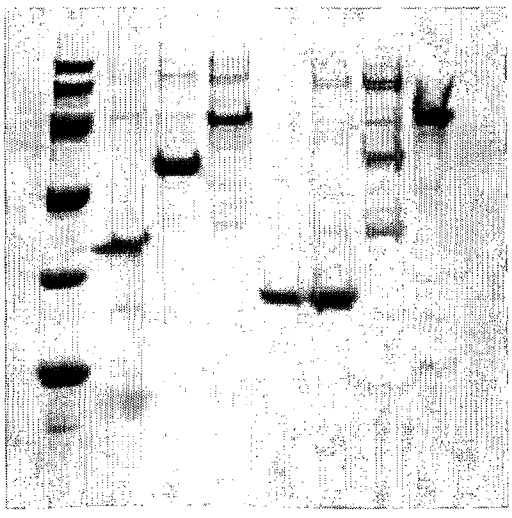

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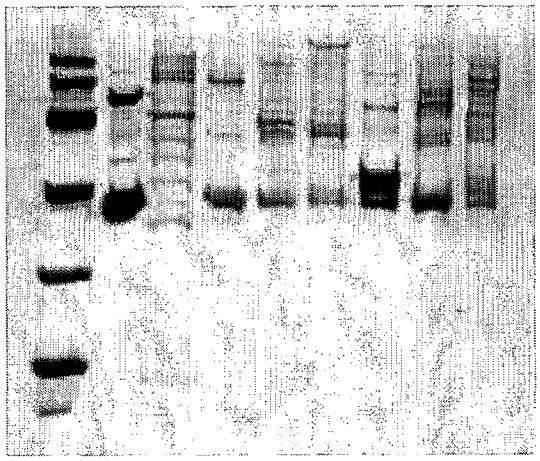

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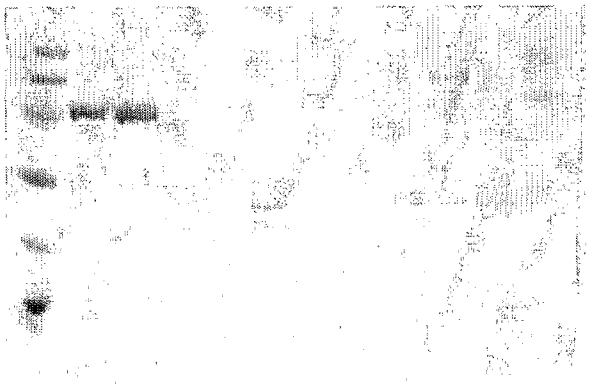

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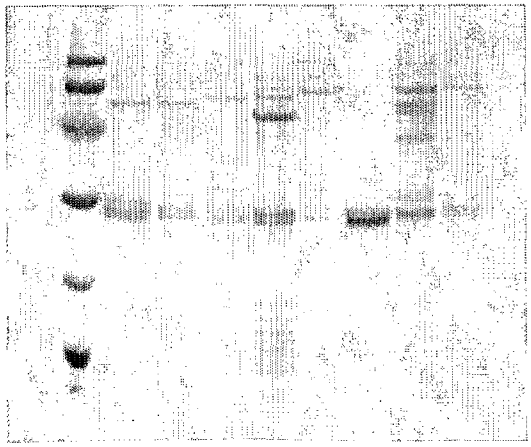

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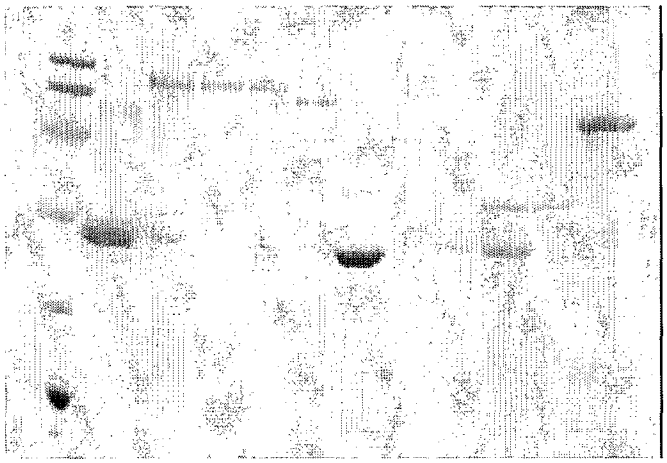
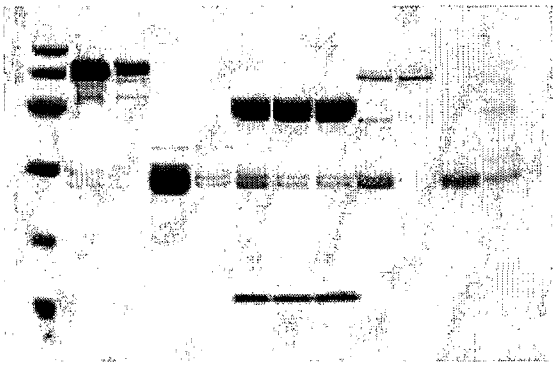


**FIGURE 219**



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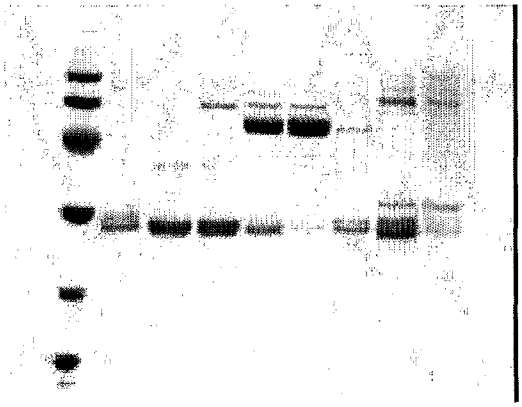


**FIGURE 221**

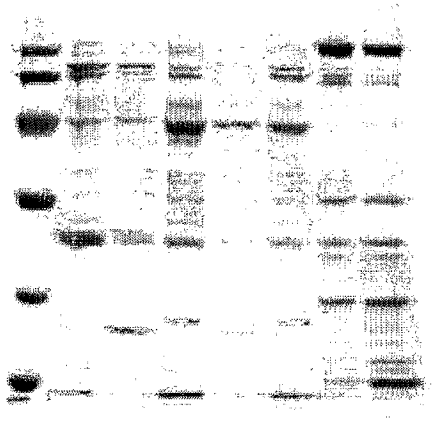


**FIGURE 222**

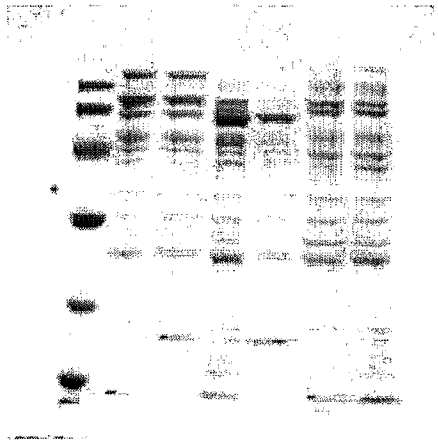


**FIGURE 223**

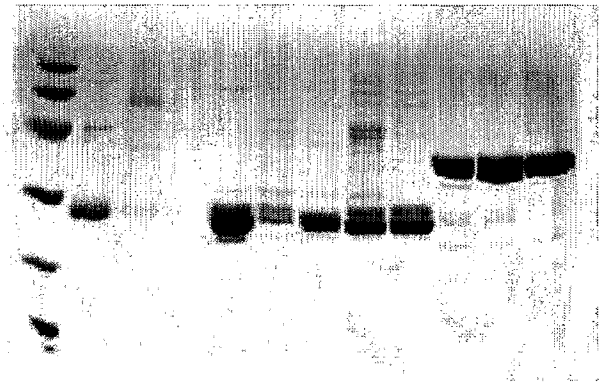
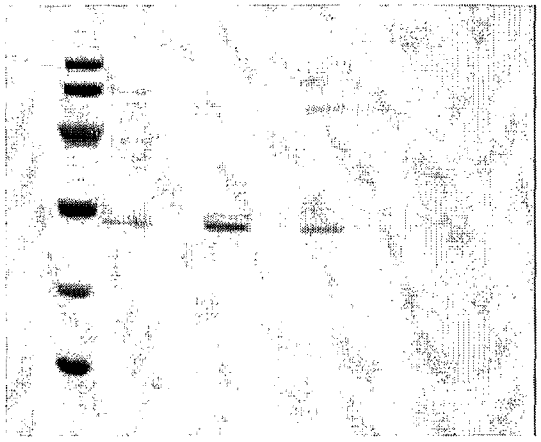


**FIGURE 224**



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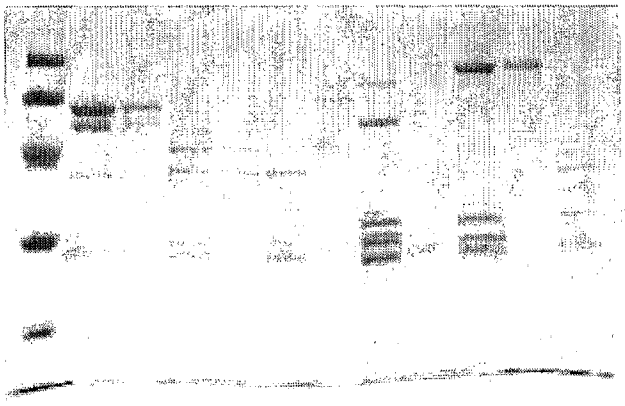


**FIGURE 226**

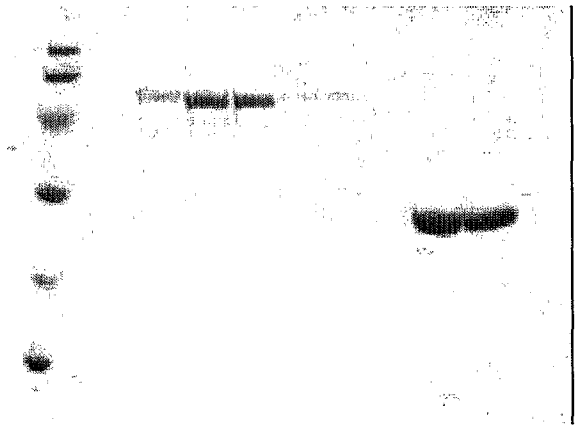


**FIGURE 227**

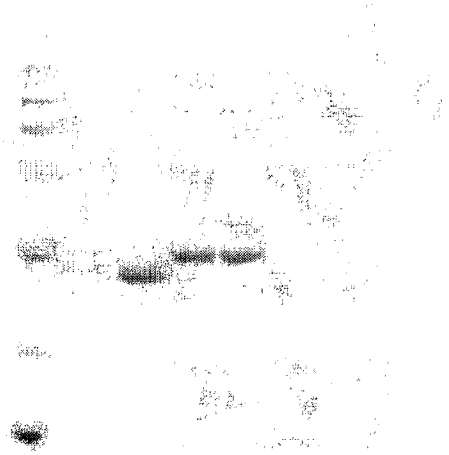


**FIGURE 228**

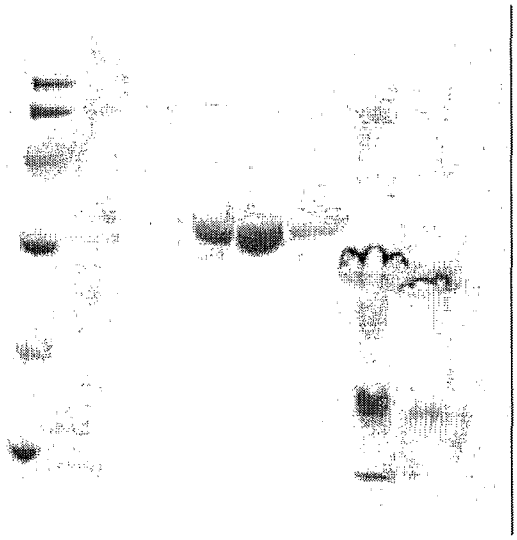
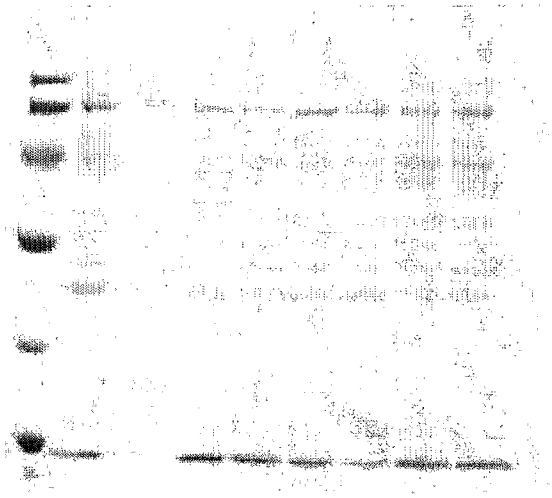


**FIGURE 229**



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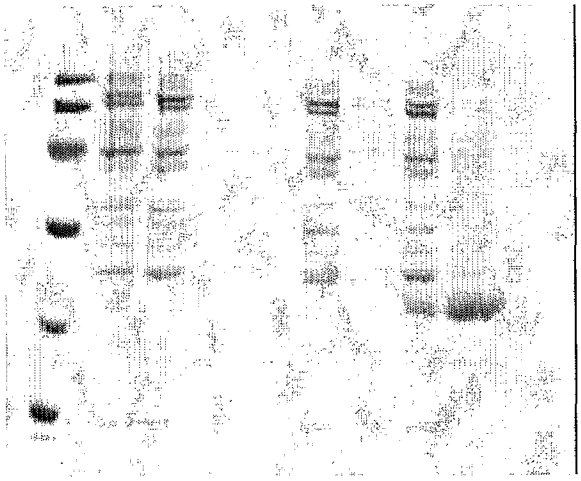


**FIGURE 231**

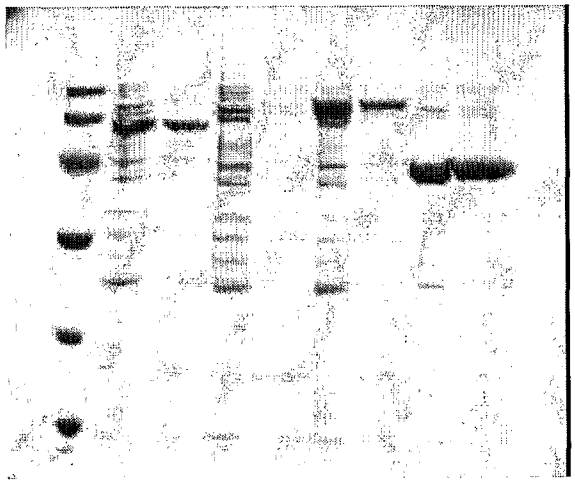


**FIGURE 232**

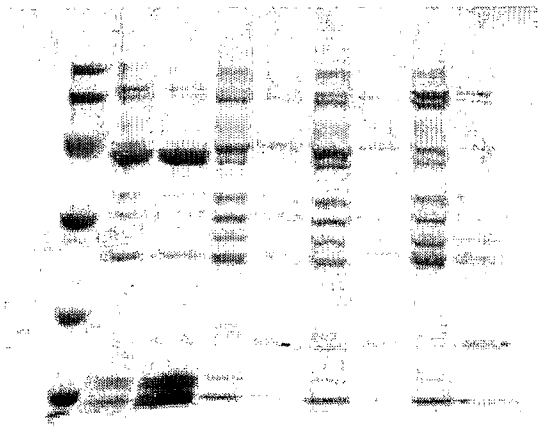


**FIGURE 233**

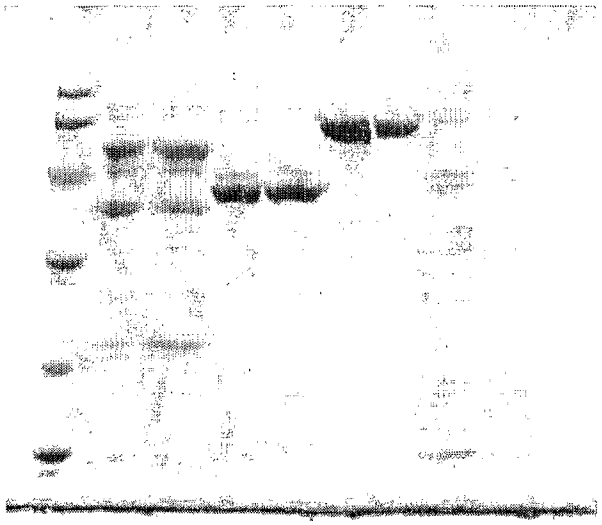


**FIGURE 234**

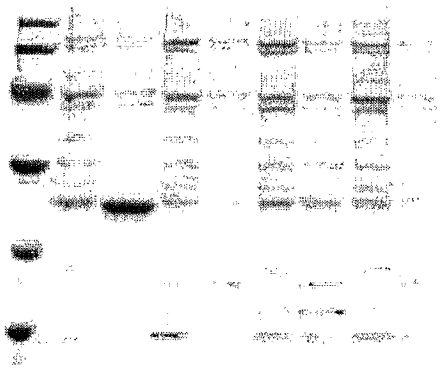


**FIGURE 235**

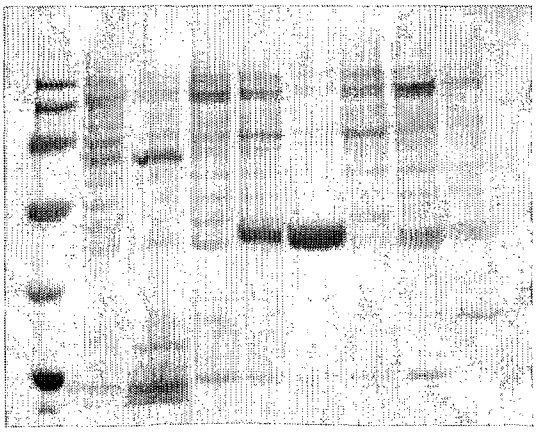


**FIGURE 236**

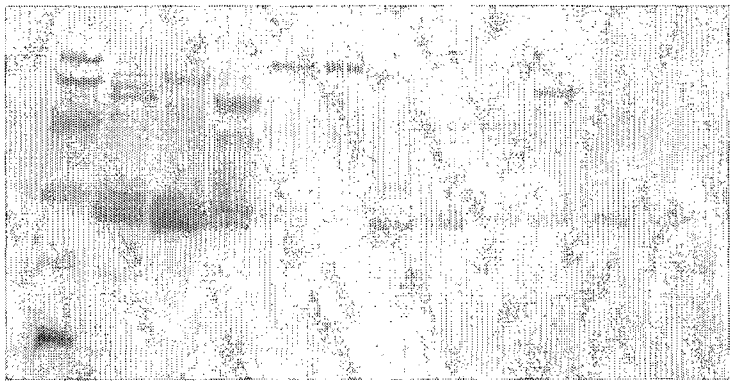


**FIGURE 237**

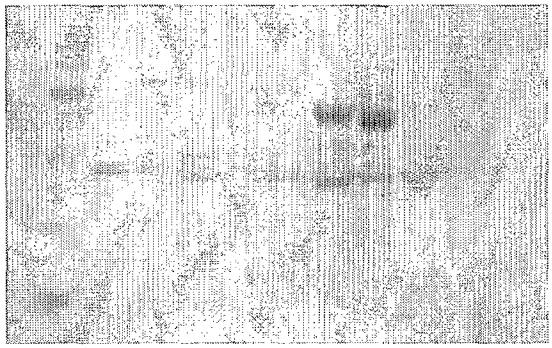


**FIGURE 238**

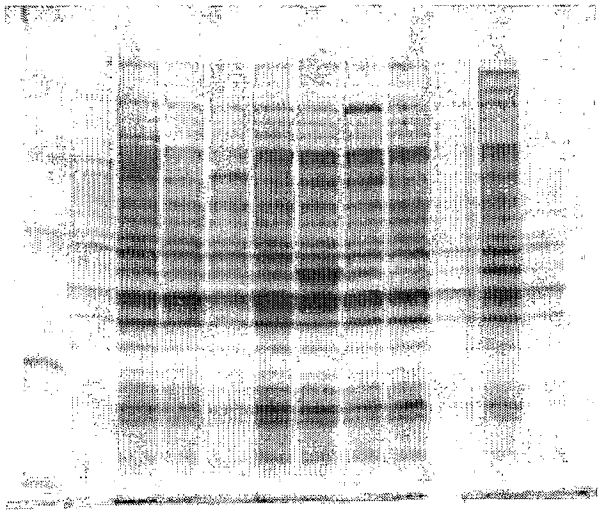


**FIGURE 239**

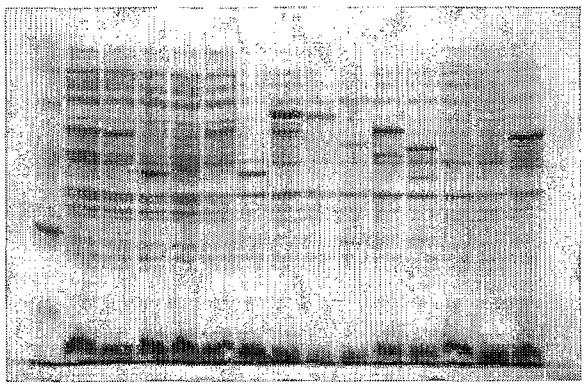


**FIGURE 240**

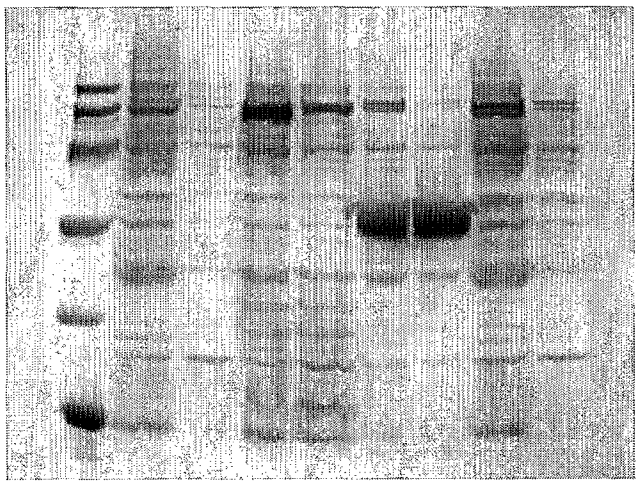


**FIGURE 241**

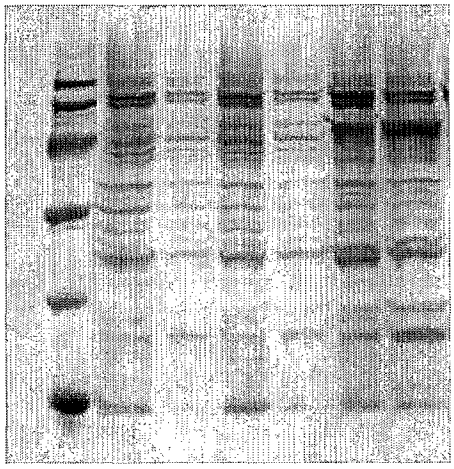


**FIGURE 242**

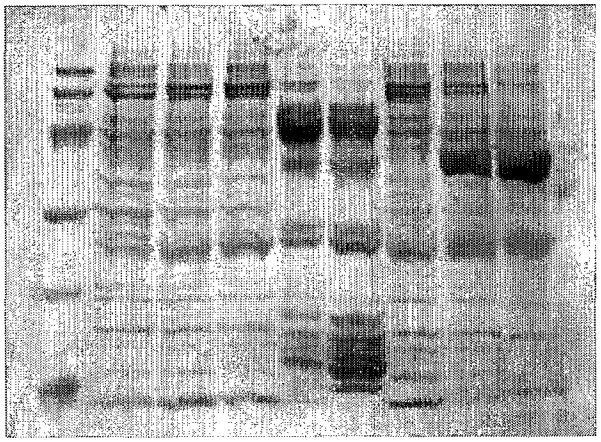


**FIGURE 243**

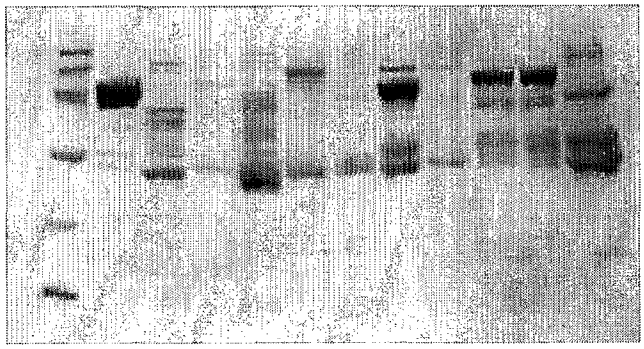
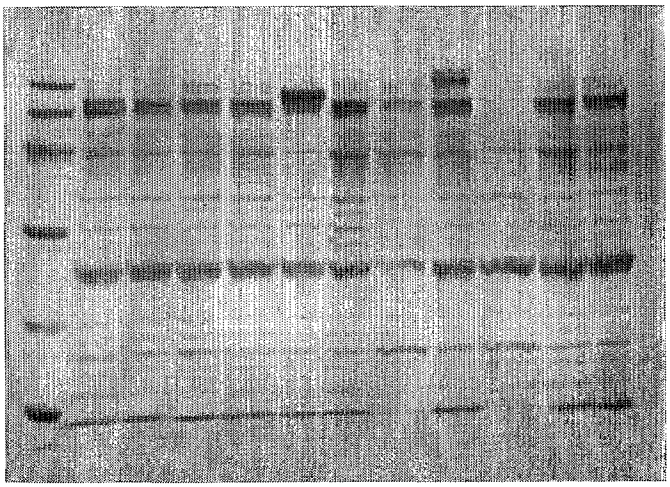
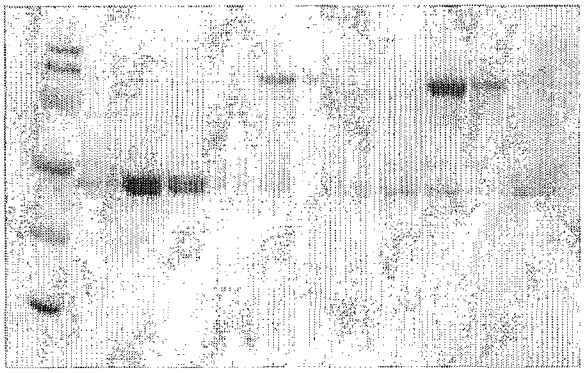


**FIGURE 244**

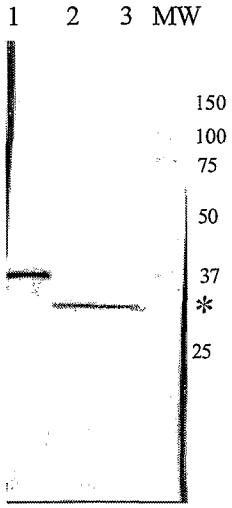


## FIGURE 245

## FIGURE 246

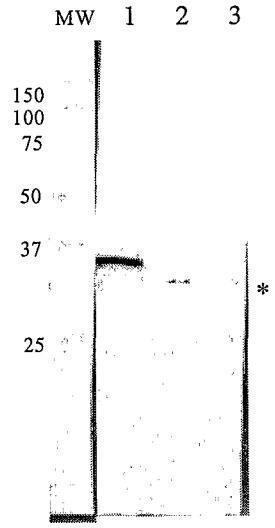


## FIGURE 247

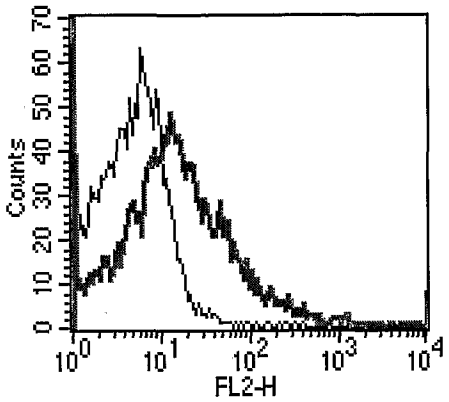


## FIGURE 248

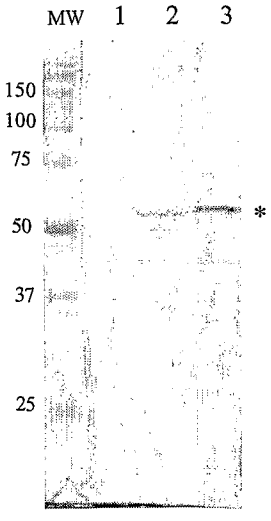
### FIGURE 248A



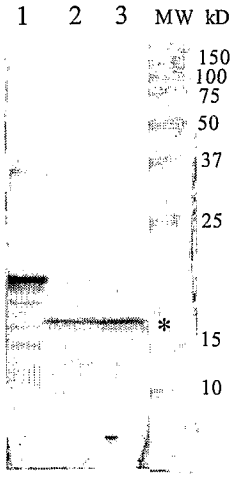

### FIGURE 248B



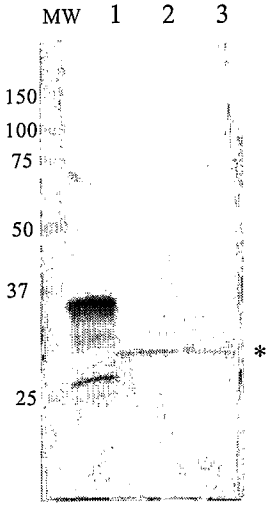

### FIGURE 249




### FIGURE 250

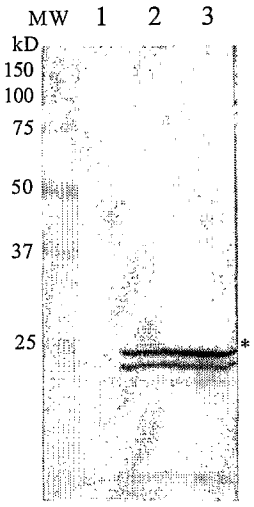



### FIGURE 251

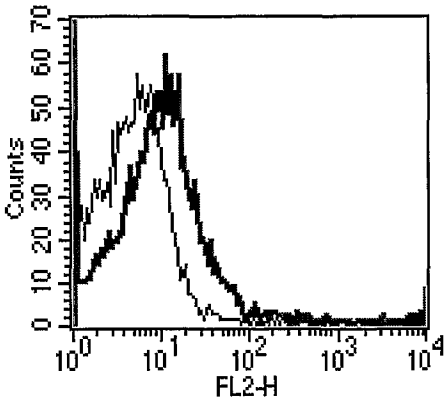


## FIGURE 252

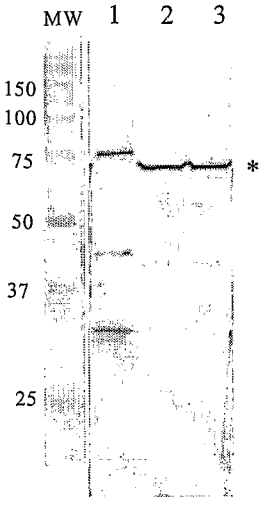
### FIGURE 252A



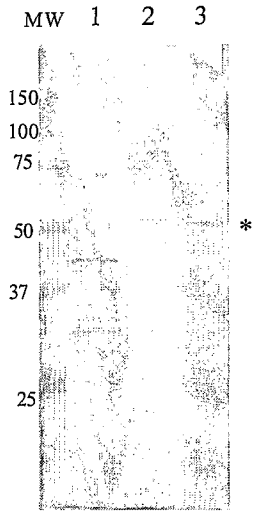

### FIGURE 252B




## FIGURE 253

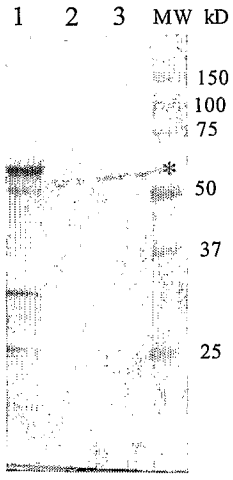


## FIGURE 254

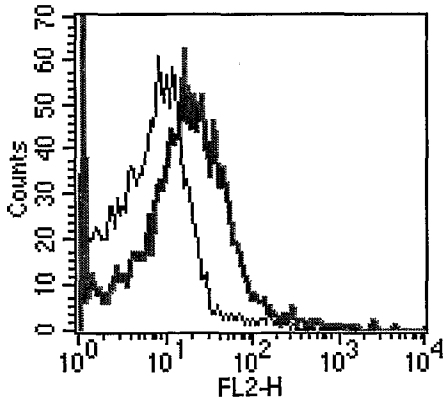



## FIGURE 255

## FIGURE 255A

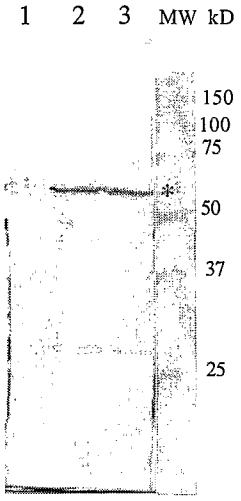



## FIGURE 255B

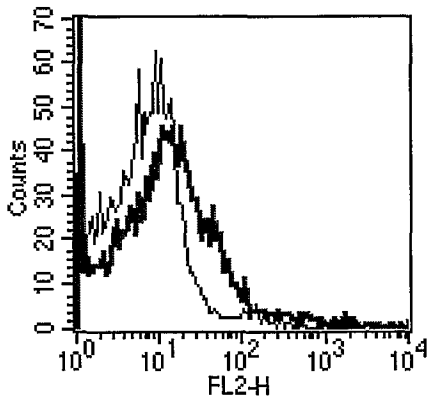


# FIGURE 256

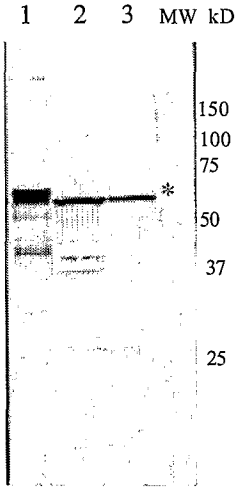
## FIGURE 256A




## FIGURE 256B




## FIGURE 257




## FIGURE 258

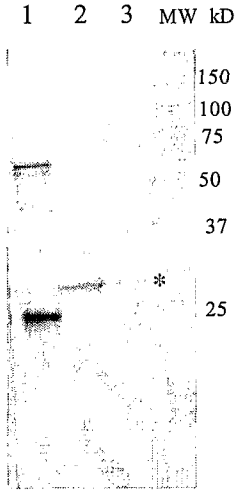


**FIGURE 259A**

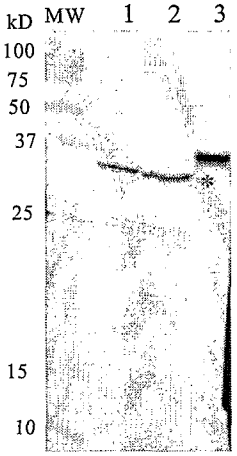



**FIGURE 259B**

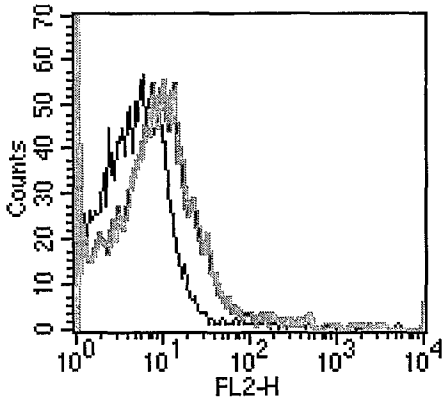



**FIGURE 260**

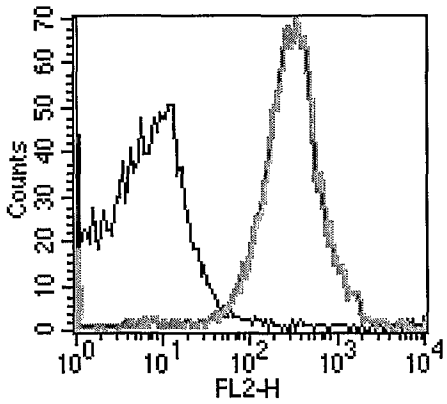



**FIGURE 261**

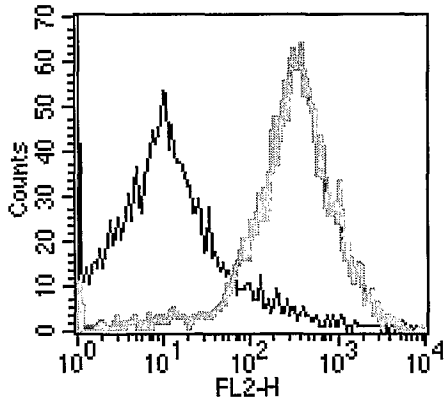


**FIGURE 262**

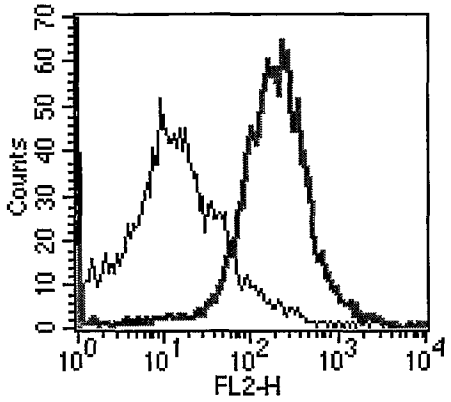



**FIGURE 263**

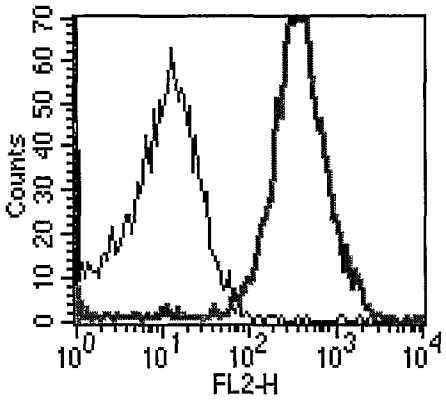



**FIGURE 264**

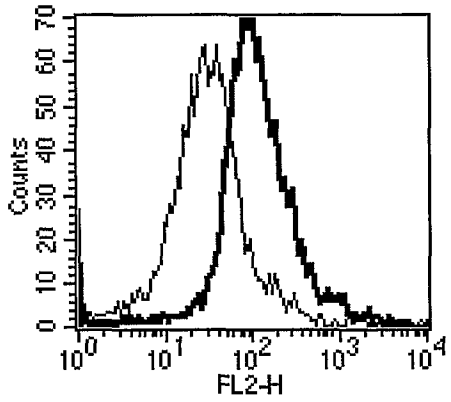



**FIGURE 265**

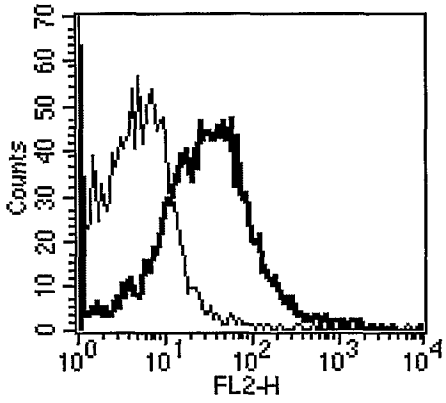



**FIGURE 266**

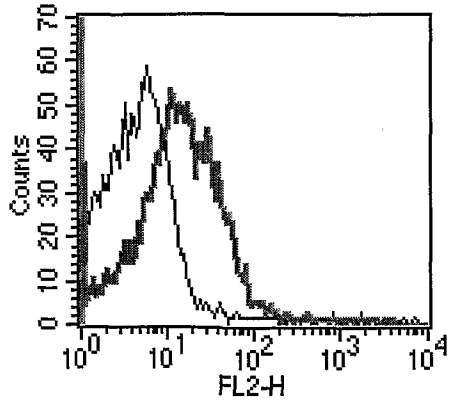



**FIGURE 267**

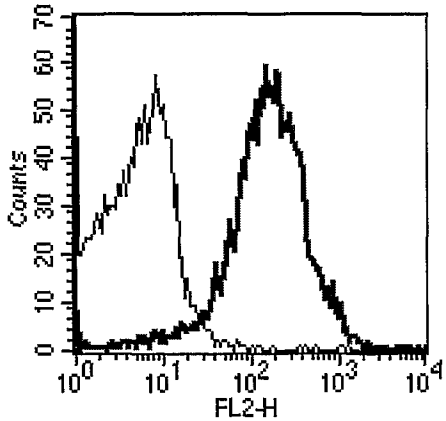


**FIGURE 268**

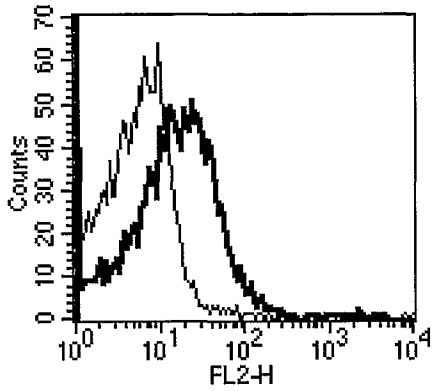



**FIGURE 269**

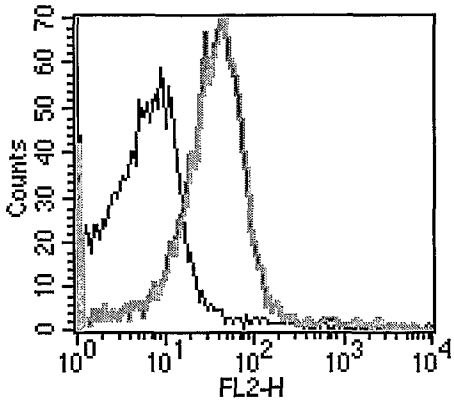



**FIGURE 270**

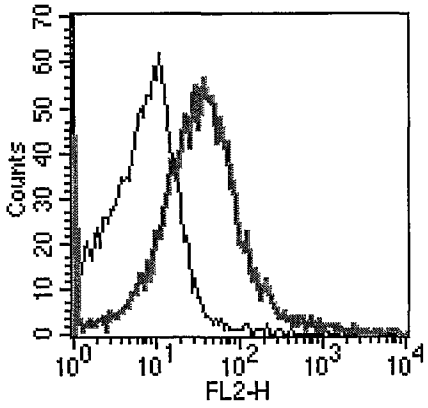



**FIGURE 271**

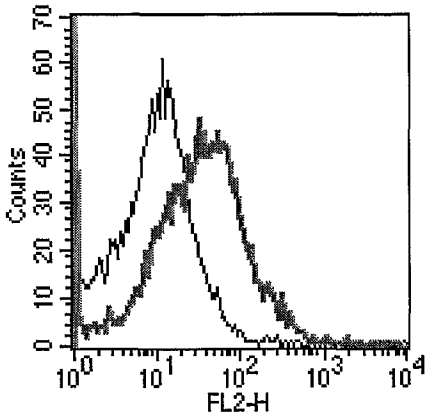



**FIGURE 272**

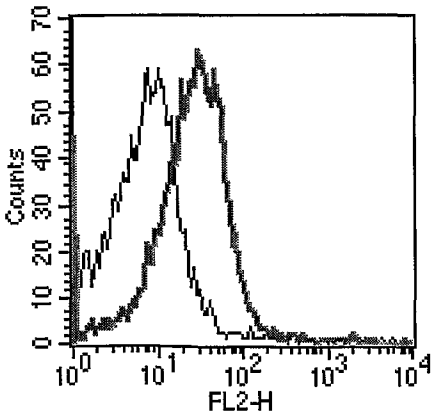



**FIGURE 273**

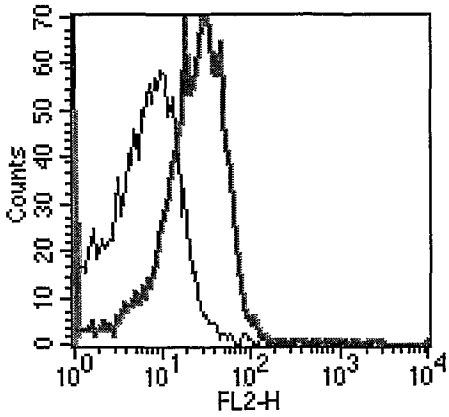


**FIGURE 274**

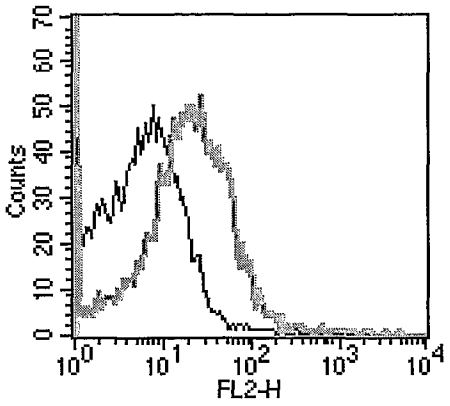



**FIGURE 275**

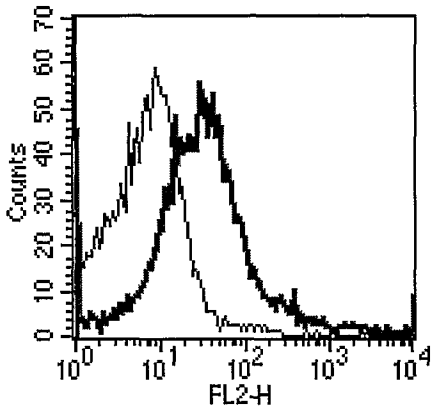



**FIGURE 276**

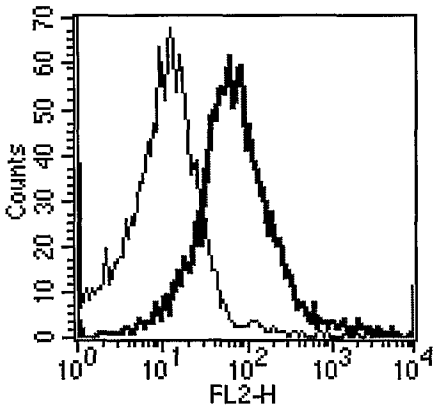



**FIGURE 277**

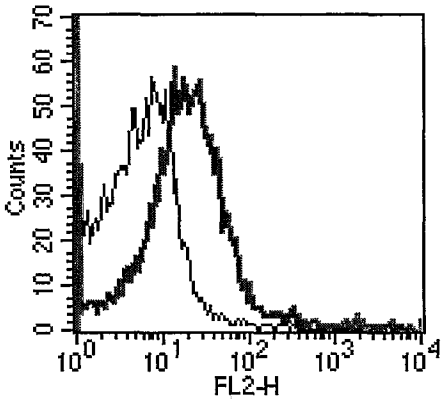



**FIGURE 278**

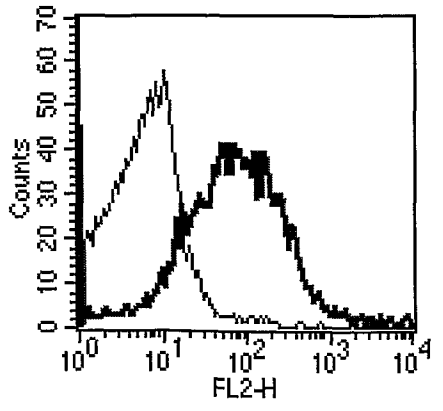



**FIGURE 279**

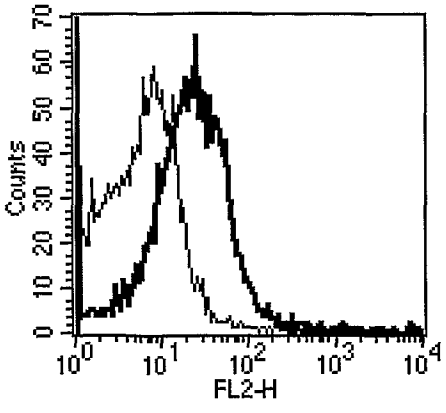


**FIGURE 280**

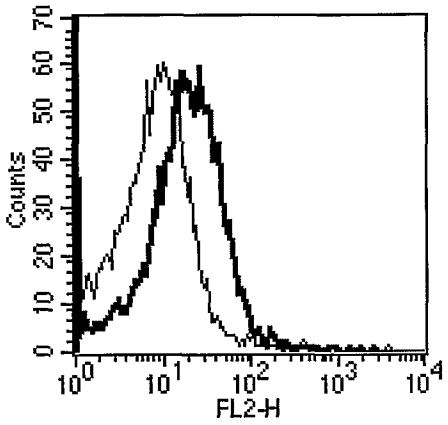



**FIGURE 281**

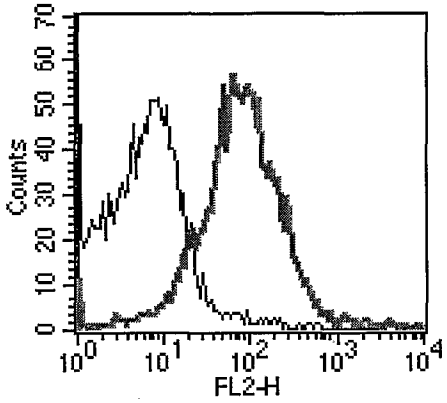



**FIGURE 282**

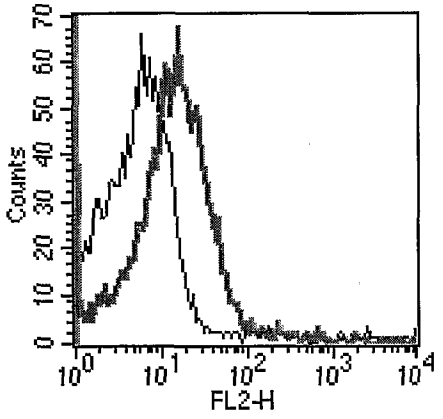



**FIGURE 283**

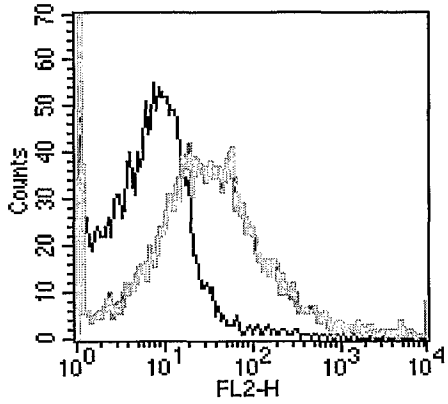



**FIGURE 284**

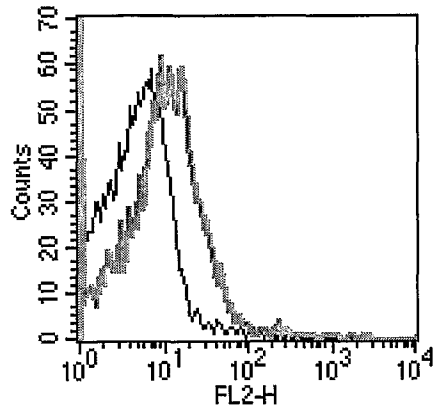



**FIGURE 285**

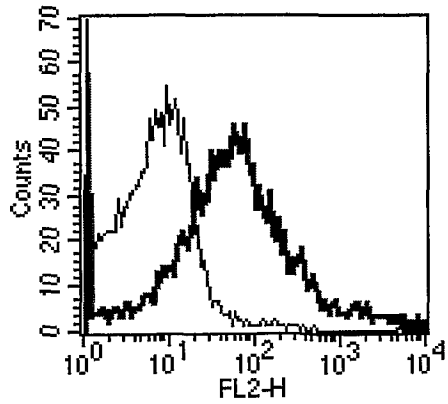


**FIGURE 286**

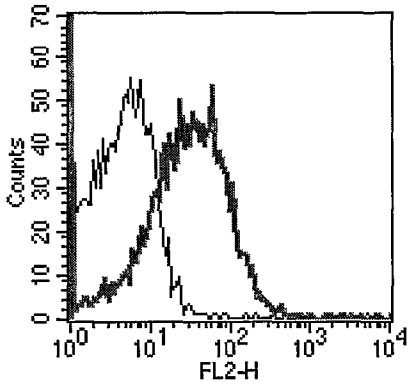



**FIGURE 287**

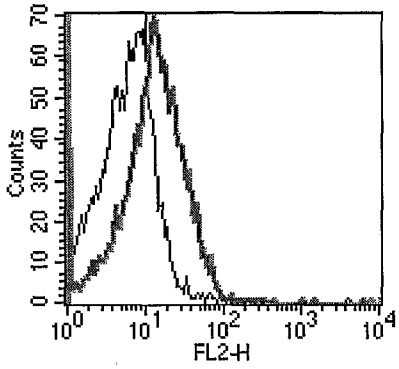



**FIGURE 288**

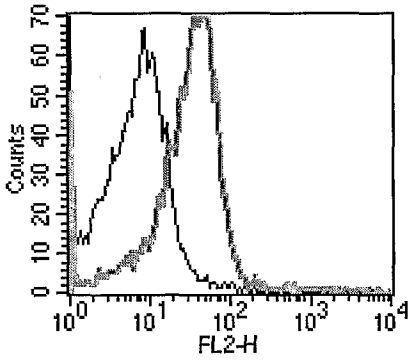



**FIGURE 289**

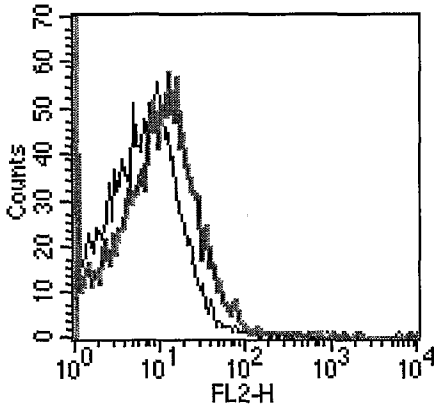



**FIGURE 290**

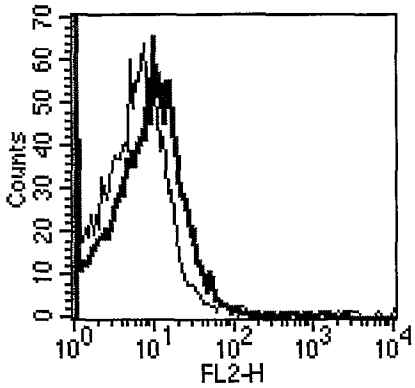



**FIGURE 291**

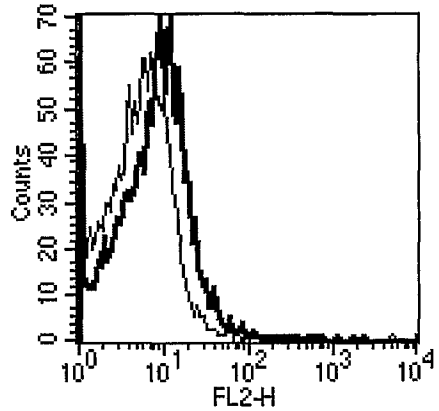


**FIGURE 292**

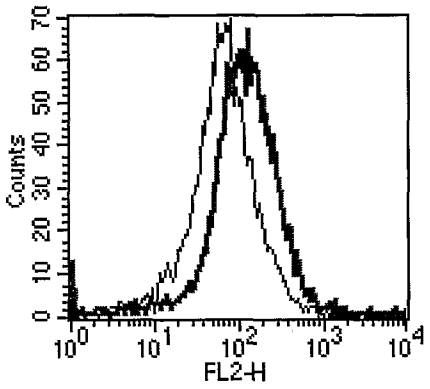



**FIGURE 293**

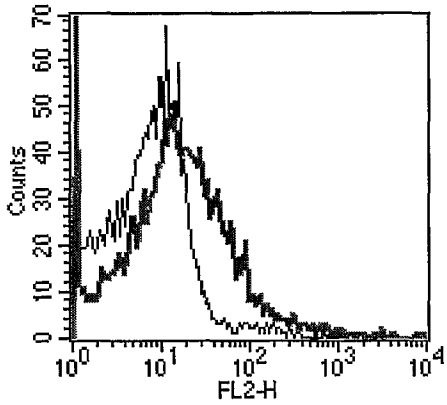



**FIGURE 294**

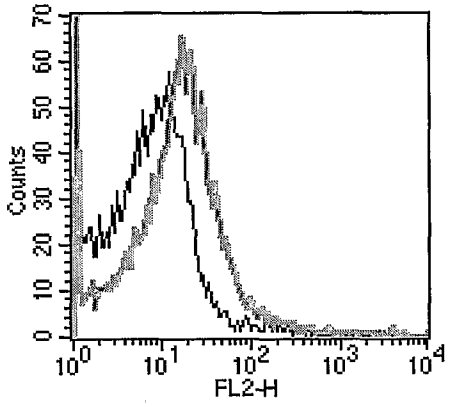



**FIGURE 295**

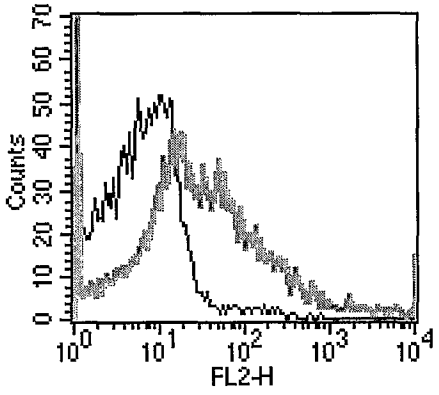



**FIGURE 296**

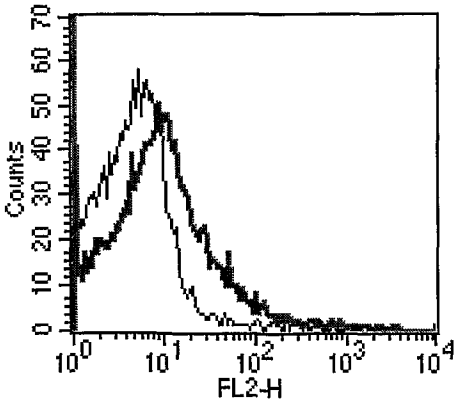



**FIGURE 297**

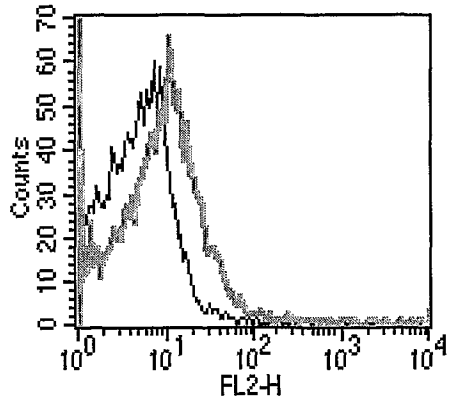


**FIGURE 298**

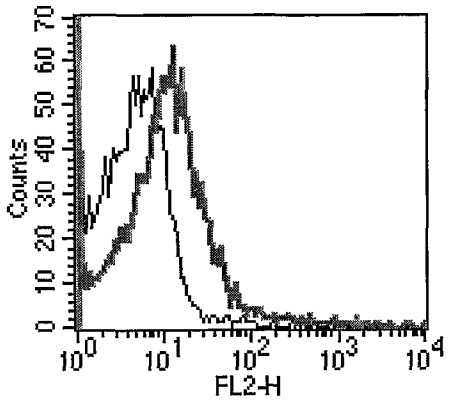



**FIGURE 299**

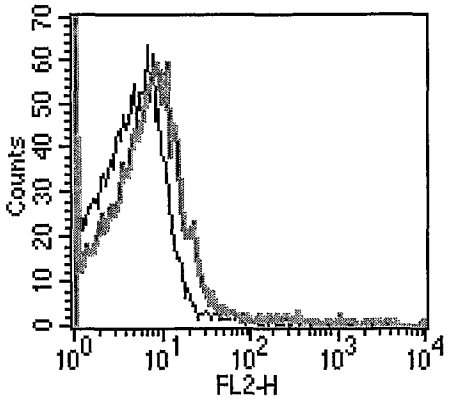



**FIGURE 300**

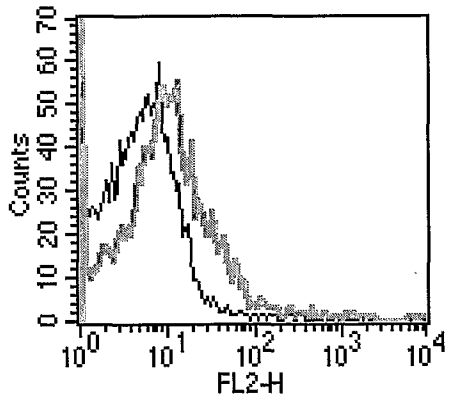



**FIGURE 301**

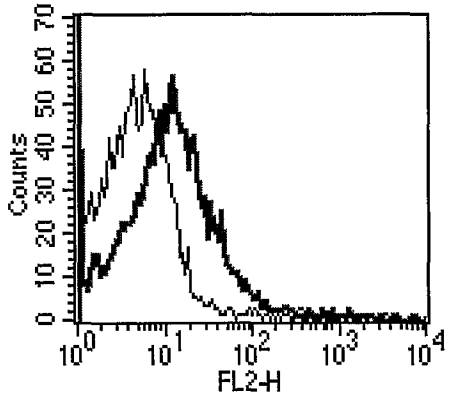



**FIGURE 302**

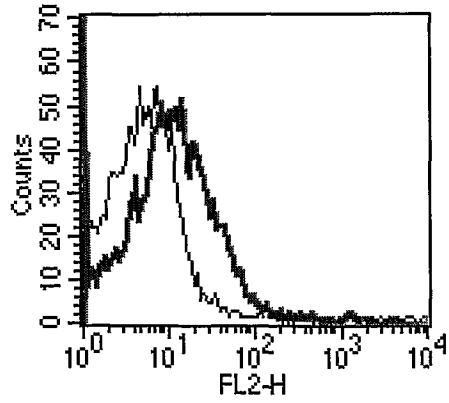



**FIGURE 303**

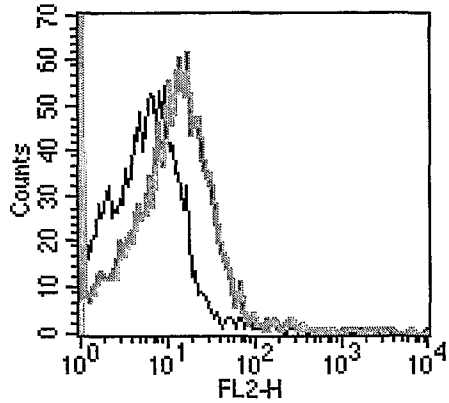


**FIGURE 304**

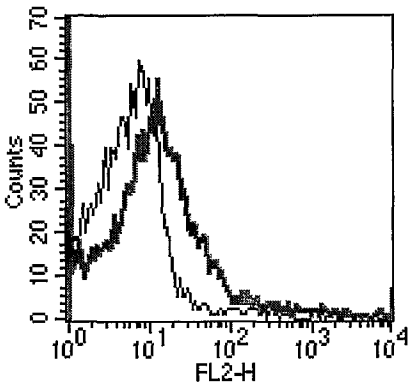



**FIGURE 305**

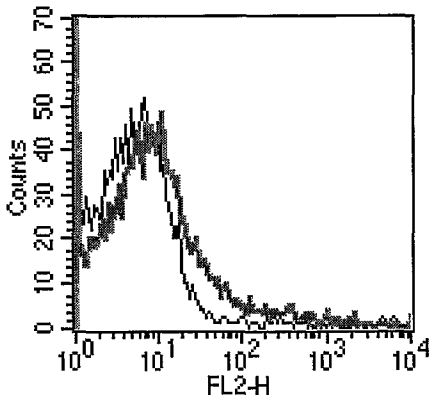



**FIGURE 306**

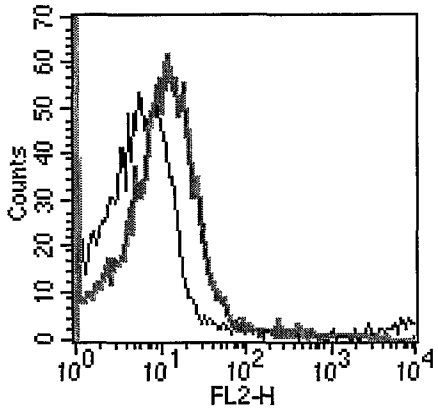



**FIGURE 307**

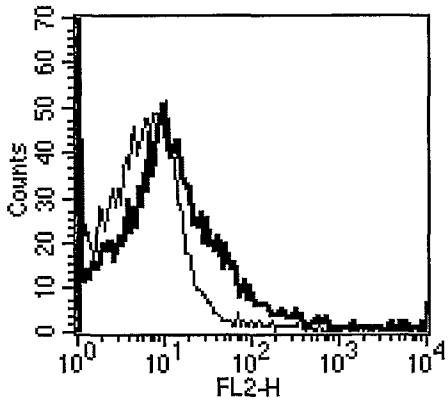



**FIGURE 308**

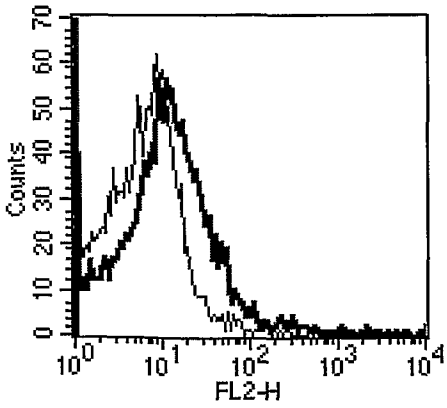



**FIGURE 309**

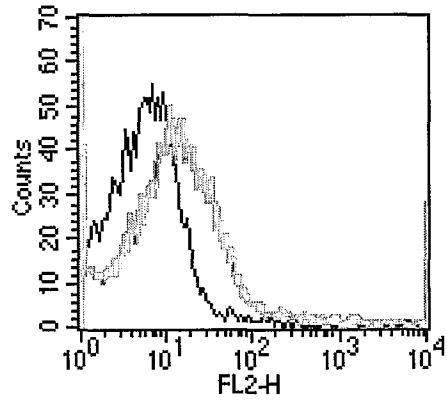


**FIGURE 310**

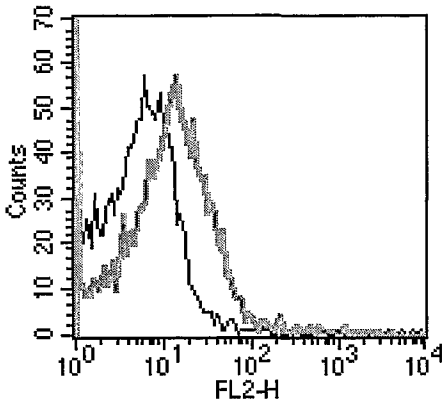



**FIGURE 311**

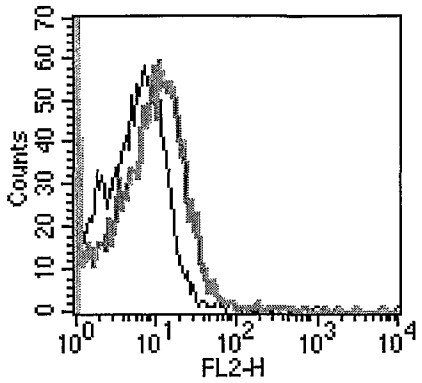



**FIGURE 312**

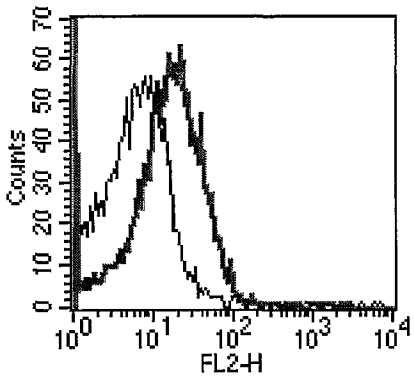



**FIGURE 313**

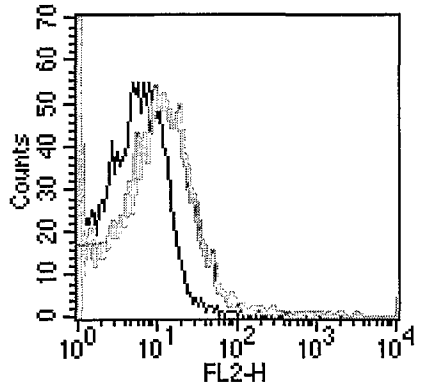



**FIGURE 314**

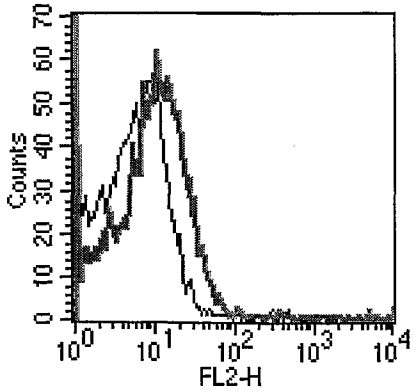



**FIGURE 315**

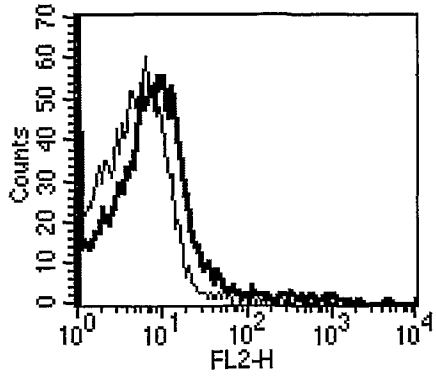


**FIGURE 316**

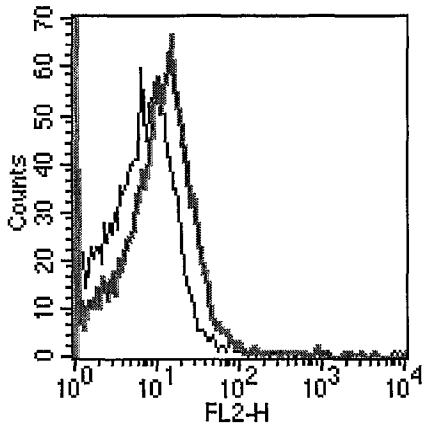



**FIGURE 317**

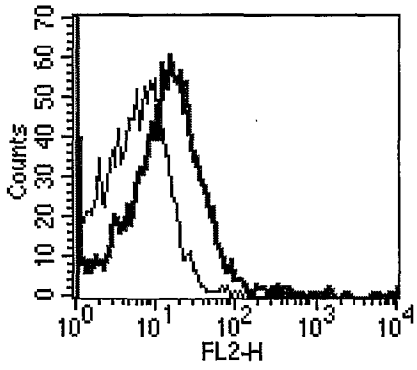



**FIGURE 318**

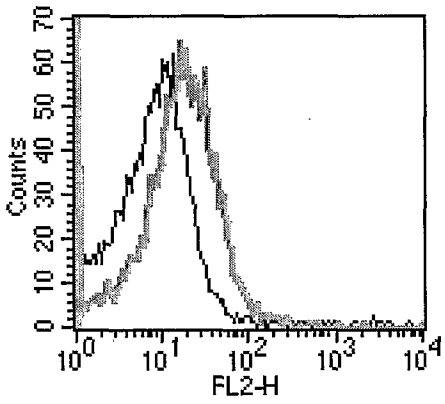
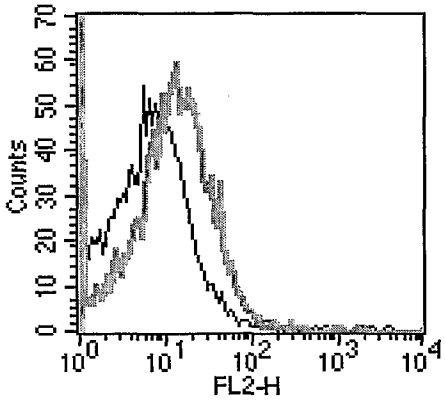



**FIGURE 319**



# SEQUENCE LISTING

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SEQ ID 2

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SEQ ID 4

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SEQ ID 11

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SEQ ID 20

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GCAGGTTATAATACAAAGGTTGAAGAGTTTAATGCTTCCTCTGAGCAAAAACAAATACCTTTGCCTTTAATCGTTGTCATTGTAGATGAATTGGCT
GACTTGATGATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATTCGTTTGGGGCAAAAAGCACGTGCTGCAGGTATCCATATGATTCTTGCAACT
CAACGTCCATCCGTAGATGTTATTTCTGGTTTGATTAAAGCAAATGTTCCGTCGCGTATTGCATTTGCTGTTTCAAGTGGTACTGATAGCCGTACG
ATCCTTGATGAAAATGGTGCTGAAAAGCTCTTGGGACGGGGTGACATGCTCTTTAAGCCTATTGATGAGAATCATCCAGTACGACTACAAGGTTCC
TTTATTTCAGATGATGATGTTGAAAGGATCGTTGGTTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTTTGATCCTGGAGAAGTATCT
GAAACAGATAACGGCTCTGGTGGTGGCGGCGGAGTACCTGAAAGTGATCCTCTTTTTGAAGAAGCCAAGGGACTCGTTTTAGAGACGCAAAAAGCA

AGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTTTCAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTGGTCCAGCA
GAAGGAACCAAGCCACGAAAAGTTTTAATGACTCCAACTCCGAGTGAA

SEQ ID 22

MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIILFFGIIRLGIFGITVYYNVIRFMVGSLAYLFIAATLIYLYFFKWLRKKDSLVAGFL
IASLGLLIEWHAYLFSMPILKDKEILRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIGAYMIGVLFIILGLFLMSSLEVYDIVEFIR
AFKNKVAEKHEQNKKERFAKREMKKAIAEQERIERQKAEEEAYLASVNVDPETGEILEDQAEDNLDDALPPEVSETSTPVFEPEILAYETSPQNDP
LPVEPTIYLEDYDSPIPNMRENDEEMVYDLDDDVDDSDIENVDFTPKTTLVYKLPTIDLFAPDKPKNQSKEKDLVRKNIRVLEETFRSFGIDVKVE
RAEIGPSVTKYEIKPAVGVRVNRISNLSDDLALALAAKDVRIETPIPGKSLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSF
NLARMPHLLVAGSTGSGKSVAVNGIISSILMKARPDQVKFMMIDPKMVELSVYNDIPHLLIPVVTNPRKASKALQKVVDEMENRYELFSKIGVRNI
AGYNTKVEEFNASSEQKQIPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVDVISGLIKANVPSRIAFAVSSGTDSRT
ILDENGAEKLLGRGDMLFKPIDENHPVRLQGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGGVPESDPLFEEAKGLVLETQKA
SASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRKVLMTPTPSE

SEQ ID 23

ATGGTTAAAAGAAATCAAAGAAAAAAAAGTGCGCCTAAGAAGCGTTTAACAAAAGCAGAAGTGGAAAAGCAACGTGCCATTAAGAGGATGATTTTA
TCTGTTTTAATGGCTTTGTTGCTTATTTTTGCGATGCTTCGCTTGGGCGTCTTTGGTGTGACAACTTATAATATGATTCGTTTTTTGGTGGGTAGT
TTAGCCTATCCGTTTATGTTTGCCTGGTTAATTTACTTATTTTGTTTTAAATGGTTACGGCAAAAAGATGGAATGATTGCGGGAGTTGTTATTGCC
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AGAGATTTACTAGCCCTGCGCGTGACTGAATTTGTTGGTGGAGGAATGCTTGGTGCATTACTTTATAAACCCATAGCCTTTTTATTTTCGAATATC
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GTTGATAAACTAGCAGTGGCTTATCAGGAAAATAAAGAAAAGCGGTTCATCAAACGAGAAGAGCACCGCTTACAAGCTGAAAAAGAGGCTTTAGAG
AAACAAGCACAAGAGGAAGAAAAACGTCTAGCAGAATTGACGGTTGATCCTGAGACGGGAGAGATTGTTGAGGATAGTCAGTCTCAAGTCAGCTAT
GATTTGGCTGAGGATATGACAAAAGAACCAGAGATTCTTGCTTATGATAGTCACCTCAAAGACGATGAGACAAGCTTATTTGATCAAGAAGACTTG
GCTTACGCTCATGAGGAAATTGGGGCTTATGACTCTTTATCTGCTTTAGCATCTTCTGAAGATGAGATGGATATGGATGAACCTGTTGAAGTTGAT
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CGCAAAAATATCAAGGTGCTTGAAGATACCTTCCAAAGTTTTGGGATTGATGTCAAGGTAGAGCGAGCAGAAATCGGGCCTTCCGTCACCAAATAT
GAAATCAAGCCAGCTGTCGGGGTCCGAGTTAATCGTATTTCAAATCTTGCTGATGATTTGGCACTTGCTCTGGCTGCTAAAGATGTTCGTATTGAA
GCACCAATTCCTGGAAAATCCTTAATAGGTATTGAAGTTCCTAACTCAGAAATTGCAACGGTTTCTTTCCGCGAACTTTGGGAACAATCTGATGCC
AATCCTGAAAACCTTTTAGAAGTACCACTAGGTAAAGCTGTTAATGGCAATGCGCGCAGTTTTAACTTAGCTAGAATGCCGCATCTTTTGGTAGCT
GGTTCAACTGGTTCAGGTAAATCTGTGGCAGTTAATGGCATTATTTCAAGTATTTTGATGAAGGCACGTCCAGATCAAGTTAAGTTTATGATGATT
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AACTTTATCAAAGACCAAACTGAAGCGGATTATGATGACGCCTTTGATCCTGGTGAAGTTAGCGACAATGATCCTGGTTTTTCTGGAAATGGCGGA
GCTGCTGAAGGTGATCCTCTTTTTGAAGAAGCAAAAGCCTTGGTCTTAGAAACACAAAAAGCTAGTGCCTCAATGATTCAAAGGCGTTTGTCGGTT
GGATTTAATCGTGCCACGCGCTTGATGGATGAATTGGAAGAAGCAGGTGTTATCGGTCCAGCAGAAGGAACCAAGCCTCGTAAGGTATTGCAGACA
AAC

SEQ ID 24

MVKRNQRKKSAPKKRLTKAEVEKQRAIKRMILSVLMALLLIFAMLRLGVFGVTTYNMIRFLVGSLAYPFMFAWLIYLFCFKWLRQKDGMIAGVVIA
FLGLLVEWHAFLFAMPRMLDQDIFLGTARLITRDLLALRVTEFVGGGMLGALLYKPIAFLFSNIGSYFIGFLFILLGLFLMTPWDIYDVSHFVKEA
VDKLAVAYQENKEKRFIKREEHRLQAEKEALEKQAQEEEKRLAELTVDPETGEIVEDSQSQVSYDLAEDMTKEPEILAYDSHLKDDETSLFDQEDL
AYAHEEIGAYDSLSALASSEDEMDMDEPVEVDFTPKTHLLYKLPTIDLFAPDKPKNQSKEKNLVRKNIKVLEDTFQSFGIDVKVERAEIGPSVTKY
EIKPAVGVRVNRISNLADDLALALAAKDVRIEAPIPGKSLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPHLLVA
GSTGSGKSVAVNGIISSILMKARPDQVKFMMIDPKMVELSVYNDIPHLLIPVVTNPRKASKALQKVVDEMENRYELFSKIGVRNIAGYNTKVEEFN
ASSEQKQIPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVDVISGLIKANVPSRMAFAVSSGTDSRTILDENGAEKLL
GRGDMLFKPIDENHPVRLQGSFISDDDVERIVNFIKDQTEADYDDAFDPGEVSDNDPGFSGNGGAAEGDPLFEEAKALVLETQKASASMIQRRLSV
GFNRATRLMDELEEAGVIGPAEGTKPRKVLQTN

SEQ ID 25

ATGCATATTGAGACTGTTATTGATTTCAAAGAATTAGGAAAAAGATATCGTTTTAAAAATCCTACAAAAGAATTAATAGCTGATACTTTAGAACAA
GTCTTAGAAGTGATAAAAGAAGTTGATTATTATCAATCTCAAAATTATTATGTTGTTGGTTATTTATCTTATGAAGCATCTGCTGCTTTTGATTCA
CATTTTAAAGTTTCTCAACAGAAGTTGGCTGGAGAACATCTAGCTTATTTTACAGTACATAAAGATTGTGAGAACGAAGCTTTTCCTTTAAGTTAT
GAAAATGTTAGATTAGCAGATAATTGGACTGCTAATGTTTCTGAGCAAGAATATCAAGAGGCAATTGCTAATATTAAAGGACAAATTAGACAAGGA
AATACTTATCAAGTAAATTATACACTAGAGCTTAGCCAACAATTATGCTCGGATCCCTTTAGTGTTTATGAACGCCTAATGGTAGAACAAGGAGCA
GGATATAATGCTTATATTGCCTACGACGATAAAAGGATTTTATCTGTAAGCCCGGAATTGTTCTTTAAGAAGAAGGATGAAGTCTTAACAACTAGA
CCAATGAAGGGAACAAGCGCTAGAAAGCCTACTTATCAAGAAGATGTGGCGGAGCGAGATTGGTTGGCAAATGATCCTAAAAATCGTTCTGAAAAT
ATGATGATTGTTGATTTATTAAGAAACGATATGGGCCGTATCTGTGATGTTGGAACAGTTAAGGTAAAAAAACTATGTCAAGTGGAGCAGTATGCA
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ACTGGAGCTCCTAAGATATCAACAATGGCTATTATTAATGAGTTGGAAAAACGGCCAAGAGGTATTTATTGTGGGACGATAGGACTTTGCATGCCA
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CAGACAGATTCTGAATATGAAGAAACCCGTCAAAAATCAGCTGTTTTAACACGTGTCAATCCAAAATTTCAATTAATAACTACAGGAAGAGTGACT
GAAAATAAACTTCTTTTCTCTCAACAACATGTCGAGAGATTAGTTGAATCAGCGTCTTATTTTGCTTATTCTTTTGATAAAAGTAAATTCGAAAGG
GAACTGAAAAAATACCTTCATCAGCTAGATGAGAAGGATTACCGCTTGAAAATAATGCTTGATAAAACTGGTAAGGTAACGTTTGAGGTAAAACAA
CTAGTGAATTTATCAAAAAAGTTTTTAACGGCAGAGGTGGTCGTACAAGACTACCCTATTAAATTATCCCCGTTTACTTATTTTAAAACTTCTTAT
CGCCCACATATTATTGAAGGTCAGAATGAAAAGATATTTGTATCTCCTGAGGGGTTGCTATTGGAAACAAGTATTGGGAATATTGTTTTAGAAAAA
AATGGAAGGTTTTTAACCCCAGATTTATCAGAAGGAGGGTTGAATGGGATTTATCGTCGTCATCTCCTTAAAAACCAAAAAGTAATTGAAGCACCA
CTAACTTTAAAAGATTTAGAATCAGCCGATGCTATATACGCCTGTAATGCTGTTAGAGGGCTTTATCCTCTAAACCTAAAG

SEQ ID 26

MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYYVVGYLSYEASAAFDSHFKVSQQKLAGEHLAYFTVHKDCENEAFPLSY
ENVRLADNWTANVSEQEYQEAIANIKGQIRQGNTYQVNYTLELSQQLCSDPFSVYERLMVEQGAGYNAYIAYDDKRILSVSPELFFKKKDEVLTTR
PMKGTSARKPTYQEDVAERDWLANDPKNRSENMMIVDLLRNDMGRICDVGTVKVKKLCQVEQYATVWQMTSTIEGVLSPEVTLMSIFQALYPCGSI
TGAPKISTMAIINELEKRPRGIYCGTIGLCMPDGQAIFNVPIRTVQMKGQQAYYGVGGGITWESQTDSEYEETRQKSAVLTRVNPKFQLITTGRVT
ENKLLFSQQHVERLVESASYFAYSFDKSKFERELKKYLHQLDEKDYRLKIMLDKTGKVTFEVKQLVNLSKKFLTAEVVVQDYPIKLSPFTYFKTSY
RPHIIEGQNEKIFVSPEGLLLETSIGNIVLEKNGRFLTPDLSEGGLNGIYRRHLLKNQKVIEAPLTLKDLESADAIYACNAVRGLYPLNLK

SEQ ID 27

TTGGGTATGCATAGAAAAACTATTATTGATTTCAAAGAGCTCGGGCAACGCTATCTTTTTGATGAGCCATTAGTAGAATTGGTAGCCAAGTCCTTA
GATCAGGTCGGTCCAGTCATTGAAAAAGTACAACACTACCAACAGCTGGGCTATTACGTGGTGGGCTATCTCAGTTATGAAGCAGCTGCTTTTTTT
GACAATGCCCTACAAACCCATAATGACAGACTAGGCAACGAGTACCTTGCCTATTTTACAGTGCACAAAACCTGTCAAAAAAAAGACCTACCTCTT
GATTATGACAGCATTACTATCCCTAACCAATGGGTCAGCGCAACTCAAAAAGAAGCCTATCAAAAAGCCATTGAAACCATTCACCGTGAGATGCAA
CAGGGCAATACTTATCAGGTTAACTACACCCTTCAATTAACTCAGGAACTCAATGCAGCTGATAGTTTAGCCATTTACAATAAACTCGTCGTTGAA
CAGGCTGCTGGCTACAATGCCTACATCGCCCATGATGAGTTTGCCGTTATTTCAGCTAGTCCTGAATTGTTCTTTAAACAAGAGGGCAACAGGTTA
ACTACTAGGCCTATGAAAGGCACCACCAAACGAGGGGTTAATAGCTGGCTGGATCAACAAGAACATGACTGGCTCCAAGCTGACGGGAAAAACCGT
TCTGAAAACATGATGATTGTGGATTTGCTCCGCAATGACATGGGGAAAATTTGCCAAACAGGCAGTGTTCGTGTTGATAGGCTCTGTGAGGTCGAG
CGATACTCTACCGTCTGGCAAATGACCTCAACTATTGTTGGTGACCTCAAAGCGGACTGTGACCTGATAGACATTCTCAAAGCTCTCTTTCCTTGT
GGCTCTATCACAGGGGCACCAAAAGTCTCCACCATGGCAATTATCACATCTCTGGAGCCAAAACCAAGGGGGATTTATTGTGGAAGTATTGGCATT
TGCCTACCTGATGGTCGCCGTTTCTTCAATGTTCCCATTAGAACCATCCAGCTCAGTCATAATCAAGCTACTTATGGTGTCGGAGGCGGCATCACT
TGGCAAAGCAAGTGGGAAGACGAATACGAGGAAGTCCATCAAAAAACAGCTTTTCTCTATCGGCACAAACAAATCTTTGACCTCAAAACAACCGCC
AAGGTGGAACACAAAAAAATAGCCTTCCTTGAGCAACACCTCAATCGCCTTAAAGAAGCAGCCACTTATTTTGCTTACCCTTATAATGAAAAAGCT
TTGCAGAAACAACTGTCAACCTATTTGGAAAATAAGAATAATGCTGCCTACCGTTTGATGATTCGTTTATCCAAAGATGGAAAGATTAGCCTCTCT
GATCAACCCTTGGAACCTTTGTCAGCCGATTTTCTGACAGCTCAACTCTCTTTACAGAAAAAGGACGTGACAGCTTCGCCTTTTACCTACTTTAAG
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GTTCAGCTGGGTCAGACCCTCTACACACCACCAGTGGCTGTGGGGATTTTACCAGGACTTTTTCGCCAAGAACTGCTAGCTACTGGTCAAGCTCAG
GAAAAAGAGGTGACACTAGCTGATTTAAAAGAGGCTAGCGCTATTTTTGGAGGAAATGCTGTCCGTGGCCTTTATCCTCTCAACCTTGAGCTTACT
CACCTTGATGCCCTCTTAGCTAAGAGTCAAGCC

SEQ ID 28

LGMHRKTIIDFKELGQRYLFDEPLVELVAKSLDQVGPVIEKVQHYQQLGYYVVGYLSYEAAAFFDNALQTHNDRLGNEYLAYFTVHKTCQKKDLPL
DYDSITIPNQWVSATQKEAYQKAIETIHREMQQGNTYQVNYTLQLTQELNAADSLAIYNKLVVEQAAGYNAYIAHDEFAVISASPELFFKQEGNRL
TTRPMKGTTKRGVNSWLDQQEHDWLQADGKNRSENMMIVDLLRNDMGKICQTGSVRVDRLCEVERYSTVWQMTSTIVGDLKADCDLIDILKALFPC
GSITGAPKVSTMAIITSLEPKPRGIYCGSIGICLPDGRRFFNVPIRTIQLSHNQATYGVGGGITWQSKWEDEYEEVHQKTAFLYRHKQIFDLKTTA
KVEHKKIAFLEQHLNRLKEAATYFAYPYNEKALQKQLSTYLENKNNAAYRLMIRLSKDGKISLSDQPLEPLSADFLTAQLSLQKKDVTASPFTYFK
TSYRPHIEQKSYEQLFYNQAGQLLETSIGNLFVQLGQTLYTPPVAVGILPGLFRQELLATGQAQEKEVTLADLKEASAIFGGNAVRGLYPLNLELT
HLDALLAKSQA

SEQ ID 29

ATGGTCACAGGAGGATTCCGACTAGACCTCTTACTTGAGATAACTAAGATAGCTCGTGCAACTTACTATTATCAACTAAAGAAACTGAATAAACCA
AATAAAGACAAAGCAATCAAATCTGACATTCAATCCATTTATGATGAACATAGAGGAAACTATGGCTATCGTCGGATTTATTTAGAACTGCGAAAT
CGTGGCTTTGTCATCAACCACAAAAGGGTGCAAGGCTTGATGAAAAGTATGGGCTTGACTGCTCGTATTCGTCGTAAGCGCAAGTATGCCTCTTAC
AAAGGTGAGGTTGGTAAGAAGGCTGATAACCTGATTCAACGCCAGTTTGAGGGGTCGAAGCCCTATGAGAAGTGCTATACCGATGTGACGGAGTTT
GCTTTACCTGAAGGGAAACTTTATCTATCGCCTGTTCTTGATGGCTATAACAGTGAGATAATTGATTTTACCCTGTCTCGGTCTCCTGACTTGAAA
CAGGTTCAAACCATGCTTGAGAGGGCTTTTCCTGCGGCTTCATACAGCGAAACCATTCTCCACAGCGACCAAGGCTGGCAGTACCAGCACAAGTCC
TACCATCAATTTCTGGAGGACAAAGGCATTCGTCCTTCTATGTCACGGAAGGGGAACAGTCCTGACAACGGTATGATGGAATCTTTCTTTGGGATT
CTAAAATCTGAGATGTTCTATGGCTTGGAGAAGTCTTACAAATCACTTGATGACCTTGAGCAAGCTATCACAGATTACATTTTTTACTACAACAAC
AAGCGAATCAAAGCAAAACTAAAAGGACTTAGTCCTGTGCAATACAGAACTAAATCCTTCACT

SEQ ID 30

MVTGGFRLDLLLEITKIARATYYYQLKKLNKPNKDKAIKSDIQSIYDEHRGNYGYRRIYLELRNRGFVINHKRVQGLMKSMGLTARIRRKRKYASY
KGEVGKKADNLIQRQFEGSKPYEKCYTDVTEFALPEGKLYLSPVLDGYNSEIIDFTLSRSPDLKQVQTMLERAFPAASYSETILHSDQGWQYQHKS
YHQFLEDKGIRPSMSRKGNSPDNGMMESFFGILKSEMFYGLEKSYKSLDDLEQAITDYIFYYNNKRIKAKLKGLSPVQYRTKSFT

SEQ ID 31

ATGCTACTTGAAATCCTTGATTTATCACGCTCCACCTATTACTATCAAGTGAAGCGACTAGCTCAAGGAGATAAGGATATAGAACTAAAGCATGTG
ATTCGAGAGATTTATGATGAGCATAAAGGTAATTACGGTTATCGTCGGATTCATATGGAGTTGCGTAACCGAGGATTTGTGGTCAATCATAAGAAA
GTTCAACGTCTCATGAAAGTCATGGGCTTAGCAGCCCGCATTCGTCGGAAGCGCAAGTATTCTTCTTACAAAGGAGAGGTTGGTAAGAAGGCTGAT
AATCTGATTAAACGTCACTTCGAAGGCTCTAAACCTTACGAAAAATGTTACACTGATGTGACGGAGTTGGCCTTACCTGAAGGAAAACTCTACTTA
TCACCTGTTCTTGATGGCTATAACAGTGAGATTATTGATTTCACTCTATCTCGGTCTCCTAACTTGAAACAGGTTCAAACCATGCTTGAGAAGACT
TTTCCAGCAGATTCATACAGCGGAACTATTCTTCATAGTGACCAGGGGTGGCAATACCAACACCAGTCCTACCATGATTTTTTAGAGTCTAAAGGT
ATTCTGGCATCCATGTCCCGCAAAGGGAATAGTCCGGATAACGGCATGATGGAATCCTTCTTTGGCATTCTCAAATCTGAAATGTTTTATGGACTC
GAGACAACTTATCAATCACTTGACAAGCTTGAAGAAGCTATTACAGATTACATTTTTTACTACAACAACAAACGAATTAAAGCAAAACTAAAAGGA
TTTAGTCCTGTCCAATACAGAACTAAATCCTTTCAA

SEQ ID 32

MLLEILDLSRSTYYYQVKRLAQGDKDIELKHVIREIYDEHKGNYGYRRIHMELRNRGFVVNHKKVQRLMKVMGLAARIRRKRKYSSYKGEVGKKAD
NLIKRHFEGSKPYEKCYTDVTELALPEGKLYLSPVLDGYNSEIIDFTLSRSPNLKQVQTMLEKTFPADSYSGTILHSDQGWQYQHQSYHDFLESKG
ILASMSRKGNSPDNGMMESFFGILKSEMFYGLETTYQSLDKLEEAITDYIFYYNNKRIKAKLKGFSPVQYRTKSFQ

SEQ ID 33

ATGAAATTAAGTTATGAAGATAAACTAGAAATATACGAGTTAAGAAAGATCGGGATGTCCTGGTCTCAGATTAGTCAACGATATGATGTTCGTATC
TCGAATCTTAAATACATGATAAAACTCATGGATCGGTATGGTGTAGAAATCGTCGAAAAAGGTAGAAATGAGTATTATCCACCTGAATTAAAGCAG
GAAATGATAGATAAAGTCTTGATTCATGGTTGTTCTCAACTCTCTGTTTCTCTTGATTATGCTCTCTCTAATTGTTCTATACTCACAAATTGGCTT
TCCCAATTTAAGAAAAATGGTTATACTATTGTTGAGAAAACAAGAGGGAGACCGAGTAAAATGGGACGTAAGCGTAAGAAAACTTGGGAAGAAATG
ACAGAGCTCGAGCGACTTCAGGAAGAAAATGAGCGCTTGAGAACGGAGAATGCCTTTCTAAAAAAGTTGAGGGATTTGCGCTTGAGGGACGAAGCC
TTACAGAGCGAACGGCAGAAACAATTAGAGAAATGGTCACAGGAGGATTCCGAC

SEQ ID 34

MKLSYEDKLEIYELRKIGMSWSQISQRYDVRISNLKYMIKLMDRYGVEIVEKGRNEYYPPELKQEMIDKVLIHGCSQLSVSLDYALSNCSILTNWL
SQFKKNGYTIVEKTRGRPSKMGRKRKKTWEEMTELERLQEENERLRTENAFLKKLRDLRLRDEALQSERQKQLEKWSQEDSD

SEQ ID 35

ATGAAATTTAATCAAGAAACGAAAGTTAAGATTTATGAGTTACGGCAAATGGGAGAGTCCATTAAATCCATATCAAAAAAGTTTGATATGGCAGAA
TCCGATCTCAAATATATGATTCGCTTGATTGATAGGTATGGGGTAACCATTGTTCAAAAATGTAAGAATCATTATTATTCTCCAGAACTGAAGCAA
GAGATAATAAATAAAGTCCTGATTGACGGCCAATCTCAGAAACAAACATCCTTAGATTATGCTTTACCAACTTCTAGTATGCTCTCAAGGTGGATA
GCGCAATACAAGAAAAACGGTTATACTATTCTTGAAAAACCAAGAGGGAGACCGAGTAAGATGGGGCGTAAACGTAAGAAAAATTTGGAAGAGATG
ACAGAGGTTGAACGTCTTCAGAAGGAATTAGAATACCCTAGAGCGGAGAATGCTGTGCTAAAAAAGCTGAGAGAATACCGCTTGAGGGACGAAGCA
AAACTCAAAGAGCAACAGAAATCATTCAAGCAT

SEQ ID 36

MKFNQETKVKIYELRQMGESIKSISKKFDMAESDLKYMIRLIDRYGVTIVQKCKNHYYSPELKQEIINKVLIDGQSQKQTSLDYALPTSSMLSRWI
AQYKKNGYTILEKPRGRPSKMGRKRKKNLEEMTEVERLQKELEYPRAENAVLKKLREYRLRDEAKLKEQQKSFKH

SEQ ID 37

TTGAAAAATCAACAAAAATTAATGTATCTAGAGAGTATCGAGCTATACTCAAACATCACTAAAGCCGCTGCACACCTTTTTATTTCTCAACCTTAC
CTAAGCAAAGTGATCAAGCAATTAGAAAATGAGTTAGAAATAAAACTCATCCAGAGCCAAGGACACCAAACCTTTTTAACTTATGCTGGACAGAGA
TATCTATTCTACCTAAAAGAAATTGATATGATTGAGCGTCAAATGGCCAAAGAACTATATCTCATCCGTTCTGATAAAAAAGGAGAAATCACACTT
GGGATTAACTCTGGCTTAGCAAGTTCTATTCTGGCAAATGTACTTCCCAAATTTAACTTGGAGCACCCAGAAATTTCTGTCAAATTACTCGAAAAC
AATCAAAATATTTCTGAACAATTGGTAGCGAGTGGTGATATTGACCTAGCTGTTGGGATGGCTCCTATCCTTTATAAAGATGGAATTGCATCAACC
ACTATTTACCGCGACGAATTGTTTTTAATGATACCTACCACCAGCCAACTCTACAACGCTGAAAAACGTGGACAGATTATTCCTTTTGAATATCCT
ATTTCAGTTCTAGACAATGAACCTCTTATCCTAACACCATTAGAGTACGGAATTGGCAAAACAATTGCACAATTCTATGAGCTTCATCACATGTCA
TTAAATCAGATGATTACAACTAGTACCGTTCCTACAGCAGCTAGCCTATCTTTGTCAGGGATGGGAGCAACATTTGTTCCACAAACTCTCATTCAT
CGCTATTTGGATAAAGAGTGCAATGTCTACCATTTTCATAAGAATAAGTTATTTTCAGAGTACATTATGATTTATAAAAAAGATGTTGAATTATCT
GGAATTGCTCTCCTACTTTATAAAGCTTTTTTAACCAAG

SEQ ID 38

MKNQQKLMYLESIELYSNITKAAAHLFISQPYLSKVIKQLENELEIKLIQSQGHQTFLTYAGQRYLFYLKEIDMIERQMAKELYLIRSDKKGEITL
GINSGLASSILANVLPKFNLEHPEISVKLLENNQNISEQLVASGDIDLAVGMAPILYKDGIASTTIYRDELFLMIPTTSQLYNAEKRGQIIPFEYP
ISVLDNEPLILTPLEYGIGKTIAQFYELHHMSLNQMITTSTVPTAASLSLSGMGATFVPQTLIHRYLDKECNVYHFHKNKLFSEYIMIYKKDVELS
GIALLLYKAFLTK

SEQ ID 39

TTGATAAGACAAGGAGAATCCTATTTGGATATTAAACAAATTCGTTATTTTATCGCAATCGTTGAAAATCATTTTAACTTGAGCCAGGCGGCGGAA
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AAAGGGTTAAAGGGAAGTATCAATATTGGTATTCCTCCTCTTATTTTATCAGTTGTTTTCTCAGAAGTAATGCCAAAACTGATTTTAGAAAATCCG
GGGATTCAATTCAATGTTAAGGAGATTGGTGCTTACCAACTAAAAAATGAACTACTCGTGGGAAATGTTGACGTCGCAGTCTTGTTATCCCCAACA
GGCATCGCTGATAATTTGGTTGAGACTTATGAAATCCAGAGATCAGAATTATCTGTATGCCTGTCTCCACGCCATCGTTTAGCTTCCAAAAAAGTT
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GTCAGACCTAATATTATTTTGACGTCCTCTTCCTGGGATTTTATGCTTAATTCTACCAAGATTAATCACAACGTCTTAACTATTTGTCCCAAACCT
ATTACAGAATTATACCAATTAAAGGACATTAAGTGTATTCCAATGGAACGTCCCATTTCTTGGCGTGTTGTCTTAACACGCCTCCGGAAAAAAAGT
TATTCTGAAATAGAAGCCTACATCATGGACGACTTGCTACAGTCTTTTTTTAAG

SEQ ID 40

LIRQGESYLDIKQIRYFIAIVENHFNLSQAAELLYVSQPTLSMMINDFEKRENVKLFKRKRGRIIGLTYLGDNYYKDAQKVLSLYDDMFLKLHDHS
KGLKGSINIGIPPLILSVVFSEVMPKLILENPGIQFNVKEIGAYQLKNELLVGNVDVAVLLSPTGIADNLVETYEIQRSELSVCLSPRHRLASKKV
IQWEDLTDEQLALFDPSFMVHHLVLEACERHQVRPNIILTSSSWDFMLNSTKINHNVLTICPKPITELYQLKDIKCIPMERPISWRVVLTRLRKKS
YSEIEAYIMDDLLQSFFK

SEQ ID 41

ATGGCCAATGCATCTTTGCGACATCAATTATTTGAAAAACTTGACCAAAAATGTGATCAAATGGTTGCTATTCGTCGCTATTTACATGAAAATCCC
GAATTATCATTTAAAGAGACAAAAACAGCAGCTTATATTTCAGATTTTTATAAAGGTAAGGACTGTCATGTTCAGACACAATTTGGTGGTATGAAT
GGCGTCGTAGTTGATATCTATGGTGATAAAGCGACAGATAAGCCCATCAAACACATTGCTTTGAGAGCCGACTTTGATGCTCTTCCAATTCAGGAA
GAGACAGGGCTTTCTTTTGCTTCAAAAACAGCGGGCGTCATGCATGCTTGTGGACATGATGCCCATACAGCTTATTTATTGATTTTGGCTGAGAGC
TTGATTGAATTAAAATCAGAATTTTCAGGTCATATCCGTATCTTACATCAACCGGCTGAAGAGGTGCCACCAGGCGGAGCAAAAGCAATGATTGAA
GCAGGATGTTTAGATGGCATTGATGCTGTCCTTGGTATCCATGTTATGTCAACGATGGAAGAGGGAACGGTACAATATCACGCAGGTCCCATTCAA
ACAGGGCGTGCCACTTTTAAAGTTATTTTGCAAGGTAAGGGTGGACATGGTTCCATGCCACATCGTGCAAATGATACAATTGTTGCAGCTTCTAGT
TTTGTTATGGCAGCGCAAACGATTGTCAGTCGTCGAGTTAATCCATTTGACACAGCAGTAGTTACTATCGGATCTTTTGATGGTAAAGGTTCTGCT
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GATGGAATAGCACAAACTTATGGTGTTAGTTATCAGTTAGACTATCAGAATGATTATCCTGTTTTAGTTAATAACAGTGAAGTGACACAGAAAGTT
GCAAATAGTTTAAAATCTGTTGCTATAAAAGAAATTTTAGATGTCATTGATTGCGACCCTCAAACGCCGTCTGAAGATTTTGCCTATTATGCTCAA
ACAATCCCAGCTTGCTTCTTCTATGTTGGAGCACATGAAGAGGGGCAACCATATTACCCACATCATCATCCAAAATTCCAAATTGCAGAATCATCA
TTGATGGTATCTGCTAAATCAATGGCAACAGCAGCGCTTGCTATGCTTGTAGAAGGAGAA

SEQ ID 42

MANASLRHQLFEKLDQKCDQMVAIRRYLHENPELSFKETKTAAYISDFYKGKDCHVQTQFGGMNGVVVDIYGDKATDKPIKHIALRADFDALPIQE
ETGLSFASKTAGVMHACGHDAHTAYLLILAESLIELKSEFSGHIRILHQPAEEVPPGGAKAMIEAGCLDGIDAVLGIHVMSTMEEGTVQYHAGPIQ
TGRATFKVILQGKGGHGSMPHRANDTIVAASSFVMAAQTIVSRRVNPFDTAVVTIGSFDGKGSANVIKDSVTLEGDVRVMSEETRGVVEEEFKRIL
DGIAQTYGVSYQLDYQNDYPVLVNNSEVTQKVANSLKSVAIKEILDVIDCDPQTPSEDFAYYAQTIPACFFYVGAHEEGQPYYPHHHPKFQIAESS
LMVSAKSMATAALAMLVEGE

SEQ ID 43

ATGTTAACGACAAAGGAAAATTTCAAAGGAAATAACAAATTATTGGTGGGAATTGTACTCGCTGTACTATCATTTTGGTTATTTGCACAGTCTATT
TTAAACATGGGACCAGATGTTCAGTCATCATTAGGTATTTCATCTGGTGCAATGGATATTGGTGTCTCAAGTACGGCATTGTTTTCAGGTTTATTT
ATTGTTGTAACTGGTGGTTTAGCAGATAAACTTGGTCGAGTTAAATTTACTTTTATTGGTCTTTGCTTAAATATTATTGGTTCTCTACTAATTGTT
TTAGCTAATGGAGCAGTGCTATTTATTATGGGACGTATTTTTCAAGGATTGGCAGCAGCTTTTATTATGCCATCAACAATGGCCTTGGTTAAAACG
TACTATGATGGTAAAGATAGACAACGTGCAGTTAGTTTCTGGTCAATCGGATCGTGGGGTGGCTCAGGTCTATGTTCTTATTTTGGTGGAGCGGTG
GCAAGTACTCTAGGTTGGCGTTATGTCTTTATCTTTTCAATCATCGCATCAGTAGTTAGTTTTCTATTAATTTTAGGAACCCCAGAAAGTAAAAAT
GTTGGACAAAAAACTCACTTTGATTACCTTGGTTTAATTATTTTTATTATTTCAATGTTATCGTTAAATATTGGGATATCTATGGCTCAGGAACAT
GGATTGATGAACGTTATTCCATTGAGTCTTTTTACAGTGATGCTTATTGGATTTGTTCTGTTTTATTATGTTGAAACACGTAAATCTAATAGTTTT
ATTGACTTTCATCTGTTTGAAAATCGATTTTACTTAGGTGCGACAATATCAAATTTCTTACTGAATGCAGTTGCAGGAACTCTGATTGTTATTAAT
ACTTACATGCAACAAGGTCGCCAGCTAACACCAAAGGTTGCAGGTGAAATGTCTTTAGGCTATTTGGTTTGTGTACTAATTGCTATCCGAGTTGGT
GAGAAAATTTTACAACGTTTTGGTGCCCGTAAGCCAATGCTTTTGGGAGCTATGAGTACATTTGTTGGGATATTTTTAATGACTTTGGTCAATATT
CAAGGACCTTTGTATCTTGTGTTAGTCTTTGTTGGTTATGCTTTATTTGGAACAGGCTTGGGGATCTATGCGACACCATCAACAGATACAGCTATT
TCTAGTATTCCTAATGAAAAAGTAGGTTCTGCATCTGGAATTTACAAAATGGCAAGTTCACTAGGTGGTGCAATTGGTGTAGCAACTTCAATTGCG
ATTTATCATGCTTTTTCTGGTAATGCAGATTTTCACAAAGCAGCTTTGTGTGGATTAATTTTAAACCTAGTTTTTTGTAGTCTATCGATCTTATCA
ATTCTTTTTGTTATCCCTAAGAAAATTGAGGATAAA

SEQ ID 44

MLTTKENFKGNNKLLVGIVLAVLSFWLFAQSILNMGPDVQSSLGISSGAMDIGVSSTALFSGLFIVVTGGLADKLGRVKFTFIGLCLNIIGSLLIV
LANGAVLFIMGRIFQGLAAAFIMPSTMALVKTYYDGKDRQRAVSFWSIGSWGGSGLCSYFGGAVASTLGWRYVFIFSIIASVVSFLLILGTPESKN
VGQKTHFDYLGLIIFIISMLSLNIGISMAQEHGLMNVIPLSLFTVMLIGFVLFYYVETRKSNSFIDFHLFENRFYLGATISNFLLNAVAGTLIVIN
TYMQQGRQLTPKVAGEMSLGYLVCVLIAIRVGEKILQRFGARKPMLLGAMSTFVGIFLMTLVNIQGPLYLVLVFVGYALFGTGLGIYATPSTDTAI
SSIPNEKVGSASGIYKMASSLGGAIGVATSIAIYHAFSGNADFHKAALCGLILNLVFCSLSILSILFVIPKKIEDK

SEQ ID 45

ATGTCACATCATCAACAAACCGTTTCAAAACAAACAATTATGGCGATTATCGCCATAGCACTCATTGGTTTTTCAGGAATTTTGTCTGAAACCAGT
ATGAATGTCACCTTCCCGACACTGATGTCAGTCTATCAGTTACCCTTAAATAGCTTGCAATGGATGACGACCATTTATTTACTAGCAGTGGCGATT
ATGATGACCACTTCGGCTACACTGAAAAAAAATGTGCGGGAAAGACCCCTCTTTTTTATGGCCACAGGTCTTTTTACATTTGGCACCATCTTGGCC
GTTCTGACCCAGTCCTTTGCGATCATGTTGCTAGCCCGCATTTTTCAAGGCATTGGTACTGGTCTGGTAATGCCTCAGATGTTTAATATTATTTTA
GAGCGTGTCCCAATGCATAAGGTAGGTCTATTTATGGGATTTGCTGGTCTTATTATTAGCTTAGCACCTGCTTTTGGGCCTACTTATGGGGGCTTT
ATGATTAGCCATTTTAGTTGGCAATGGATTTTTATCTGTATACTCCCTGTACCACTGATTGCAGGTATTCTAGCTTATTATTACCTCGAAGATTCT
CCAGTAAGCGAAAAAGTACCCTTTGACTGGTTGGCATTTATTGCACTATCGATTAGCTTAACTTCTGCCTTATTAGCTATTACTAGTCTAGAAAAC
GGCAGTGTTAATTTGTATTACTTAGGGCTTTTTATTCTCAGCTTTATCCTCTTCCTCTACAAGAATCTCACAGCTAAGCAACCCTTTCTTGATATT
CGCATTCTCAAAATTCCCTCTCTAACCTTTGGCCTGATTCCCTTTTTTGTCTTCCAGCTGATTAATTTAGGCATAAATTTTCTAACGCCAAACTTT
ATTGTCATGGAAAAGATTGCTAATAGTTCTCAAGCTGGTATGGTGTTACTACCTGGTACCTTACTCGGAGCTCTACTAGCACCTGCTTTTGGTAAA
CTTTATGATCAAAAAGGAGCAAGACTTTCGCTTTATTTAGGAAATGCCTTATTTAGTTTATCATTGATTATTATGACACTTCAAACAAGACATTTT
ATGCTTTTACCATTCACTCTTTTATATATTTTATTCACGTTTGGGCGTAACATGGGCTTTAATAATAGCTTAGCCACGGCTATTCGAGAATTGCCT
GCCGAGAAAAATGCCGATGCCACGGCCATTTTTCAGATGATGCAGCAATTTGCTGGCGCTCTAGGAACTGCTATGGCATCACTGATAGCAAATAGT
CAAGCAGAATTCACAAGCGGTGTCCAGTCTGTCTACCTTCTCTTTACTATTTTTGCTCTACTTGATTTTATCTTTTTCTTTGCTATGTTTTACCAT
TTAGGGAAAAAAGGATTAGCC

SEQ ID 46

MSHHQQTVSKQTIMAIIAIALIGFSGILSETSMNVTFPTLMSVYQLPLNSLQWMTTIYLLAVAIMMTTSATLKKNVRERPLFFMATGLFTFGTILA
VLTQSFAIMLLARIFQGIGTGLVMPQMFNIILERVPMHKVGLFMGFAGLIISLAPAFGPTYGGFMISHFSWQWIFICILPVPLIAGILAYYYLEDS
PVSEKVPFDWLAFIALSISLTSALLAITSLENGSVNLYYLGLFILSFILFLYKNLTAKQPFLDIRILKIPSLTFGLIPFFVFQLINLGINFLTPNF
IVMEKIANSSQAGMVLLPGTLLGALLAPAFGKLYDQKGARLSLYLGNALFSLSLIIMTLQTRHFMLLPFTLLYILFTFGRNMGFNNSLATAIRELP
AEKNADATAIFQMMQQFAGALGTAMASLIANSQAEFTSGVQSVYLLFTIFALLDFIFFFAMFYHLGKKGLA

SEQ ID 47

ATGAGTTTATCCATCATGACAAAACACAAACACCTAACTCTCTTAGACCGTAATGACATCCAATCTGGTTTGGATAGAGGAGAAACCTTTAAAGCC
ATCGGGCTTAATCTACTGAAACACCCTACTACTATCGCAAAAGAAGTCAAACGAAATAAGCAACTAAGAGAATCAACCAAAGACTGCCTAGACTGT
CCGCTACTAAGAAAAGCTCCCTATGTTTGTAATGGGTGTCCAAAGAGGAGGATCAACTGTGGTTACAAGAAGACCTTCTATCTTGCTAAGCAAGCT
CAAAGAAACTATGAAAAACTTTTAGTTGAATCTAGAGAAGGAATCCCTTTGAACAAAGAGACCTTCTGGAAAATAGATAGAGTGCTTTCTAATGGG
GTCAAGAAGGGCCAACGTATCTATCATATCCTCAAAACCAACGATCTAGAAGTGAGTTCTTCAACCGTTTATCGACACATCAAGAAAGGCTACCTA
TCCATCACACCAATCGACCTACCCAGAGCTGTGAAGTTCAAAAAAAGGCGAAAGAGCACACTCCCTCCTATTCCAAAAGCGATTAAAGAAGGGCGA
CGGTACGAGGATTTTATAGAACACATAACNNNNNTTAAT

SEQ ID 48

MSLSIMTKHKHLTLLDRNDIQSGLDRGETFKAIGLNLLKHPTTIAKEVKRNKQLRESTKDCLDCPLLRKAPYVCNGCPKRRINCGYKKTFYLAKQA
QRNYEKLLVESREGIPLNKETFWKIDRVLSNGVKKGQRIYHILKTNDLEVSSSTVYRHIKKGYLSITPIDLPRAVKFKKRRKSTLPPIPKAIKEGR
RYEDFIEHITXXN

SEQ ID 49

ATGGCTAAAAAAGTTGAAAAACTTGTAAAACTTCAAATTCCTGCTGGTAAAGCAACTCCAGCTCCACCAGTTGGACCAGCACTTGGTCAAGCAGGA
ATCAACATCATGGGATTCACTAAAGAGTTTAACGCTCGTACAGCTGATCAAGCTGGTATGATTATTCCAGTTGTTATCTCAGTATATGAAGACAAA
TCATTTGATTTCATCACTAAAACACCACCAGCTGCTGTTCTTTTGAAAAAAGCTGCAGGTGTTGAAAAAGGATCAGGTGAACCTAACAAAACTAAA
GTTGCAACAATTACTCGTGCGCAAGTACAAGAAATTGCTGAAACTAAAATGCCAGATTTAAACGCTGCAAACCTTGAGTCTGCAATGCGTATGATC
GAAGGTACTGCTCGTTCTATGGGATTCACTGTTACTGAC

SEQ ID 50

MAKKVEKLVKLQIPAGKATPAPPVGPALGQAGINIMGFTKEFNARTADQAGMIIPVVISVYEDKSFDFITKTPPAAVLLKKAAGVEKGSGEPNKTK
VATITRAQVQEIAETKMPDLNAANLESAMRMIEGTARSMGFTVTD

SEQ ID 51

ATGCAATATTGCATATCTGTGGGAGGTAAAAATCTCAATTACCGCCAAAACCACAACAGGAGGATTTTTAAAATGGCTAAAAAAGTCGAAAAACTT
GTAAAACTTCAAATCCCTGCTGGTAAAGCTACACCAGCTCCACCAGTTGGACCAGCTCTTGGTCAAGCAGGTATCAACATCATGGGCTTCACTAAA
GAATTTAACGCTCGTACAGCTGATCAAGCTGGTATGATCATCCCAGTTGTTATCTCAGTTTATGAAGACAAATCATTTGATTTCATCACTAAAACA
CCACCAGCTGCTGTTCTTTTGAAAAAAGCTGCAGGTGTTGAAAAAGGATCAGGTACACCTAACACTACTAAGGTTGCGACAGTTACTCGTGCACAA
GTACAAGAAATTGCTGAAACTAAGATGCCAGATTTGAACGCTGCAAACATTGAAGCTGCAATGCGTATGATCGAAGGTACTGCTCGTTCTATGGGA
TTCACTGTTACTGAC

SEQ ID 52

MQYCISVGGKNLNYRQNHNRRIFKMAKKVEKLVKLQIPAGKATPAPPVGPALGQAGINIMGFTKEFNARTADQAGMIIPVVISVYEDKSFDFITKT
PPAAVLLKKAAGVEKGSGTPNTTKVATVTRAQVQEIAETKMPDLNAANIEAAMRMIEGTARSMGFTVTD

SEQ ID 53

ATGGCTAAAAAAAGTAAAAACTTACGTGCTGCTCTTGAGAAAATTGATAGCACTAAAGCATACAGCGTAGAAGAAGCTGTAGCTCTTGCAAAAGAA
ACTAACTTTGCTAAATTTGATGCAACTGTTGAAGTTTCTTATAACCTTAACATTGACGTTAAAAAAGCTGACCAACAAATCCGTGGTGCTATGGTT
TTACCAGCAGGTACTGGTAAAACTTCACGTGTTCTTGTTTTTGCTCGTGGTGCTAAAGCTGAAGAAGCTAAAGCAGCAGGTGCAGACTTTGTCGGT
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CGTGTCCTTGGACCTCGTAACTTGATGCCAAACCCTAAAACTGGTACAGTAACTATGGACGTTGCTAAAGCAGTTGAAGAGTCTAAAGGTGGTAAA
ATTACTTACCGTGCTGATAAAGCAGGTAACGTCCAAGCCCTTATTGGTAAAGTTTCATTTGATGATGCTAAATTAGTTGATAACTTCAAAGCATTT
AATGATGTTATTGTTAAAGCTAAACCAGCTACTGCAAAAGGAACTTACATCACAAACCTTTCAATTACAACAACACAAGGTGTTGGTATCAAAGTT
GATCCTAACTCACTT

SEQ ID 54

MAKKSKNLRAALEKIDSTKAYSVEEAVALAKETNFAKFDATVEVSYNLNIDVKKADQQIRGAMVLPAGTGKTSRVLVFARGAKAEEAKAAGADFVG
EDDLVAKIQGGWLDFDVVIATPDMMALVGRLGRVLGPRNLMPNPKTGTVTMDVAKAVEESKGGKITYRADKAGNVQALIGKVSFDDAKLVDNFKAF
NDVIVKAKPATAKGTYITNLSITTTQGVGIKVDPNSL

SEQ ID 55

ATGGCTAAAAAAAGCAAACAAATGCGTGCTGCACTTGAAAAAGTAGATAGCACAAAAGCGTACAGTGTAGAAGAAGCTGTAGCATTAGTAAAAGAA
ACGAACTTCGCAAAATTTGATGCGTCTGTTGAAGTTGCTTACAACTTGAACATTGACGTTCGTAAAGCAGACCAACAAATCCGTGGCGCAATGGTA
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GAAGACGACCTTGTTGCAAAAATCAATGGTGGATGGCTTGACTTTGACGTTGTTATCGCAACGCCAGACATGATGGCTATCGTAGGTCGTCTTGGA
CGTGTCCTTGGACCTCGTAACTTGATGCCAAACCCTAAAACTGGTACAGTAACGATGGATGTTGCTAAAGCCGTTGAAGAGTCTAAAGGTGGTAAA
ATCACTTACCGTGCTGACAAAGCAGGTAATGTTCAAGCTCTTATTGGTAAAGTTTCATTTGATGCTGACAAATTGGTTGAAAACTTCAAAGCCTTC
CACGATGTAATGGCTAAAGCTAAACCTGCAACAGCTAAAGGAACTTACATGGCAAACGTCTCAATCACATCAACACAAGGTGTTGGTATCAAGGTT
GATCCTAACTCACTT

SEQ ID 56

MAKKSKQMRAALEKVDSTKAYSVEEAVALVKETNFAKFDASVEVAYNLNIDVRKADQQIRGAMVLPNGTGKTQRVLVFARGAKAEEAKAAGADFVG
EDDLVAKINGGWLDFDVVIATPDMMAIVGRLGRVLGPRNLMPNPKTGTVTMDVAKAVEESKGGKITYRADKAGNVQALIGKVSFDADKLVENFKAF
HDVMAKAKPATAKGTYMANVSITSTQGVGIKVDPNSL

SEQ ID 57

TTGGTAAAAATGAGACGTAACATATTATTGAGCATTACTTGTTTATTGATGGTGACTCTGACTGCATGCCATTCACAGGATAGCAAAAGTCATAAA
CTAAACAGTGATAAACTCACGCTTGCTTGGGGAGAAGACTTTGGTGATGTTAATCCGCATCGCTATAACCCTGATCAGTTTGTTATCCAGGATATG
GTTTATGAGGGGTTGGTACGATATGGTGACAATGGGAAAATTGAACCAGCTTTAGCGAAAAGCTGGAGCATTAGTCAAGATGGAAAAACCTACACT
TTTAAATTGAGAAATGCTAAATATTCTGATGGCAGTAACTTTAATGCTGCGAATGTCAAACGTAATTTTGATAGTATTTTTTCGAAGTCTAATAGA
GGTAATCATAATTGGTTTAATTTAACGAATCAATTGGAAAATTATCGTGCCTTGAATCAAAGTACTTTTGAAATTAAACTGAAACAAGCTTATAGT
GCTACTTTATATGATCTCTCTATGATTCGACCAATTCGCTTTTTATCTGATAGCGCTTTCCCTAAAGGTGATGATACAACTAAGAAGAATGTAAAA
AAACCAATTGGAACGGGTCAATGGGTTGTGAAAAGTAAAAAGCAAAATGAATATATTACCTTCAAACGTAATGAGAATTACTGGGGAAAGAAACCA
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GCTAAGGAAAGTATTTTCCAAGATAAAAAAGTTCGTCAGGCAATGAATCATGCTATTGACAAGGTTTCTATTGCTAAGAACACCTTTAGAGGAACA
GAAAAGCCAGCAGACACTATTTTTTCAAAATCAACATCTCACTCAGATGCTAAGTTAAATCCTTATAGCTATAATGTTGATAAAGCAAATCAGCTA
TTGGATCAAGCTGGTTGGAAGATGGGAAAAGATAAGGTTCGTGAAAAAGATGGTAAAACTCTAACCTTACGTCTTCCTTATATCGCCACTAAGGCA
ACTGATAAAGACCTGGTAACTTATTTCCAAGGAGAATGGCGTAAAATCGGTATTAATGTTTCTCTTATTGCTATGGAAGAAGATGATTATTGGGCT
AATGCTAAAAAGGGTAATTTTGATATGATGTTAACCTATTCTTGGGGAGCACCATGGGACCCTCATGCTTGGATGTCGGCATTAACTGCCAAGGCA
GATCATGGACATCCAGAAAATATAGCTTTAGAAAATCTAGCAACTAAAACTGAAATGGATAGACTTATTAAGTCAGCTCTAGTAGATCCTAAGGAA
GAAAATGTTGATAGAGACTATAAGAAGGTTCTTGAATTATTGCATGATGAGGCTGTATATATCCCATTAACTTATCAATCGGTGATTTCTGTTTAT
AGGAAAGGTGATTTTAAAACCATGCGTTTTGCGCCAGAAGAAAATTCATTCCCATTACGCTATATAGAAAAAAACAATGTATCTAAG

SEQ ID 58

MVKMRRNILLSITCLLMVTLTACHSQDSKSHKLNSDKLTLAWGEDFGDVNPHRYNPDQFVIQDMVYEGLVRYGDNGKIEPALAKSWSISQDGKTYT
FKLRNAKYSDGSNFNAANVKRNFDSIFSKSNRGNHNWFNLTNQLENYRALNQSTFEIKLKQAYSATLYDLSMIRPIRFLSDSAFPKGDDTTKKNVK
KPIGTGQWVVKSKKQNEYITFKRNENYWGKKPKLKEVTVKVIPDAQTRALAFESGDVDLIYGNGIIGLDTFAQYTKDKKYVTAISQPMSTRLLLLN
AKESIFQDKKVRQAMNHAIDKVSIAKNTFRGTEKPADTIFSKSTSHSDAKLNPYSYNVDKANQLLDQAGWKMGKDKVREKDGKTLTLRLPYIATKA
TDKDLVTYFQGEWRKIGINVSLIAMEEDDYWANAKKGNFDMMLTYSWGAPWDPHAWMSALTAKADHGHPENIALENLATKTEMDRLIKSALVDPKE
ENVDRDYKKVLELLHDEAVYIPLTYQSVISVYRKGDFKTMRFAPEENSFPLRYIEKNNVSK

SEQ ID 59

TTGATTGTGTCAAAATACCTAAAATACTTCTCTATTATCACGTTATTTTTGACTGGGCTTATTTTAGTTGCATGTCAACAACAAAAGCCTCAAACA
AAAGAACGTCAGCGCAAACAACGTCCAAAAGACGAACTTGTCGTTTCTATGGGGGCAAAGCTCCCTCATGAATTCGATCCAAAGGACCGTTATGGA
GTCCACAATGAAGGGAATATCACTCATAGCACTCTATTGAAACGTTCTCCTGAACTAGATATAAAAGGAGAGCTTGCTAAAACATACCATCTCTCT
GAAGATGGGCTGACTTGGTCGTTTGACTTGCATGATGATTTTAAATTCTCAAATGGTGAGCCTGTTACTGCTGATGATGTTAAGTTTACTTATGAT
ATGTTGAAAGCAGATGGAAAGGCTTGGGATCTAACCTTCATTAAGAACGTTGAAGTAGTTGGGAAAAATCAGGTCAATATCCATTTGACTGAGGCG
CATTCGACATTTACAGCACAGTTGACTGAAATCCCAATCGTCCCTAAAAAACATTACAATGATAAGTATAAGAGCAATCCTATCGGTTCAGGACCT
TACATGGTAAAAGAATATAAGGCTGGAGAACAAGCTATTTTTGTTCGTAACCCTTATTGGCATGGGAAAAAACCATACTTTAAAAAATGGACTTGG
GTCTTACTTGATGAAAACACAGCACTAGCAGCTTTAGAATCTGGTGATGTTGATATGATCTACGCAACGCCAGAACTTGCTGATAAAAAAGTCAAA
GGCACCCGCCTCCTTGATATTCCATCAAATGATGTGCGCGGCTTATCATTACCTTATGTGAAAAAGGGCGTCATCACTGATTCTCCTGATGGTTAT
CCTGTAGGAAATGATGTCACTAGTGATCCAGCAATCCGAAAAGCCTTGACTATTGGTTTAAATAGGCAAAAAGTTCTCGATACGGTTTTAAATGGT
TATGGTAAACCAGCTTATTCAATTATTGATAAAACACCATTTTGGAATCCAAAAACAGCCATTAAAGATAATAAAGTAGCTAAAGCTAAGCAATTA
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AAGTCACATGACTCAGCCTTACTTTATGCCGGAGGACGTCATCACGCGCAGCAATTTTATGAATCGCATCATCCAAGCCTAGCAGGGAAAGGTTGG
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TTAGCGCAGTGGGATGGCAAAACAGGTGCTTCTACTCTTGGAGATTTGCCAAATGTATGGTTGGTGAGCCTTAACCATACTTATATTGGTGATAAA
CGTATCAATGTAGGTAAACAAGGCGTCCACAGTCATGGTCATGATTGGTCATTATTGACTAACATTGCCGAGTGGACTTGGGATGAATCAACTAAG

SEQ ID 60

LIVSKYLKYFSIITLFLTGLILVACQQQKPQTKERQRKQRPKDELVVSMGAKLPHEFDPKDRYGVHNEGNITHSTLLKRSPELDIKGELAKTYHLS
EDGLTWSFDLHDDFKFSNGEPVTADDVKFTYDMLKADGKAWDLTFIKNVEVVGKNQVNIHLTEAHSTFTAQLTEIPIVPKKHYNDKYKSNPIGSGP
YMVKEYKAGEQAIFVRNPYWHGKKPYFKKWTWVLLDENTALAALESGDVDMIYATPELADKKVKGTRLLDIPSNDVRGLSLPYVKKGVITDSPDGY
PVGNDVTSDPAIRKALTIGLNRQKVLDTVLNGYGKPAYSIIDKTPFWNPKTAIKDNKVAKAKQLLTKAGWKEQADGSRKKGDLDAAFDLYYPTNDQ
LRANLAVEVAEQAKALGITIKLKASNWDEMATKSHDSALLYAGGRHHAQQFYESHHPSLAGKGWTNITFYNNPTVTKYLDKAMTSSDLDKANEYWK
LAQWDGKTGASTLGDLPNVWLVSLNHTYIGDKRINVGKQGVHSHGHDWSLLTNIAEWTWDESTK

SEQ ID 61

ATGTATCTAAGTAGTTCGATCATCAAAAAAATATTGTCAGCTTTTTTGGCATTGTTTTTCATATCACTTCTAACATTTATTCTTATCAAACTATCA
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CCATTATGGAAGCAGTACTGGCTGTGGTTCCAAAAAGCATTAACAGGAGATTTTGGATATTCTTATGTGCTCAGGTTGCCAGTATTAGATTTGGTT
TTACAACGGTTTTTGGCTACTTTATTTTTAGGCACGAGTGCCTTCTTGCTAATTGTTACCATTTCTACCCCGTTAGGTGTGTGGGCTGGCTTACAT
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ACACATCACCTCCTTAGAAATGCCTTACCTGCGATAATGACAGCACTTAGCTTGACTTGGGTTTACTTATTAACAGGATCAATTATTGTTGAAGAA
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TTATTTTTAGCTAATAATTTTATGACACAGTGTTTTATGAATTGGGTTGATCCTCGGTTACGAAAGTCAAGGGAGAAA

SEQ ID 62

MYLSSSIIKKILSAFLALFFISLLTFILIKLSTVNSAENYLRLSKISVSPEALKEAEHYLGLDKPLWKQYWLWFQKALTGDFGYSYVLRLPVLDLV
LQRFLATLFLGTSAFLLIVTISTPLGVWAGLHESARSDHLIRFLSFSSVSMPNFWVAYLLMLLFSAKLNLLPVSGGNDLQSLILPSITLSFSTVGQ
YIALIRKAISQENRSLNVENARLRGVKERYIVTHHLLRNALPAIMTALSLTWVYLLTGSIIVEEIFSWNGIGRLFVTSLRTSDLPVIQACMLIFGT
LFLANNFMTQCFMNWVDPRLRKSREK

SEQ ID 63

GTGAAACGTACTACCATTATTATCATCTGGAAAATCATCAGATGTGTCACGCTTATTTTTGGGGTATCTGTTTTGACCTTCGTTTTGTTAAAACAA
TCTCCAGTAGATCCAGTCATGGCAAGTGTCAATTATGACACATCACTAACCCCTGCTCAGTACAAAGCGATTGCTCACCACTATGGCTTGGATAAG
CCAGCTCTAGTCCAATATTTTATTTGGTTGAAAAATGTGATACAGGGAGATTTAGGGACCTCGCTCGTTTATCGGCAACCTGTTAGTGATATTATT
AGATCACGGGCAGGTGCTTCTTTCATACTTATGGGACTCTCTTGGATCTTATCGGGTCTTATTGGATTTATCTTAGGAACGTTATCCGCTTTCCAT
CAAGGGAAATTACTTGACCGAGTTGTCAGGTGGTTTTCATACCTTCAGATATCAGTACCAACGTTTTGGATTGGACTCATTTTTTTATTAATCTTT
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TTACCTGTTTTCACGCTAAGTATTCTAGGCATTGCCAATGTCACCCTTCATACGAGAACTAAAATGATGTCGGTGCTTTCTAGTGAATATGTCTTA
TTTGCCAGAGCGCGTGGGGAAACACAGTGGCAAATTTTTAAACATCATTGCCTTAGAAATGCTATCGTACCAGCTATTACACTGCATTTTTCCTAT
TTTGGAGAATTGTTTGGAGGATCTGTTCTTGCTGAGCAAGTTTTCTCATATCCTGGCTTAGGGTCTACCCTCACTGAAGCAGGACTTAAAAGTGAT
ACACCGCTCCTTCTAGCTATTGTGATGATAGGGACATTATTTGTTTTTGCGGGCAATCTTATTGCGGATATTTTAAATAGCATCATCAATCCACAG
TTAAGGAGAAAAGTA

SEQ ID 64

VKRTTIIIIWKIIRCVTLIFGVSVLTFVLLKQSPVDPVMASVNYDTSLTPAQYKAIAHHYGLDKPALVQYFIWLKNVIQGDLGTSLVYRQPVSDII
RSRAGASFILMGLSWILSGLIGFILGTLSAFHQGKLLDRVVRWFSYLQISVPTFWIGLIFLLIFSVQLGWFPIGISSPIGTLSQDITLADRVKHLM
LPVFTLSILGIANVTLHTRTKMMSVLSSEYVLFARARGETQWQIFKHHCLRNAIVPAITLHFSYFGELFGGSVLAEQVFSYPGLGSTLTEAGLKSD
TPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV

SEQ ID 65

TTGTTAGTGATTAGTGCCATTTTTGCCCCTATTCTATCTAGCTTTGATCCACAATACGTAGATTTATCACAAAAATTATTGGCTCCCAATAATGTT
CATTTGTTAGGGACTGACCAATTGGGTAGAGATGTATTATCTCGCTTGCTTTATGGTGCTAGATATTCACTGTTTTTAGCTATTATTATTAGCTTA
TTGGAATTAACGATTGGTATGTTTGTGGGTCTTATTGTTGGTTGGTATCAAGGAAAGTTAGAAAACCTCTTTTTATGGATAGCTAATATTATTTTA
GCTTTTCCGAGCTTTTTGCTCTCTCTTGCAACCGTGGGAATCTTAGGTCATGGTCTAGGGAATTTAATTTTTGCAATTGTCTTTGTGGAATGGGTT
TACTATGCTAAATTAATGACCAATTTAGTTAAGAGTGCAAAAAAAGAGCCTTATGTGATAAATGCGCAAATTATGGGACTTTCAGTCTGGCATATT
TTAAGAAAACATATTTTTCCTTTTGTGTATCAGCCAATCCTCGTTATGGTCCTTATGAATATAGGAAATATTATTTTAATGATTTCTGGCTTTTCT
TTCTTAGGGATTGGTGTGCAACCTAATGTCACAGAATGGGGAATGATGTTGCACGATGCTAGAGGATATTTTAGGACAGCTACTTGGATGATGTTA
TCTCCTGGAATTGCGATTTTTTTAACAGTATTTTCCTTTAATACTTTAGGCGATGCCATAGATAAAAAAGATTGGAAACGACAATGGAACAGT

SEQ ID 66

MLVISAIFAPILSSFDPQYVDLSQKLLAPNNVHLLGTDQLGRDVLSRLLYGARYSLFLAIIISLLELTIGMFVGLIVGWYQGKLENLFLWIANIIL
AFPSFLLSLATVGILGHGLGNLIFAIVFVEWVYYAKLMTNLVKSAKKEPYVINAQIMGLSVWHILRKHIFPFVYQPILVMVLMNIGNIILMISGFS
FLGIGVQPNVTEWGMMLHDARGYFRTATWMMLSPGIAIFLTVFSFNTLGDAIDKKDWKRQWNS

SEQ ID 67

ATGATATTGAAACGTCGAACGATGGTTTTATGGCAACTGGGTATCGCCATTTCTCTCATTCTTAGTATTCTAGCCTTAAACCTTTATTTCTATAGG
ACGCCTTTGGAAACCAATGCAGCTTTACGCAACCTCGCTCCTTCCTTAAACCATCTTTTTGGGACAGATGGTTTAGGTAGGGATATGTTTGTCAGA
ACGATTAAAGGGCTTTATTTCTCTTTACAAGTCGGCTTATTAGGCGCCCTTATGGGAGTCTTTCTTGCGACCGTTTTTGGAGTGCTTGCAGGTCTA
GGAAATAGCCTTATTGATAAAATAATAGCCTGGTTGGTTGATTTGTTTATTGGTATGCCTCATTTGATTTTTATGATTCTCATTTCTTTTGTTGTT
GGGAAAGGGGCTCAAGGGGTTATCATTGCAACAGCTGTTACCCATTGGCCCTCTCTAGCAAGGCTTATCCGCAATGAAGTCTATGATCTAAAGAAT
AAAGCCTTTGTCCAGCTCTCTAAAAGCATGGGAAAAACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTCAAATTTTCATT
GGGTTTATCCTCTTATTTCCGCACGTCATCTTGCATGAAGCATCCATGACTTTCTTAGGATTTGGCCTTTCTGCCGAACAACCTTCGGTTGGTATC
ATTTTGTCAGAGGCAGCTAAGCATATCTCTCTTGGCAATTGGTGGTTGGTGATTTTTCCAGGCCTTTATCTTATTTTGGTTGTCAATGCCTTTGAT
ACTATCGGAGAATCTTTAAAGAAACTCTTTTACCCTCAAACGGATCATTTT

SEQ ID 68

MILKRRTMVLWQLGIAISLILSILALNLYFYRTPLETNAALRNLAPSLNHLFGTDGLGRDMFVRTIKGLYFSLQVGLLGALMGVFLATVFGVLAGL
GNSLIDKIIAWLVDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYDLKNKAFVQLSKSMGKTPYYIVRHHILPLIASQIFI
GFILLFPHVILHEASMTFLGFGLSAEQPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF

SEQ ID 69

TTGGAAACGACAATGGAACAGTTAGAAATAAGAAAATTGTCATTACAGATAGGAGAGGTCCCTGTACTAAGAGATTTTAGTTGTAAAATAGATATG
GGAGAATCGCTAACTATTATTGGTGAGAGTGGTTCAGGGAAAACCCTCTTGGCAAAATTATTGGTTGGTCACATTCCACAAGGTATGACAGTTAGA
GGAAACATATTTTTTAAGGGAGTTGATTTAGGTAAACTAACTGTAAAGCAGTGGCAGAAATTAAGGGGACGAGATATTGCCTATTTAGTGCAAAAT
CCCATGTCTATGTTTAATCCTTTTCAAAAAATTGAAGCGCATATTTTGGAAACAATCCTTAGTCATGAGAAATGTTCAAAGAGAGTAGCCTTATCT
AAAGCGTTAGAATGGATGAAACGTTTAAATTTAGATGATGCGATATCCCTGTTAAAAAAATACCCTTTTGAGCTTAGTGGAGGAATGCTACAAAGA
ATTATGTTAGCCACTATATTATCTCTTGATCCTCAGGTAATCATATTAGATGAGCCGACCTCAGCGGTTGATTGTCATAATTGTTCTACTATATCA
GCTATTTTGCAGGAATTGCAAAATAATGGAAAAACCTTGATTACTGTAACGCATGATTATCAGTTAGCTAGAGACCTGGGGGGACAATTATTAGTT
ATAAGTGAGGGAGAAGTTGTTGAACAGGGACAAACCCAAGCTATTTTAAGCAATCCTCAACATAACTATACGAAAGCACTGACAGTGCAAATGGAG
TATGAAGGAGATATTCTTAATGTTGGTTTG

SEQ ID 70

METTMEQLEIRKLSLQIGEVPVLRDFSCKIDMGESLTIIGESGSGKTLLAKLLVGHIPQGMTVRGNIFFKGVDLGKLTVKQWQKLRGRDIAYLVQN
PMSMFNPFQKIEAHILETILSHEKCSKRVALSKALEWMKRLNLDDAISLLKKYPFELSGGMLQRIMLATILSLDPQVIILDEPTSAVDCHNCSTIS
AILQELQNNGKTLITVTHDYQLARDLGGQLLVISEGEVVEQGQTQAILSNPQHNYTKALTVQMEYEGDILNVGL

SEQ ID 71

ATGACAAAAGAAAATAATGTAATCTTAACTGCCAAAGATGTGGTGGTAGAATTTGATGTGCGTGATCGTGTTTTAACAGCTATCCGTAACGTCTCA
CTGGAACTTGTTGAAGGAGAAGTCCTTGCTTTTGTAGGGGAATCAGGCTCAGGTAAATCTGTTTTAACAAAGACCTTTACAGGGATGTTGGAGTCT
AATGGACGCATTGCTAATGGTTCAATTGTCTATCGTGGGCAAGAATTGACAGATTTAAAAACAAATAAAGAGTGGGCAAAGATTCGCGGCTCAAAA
ATCGCAACGATTTTCCAAGACCCAATGACCAGTCTTAGTCCCATTAAAACTATCGGTAGCCAAATCACAGAAGTGATTATTAAGCACCAAAAAGTA
AGTCATGCCAAAGCTAAAGAAATGGCCCTTGATTACATGAATAAAGTGGGTATCCCAAATGCCAAAAAACGCTTTGAAGATTACCCATTTGAGTAT
TCAGGAGGAATGCGTCAACGTATTGTTATCGCTATTGCTTTAGCTTGTCGCCCAGATATTCTTATCTGTGATGAGCCAACAACAGCCCTTGATGTG
ACTATTCAAGCTCAAATCGTTGAGTTATTGAAGTCGCTTCAACGAGAATATCATTTCACCATTATCTTTATTACGCACGATTTAGGTGTTGTGGCA
AGCATTGCAGATAAAGTGGCTGTCATGTATGCAGGAGAAATTGTTGAATTTGGAACAGTCGAAGAGATTTTCTATGATCCAAGACACCCCTATACA
TGGAGTTTGCTGTCTAGCTTACCGCAGTTGGCAGATGAATCTGGTGAACTTTACGCTATTCCAGGAACGCCTCCATCACTTTATTCACCAATTATC
GGAGATGCCTTTGCACTTCGCTCAGAATATGCTATGGTTTTAGACTTTGAAAAAGCACCTCCGGCGATTAACGTATCTGAGACTCATTGGGCCAAA
ACATGGCTTTTACACCCAGAGGCTCCAAAAGTTCAAAAACCAGAAGTCATTCAAGATTTGCATCAAAAAATCTTAAGAAAAATGTCACAACAGGAG
GAAGGAAATGTC

SEQ ID 72

MTKENNVILTAKDVVVEFDVRDRVLTAIRNVSLELVEGEVLAFVGESGSGKSVLTKTFTGMLESNGRIANGSIVYRGQELTDLKTNKEWAKIRGSK
IATIFQDPMTSLSPIKTIGSQITEVIIKHQKVSHAKAKEMALDYMNKVGIPNAKKRFEDYPFEYSGGMRQRIVIAIALACRPDILICDEPTTALDV
TIQAQIVELLKSLQREYHFTIIFITHDLGVVASIADKVAVMYAGEIVEFGTVEEIFYDPRHPYTWSLLSSLPQLADESGELYAIPGTPPSLYSPII
GDAFALRSEYAMVLDFEKAPPAINVSETHWAKTWLLHPEAPKVQKPEVIQDLHQKILRKMSQQEEGNV

SEQ ID 73

ATGAAGGAGATATTCTTAATGTTGGTTTGTAATCATGTCGGAAAAACATTTGGACGACAAGAGGTTTTAAAGGACTGTCATTTTCATCTTAAAAGA
GGAGAAATAATTGGTATAATGGGTAAAAGTGGCAGTGGTAAAAGTAGCCTTGCCCGACTCATTATAGGACTAGATAGTCCTACTTGTGGTTCGATA
TATTTTCAAGGAAAAATTTACACACCTAAAGATGGTAAGGCGCAGATTATCCTTGTTTTTCAAGATGCGCTTAGTTCGGTCAATCCATATTTTAGT
ATTGAGGAAATTTTGAATGAAGCTTTTTATGGAAAAAAAACAACTTTTGAATTATGTCAAATATTAGAAGCGGTGGGTTTAGATGGAACTTATCTA
AAATATAAAGCTAGACAACTTAGTGGTGGTCAGCTACAGAGAGTTTGTATCGCTAGAGCTTTACTCTTAAAGCCTAAAATTATTATTTTTGATGAA

TCCTTAAGTGGATTAGACCCAGTAACTCAAATTAAAATGCTACGTTTATTACAAAAAATAAAACGCCGTTATGAATTAAGTTTTATAATGATTTCT
CATGACCCTAAAATTTGTCAAGCTATCTGTAACCGGGTCTTTCTGATAAAAAATGGTTATTTAGTAGAAGATAATGAATTCTTGAAGAGAGCGTGT
TCTACTAACTGTTTGACCAATCTC

SEQ ID 74

MKEIFLMLVCNHVGKTFGRQEVLKDCHFHLKRGEIIGIMGKSGSGKSSLARLIIGLDSPTCGSIYFQGKIYTPKDGKAQIILVFQDALSSVNPYFS
IEEILNEAFYGKKTTFELCQILEAVGLDGTYLKYKARQLSGGQLQRVCIARALLLKPKIIIFDESLSGLDPVTQIKMLRLLQKIKRRYELSFIMIS
HDPKICQAICNRVFLIKNGYLVEDNEFLKRACSTNCLTNL

SEQ ID 75

ATGAATGAAGCAATAATTCAATTAGATCATATTGATATTACCTTCCGTCAAAAAAAACGGGTTATCGAAGCTGTTAAAGATGTCACGGTTCATATC
AATCAAGGAGATATTTATGGCATTGTTGGGTATTCAGGTGCCGGGAAATCAACTCTTGTGCGTGTGATTAACCTGCTACAGGCACCAACAAACGGG
AAAATCACTGTTGATGGGGATGTGACTTTTGACCAGGGGAAAATTCAATTGTCAGCTGATGCCCTTCGCCAAAAACGACGTGATATTGGTATGATC
TTCCAACATTTCAATTTGATGGCCCAAAAAACAGCCAAAGAAAATGTAGCATTTGCGCTCCGTCATTCGTCGTTAAGTAAGACTGAGAAAGAACAC
AAAGTTATCGAACTGCTAGAACTTGTAGGTTTATCAGAGCGAGCAGATAACTACCCTGCCCAGTTATCGGGTGGGCAAAAACAAAGGGTGGCTATT
GCGCGTGCTCTAGCTAACGATCCAAAAATTTTGATTTCAGATGAGGCCACATCAGCACTAGATCCAAAAACCACTAAACAAATTTTGGCGCTCTTG
CAAGAATTAAACCGCAAACTTGGCCTTACCATTGTTATGATTACTCATGAAATGCAAATTGTTAAGGATATTTGTAATCGTGTTGCTGTTATGCAA
AATGGTGTTTTGATTGAAGAAGGTTCTGTCCTTGATATCTTTTCAAATCCAAAAGAAGCCTTGACACAGGAATTTATCACAACAGCTACAGGGATT
GATGAGGCTTTAGAAAAAATTAACCAACAAGACATTGTTAAACATTTGCCTGCAAATGCCCTTCTAGCTCAGTTGAAATATGCAGGAACTTCTACG
GATGAGCCTCTACTTAATAGCATTTACCGTCAGTTTGAAGTGACAGCTAATATTTTGTATGGCAATATTGAGATTTTAGATCATATTCCAGTTGGT
GACATGATTGTTGTCTTGGAAGGGCAAGCTGAAAATATTCTTGCGGCTGAGAAAGCCTTGCATGAAGCTGGTGTTGATGTTAGTATTTTAAAGAGA
GGAGCC

SEQ ID 76

MNEAIIQLDHIDITFRQKKRVIEAVKDVTVHINQGDIYGIVGYSGAGKSTLVRVINLLQAPTNGKITVDGDVTFDQGKIQLSADALRQKRRDIGMI
FQHFNLMAQKTAKENVAFALRHSSLSKTEKEHKVIELLELVGLSERADNYPAQLSGGQKQRVAIARALANDPKILISDEATSALDPKTTKQILALL
QELNRKLGLTIVMITHEMQIVKDICNRVAVMQNGVLIEEGSVLDIFSNPKEALTQEFITTATGIDEALEKINQQDIVKHLPANALLAQLKYAGTST
DEPLLNSIYRQFEVTANILYGNIEILDHIPVGDMIVVLEGQAENILAAEKALHEAGVDVSILKRGA

SEQ ID 77

GTGGAACCTAAATATCAACGTATATTAATTAAGTTATCTGGTGAAGCATTGGCGGGAGATAAGGGTGTCGGTATTGACATTCCTACCGTTCAATCT
ATTGCAAAAGAAATTGCCGAAGTACACAATTCAGGTGTTCAAATAGCGCTTGTCATTGGTGGAGGTAATCTTTGGCGTGGAGAACCTGCAGCAGAA
GCAGGGATGGATCGTGTTCAAGCTGATTATACAGGGATGTTAGGGACAGTAATGAATGCTCTTGTAATGGCTGATAGCCTTCAACAATATGGGGTA
GATACTAGAGTTCAAACAGCTATTCCAATGCAAACTGTTGCTGAGCCTTACGTACGTGGTCGTGCTTTACGTCATCTAGAGAAGAATCGTATTGTT
GTCTTTGGAGCGGGTATTGGTTCGCCTTATTTCTCAACTGATACAACAGCAGCGCTTCGTGCTGCTGAGATTGAGGCAGAAGCAATTTTAATGGCT
AAAAATGGAGTAGATGGTGTTTATAATGCTGATCCAAAGAAAGATGCCAATGCTGTCAAATTTGATGAATTAACTCACGTTGAAGTAATAAAACGA
GGGTTAAAAATCATGGATGCAACCGCATCAACTATTTCAATGGATAATGATATTGACCTTGTTGTTTTCAATATGAATGAGACTGGTAATATTAAG
CGTGTTGTTCTTGGAGAACAAATCGGAACAACTGTTTCAAACAAAGCATCTGAA

SEQ ID 78

MEPKYQRILIKLSGEALAGDKGVGIDIPTVQSIAKEIAEVHNSGVQIALVIGGGNLWRGEPAAEAGMDRVQADYTGMLGTVMNALVMADSLQQYGV
DTRVQTAIPMQTVAEPYVRGRALRHLEKNRIVVFGAGIGSPYFSTDTTAALRAAEIEAEAILMAKNGVDGVYNADPKKDANAVKFDELTHVEVIKR
GLKIMDATASTISMDNDIDLVVFNMNETGNIKRVVLGEQIGTTVSNKASE

SEQ ID 79

GTGGAACCTAAATATCAACGTATATTAATTAAGTTATCTGGTGAAGCATTAGCAGGTGAAAAAGGAGTTGGCATTGACATTCCAACTGTTCAGGCT
ATTGCAAAAGAAATTGCCGAAGTTCATGTGTCGGGAGTACAGATCGCTCTTGTTATTGGTGGAGGCAATCTCTGGCGTGGAGAGCCTGCAGCAGAC
GCTGGAATGGACCGTGTTCAGGCTGATTACACTGGCATGCTTGGAACGGTGATGAATGCCCTAGTCATGGCTGATAGTCTTCAACATTATGGTGTT
GATACCCGTGTGCAAACAGCTATTCCTATGCAAAATGTAGCAGAACCTTATATTCGCGGACGTGCCTTGCGCCATCTAGAAAAAAATCGGATTGTT
GTTTTTGGAGCTGGTATTGGCTCGCCTTATTTTCAACAGACACCACCGCGGCACTGCGTGCTGCTGAGATTGAAGCAGATGCTATTTTAATGGCA
AAAAATGGTGTGGATGGGGTCTATAATGCTGATCCTAAAAAAGATGCTAATGCGGTTAAATTTGATGAATTAACACATGGTGAAGTGATCAAACGT
GGTCTCAAAATCATGGATGCAACGGCATCGACCTTATCGATGGATAACGATATTGATTTGGTGGTTTTCAATATGAATGAAGCTGGCAATATTCAA
CGTGTTGTCTTTGGAGAACATATTGGAACTACTGTATCAAATAAAGTTTGTGAC

SEQ ID 80

VEPKYQRILIKLSGEALAGEKGVGIDIPTVQAIAKEIAEVHVSGVQIALVIGGGNLWRGEPAADAGMDRVQADYTGMLGTVMNALVMADSLQHYGV
DTRVQTAIPMQNVAEPYIRGRALRHLEKNRIVVFGAGIGSPYFSTDTTAALRAAEIEADAILMAKNGVDGVYNADPKKDANAVKFDELTHGEVIKR
GLKIMDATASTLSMDNDIDLVVFNMNEAGNIQRVVFGEHIGTTVSNKVCD

SEQ ID 81

TTGATTGATGATTTATCAAATGGTGAAATTAAAAGAACACGAGCTTCAGGTACAGTAATAGAAGCTAATTGGTTAAGGGGGGTTGGCGCTCCA

SEQ ID 82

MIDDLSNGEIKRTRASGTVIEANWLRGVGAP

SEQ ID 83

ATGACTAAGGAAATCGTTACAAAAGCTCAAGAGCGTTTTGAGCAATCACACCAAAGTTTATCAAGAGAATTTGCAGGGATTCGTGCAGGACGTGCT
AATGCTAGCTTGCTTGATCGTATTCAAGTTGAGTATTATGGAGCGCCAACCCCCCTTAACCAATTAGCTTCTATTACTGTACCTGAAGCTCGTGTT
CTTTTAATTTCACCATTTGATAAATCATCAATCAAAGATATTGAGCGTGCTATTAACGAATCAGATTTAGGTATTAATCCTGCAAATGATGGTTCA
GTTATTCGTCTTGTTATTCCAGCTTTGACAGAAGAAACACGTCGTGATTTAGCTAAAGAAGTGAAAAAAGTCGGAGAAAATGCTAAGATTGCTATC
CGTAATATTCGCCGTGATGCTATGGATGAAGCTAAGAAGCAAGAAAAGAATAAAGAAATTACAGAAGATGACTTGAAATCTCTTGAAAAAGATATT
CAAAAGGCTACTGATGATGCTGTAAAACATATTGATGAGATGACTGCTAATAAAGAAAAAGAATTGTTGGAAGTT

SEQ ID 84

MTKEIVTKAQERFEQSHQSLSREFAGIRAGRANASLLDRIQVEYYGAPTPLNQLASITVPEARVLLISPFDKSSIKDIERAINESDLGINPANDGS
VIRLVIPALTEETRRDLAKEVKKVGENAKIAIRNIRRDAMDEAKKQEKNKEITEDDLKSLEKDIQKATDDAVKHIDEMTANKEKELLEV

SEQ ID 85

ATGGCAAATGCAATTATTGAAACTGCAAAAGAACGTTTTGCACAATCCCATCAGTCTTTATCACGTGAATATGCCAGCATTCGTGCGGGTCGTGCC
AACGCTAGTCTTTTAGACCGTATCCAAGTTGATTATTACGGGGCACCGACACCATTAAATCAATTGGCTTCAATCACTGTACCAGAAGCGCGTGTC
TTATTGATCTCGCCTTTTGATAAATCTTCTATCAAAGATATCGAGCGCGCTCTTAACGCATCAGATTTAGGCATTACACCTGCTAACGATGGCTCT
GTCATTCGTTTGGTTATTCCAGCTTTGACCGAAGAAACACGTAAAGAATTAGCCAAAGAAGTGAAAAAAGTTGGTGAAAATGCTAAAATTGCAATC
CGTAATATCCGCCGCGATGCTATGGATGATGCTAAAAAGCAAGAAAAAGCAAAAGAAATCACTGAAGATGAGTTAAAAACACTTGAGAAAGATATC
CAAAAAGCAACCGATGATGCTATCAAAGAAATTGACCGCATGACGGCTGAAAAAGAAAAAGAATTGCTCTCAGTG

SEQ ID 86

MANAIIETAKERFAQSHQSLSREYASIRAGRANASLLDRIQVDYYGAPTPLNQLASITVPEARVLLISPFDKSSIKDIERALNASDLGITPANDGS
VIRLVIPALTEETRKELAKEVKKVGENAKIAIRNIRRDAMDDAKKQEKAKEITEDELKTLEKDIQKATDDAIKEIDRMTAEKEKELLSV

SEQ ID 87

TTGGCAAGTAATAAAATGATTATGGAGGTAACTGATAGAATCAAAACCAGATGGATTTGGTTTGTCGGTTACCTTTTTAAAAGGAGAAAAATGAAT
ACATTATTAGCGACAGTCATAACAGGCTTAGTAACTGATGAAAACAAAGATTTTTACTTTATCCAAAAAGATGGCTTTACCTTTGCATTATCAAAG
TCAGAAGGAGAGCATCACATTGGTGAAATGGTTAAAGGATTCGCCTATACAGATATGCAACAAAAAGCACGTCTTACAACTAAAGAAACATTTGCG
ACTCGAGATCATTATGGTTGGGGGACAGTTACTGAGGTACGTAAAGACTTGGGAGTATTTCTTGATACTGGTCTTCCAGATAAGCAAGTGGTTGTT
TCTTTGGATGTTCTTCCTGAATTGAAAGAACTTTGGCCTAAAAAAGGTGATCGCCTCTACGTTTGCTTAGATGTTGATAAAAAAGATCGTCTCTGG
GCTCTCCCTGCAGATCCTGAAGTGTTTCAACGAATGGCAACCCCTGCATATAACAATATGCAAAATCAAAATTGGCCAGCAATCGTTTATCGCTTA
AAATTGTCAGGAACTTTTGTTTATCTACCAGAAAATAATATGCTCGGCTTTATTCACCCTAGTGAACGTTACAGTGAACCTCGTTTAGGGCAAGTG
CTGGATGCACGAGTTATTGGCTTCAGAGAAGTTGATAGAACCTTAAATTTATCATTAAAGCCTCGTTCTTTTGAAATGTTAGAAAATGACGCACAA
ATGATTTTAACGTATTTAGAAAGTAACGGAGGATTCATGACTTTAAATGATAAATCTTCTCCAGAGGAAATTAAAGCTACTTTTGGAATTTCCAAA
GGTCAGTTTAAAAAAGCACTTGGAGGACTCATGAAAGCTAAAAAGATCAAACAAGATCAGCTAGGTACAGAATTATTA

SEQ ID 88

MASNKMIMEVTDRIKTRWIWFVGYLFKRRKMNTLLATVITGLVTDENKDFYFIQKDGFTFALSKSEGEHHIGEMVKGFAYTDMQQKARLTTKETFA
TRDHYGWGTVTEVRKDLGVFLDTGLPDKQVVVSLDVLPELKELWPKKGDRLYVCLDVDKKDRLWALPADPEVFQRMATPAYNNMQNQNWPAIVYRL
KLSGTFVYLPENNMLGFIHPSERYSEPRLGQVLDARVIGFREVDRTLNLSLKPRSFEMLENDAQMILTYLESNGGFMTLNDKSSPEEIKATFGISK
GQFKKALGGLMKAKKIKQDQLGTELL

SEQ ID 89

ATGAATGATTTACTAGCAACAGTCATTACTGGGCTTATTAAAGAAGAAAACGCTAATGACTATTTTATCCACAAAGAAGGGTTTACCTTTACCTTG
TCTAAAGCAGAAGGAGAACGCCAGATTGGTGATATGGTCACAGGCTTTGCCTATACAGACATAGAGCAAAAGGCACGTCTCACAACCAAAGAGATC
CGTTCAACACGGACAAGTTATGGCTGGGGGGAAGTGACAGAGGTTCGTCGTGACCTAGGCGTTTTTGTCGATACAGGAATTCCAAATAAAGAAATT
GTGGTTTCTTTGGACGTGTTGCCTGAGATGAAAGAACTATGGCCTAAAAAAGGGGATAAACTTTACATTCGTTTGGATGTGGATAAAAAAGACCGT
ATTTGGGGACTTCCAGCAGAGCCTGAGGTCTTTCAAAAGATGGCTAGCCCTGCTTACAATAACATGCAAAATCAACATTGGCCAGCAATTGTTTAC
CGCCTAAAATTAACAGGAACGTTTGTTTACCTGCCTGAAAACAACATGTTGGGCTTTATTCACTCAAGTGAACGCTACGCAGAACCGCGCTTAGGT
CAGGTTTTAGATGCCCGTGTGATTGGGTTTAGAGAGGTCGATCGTACCTTGAATTTATCGTTGAAACCACGTTCTTTTGAGATGTTGGAGAATGAC
GCTCAGATGATTGTTACTTATCTGGAAGCCAATGGTGGTTTCATGACTTTAAATGACAAATCAAGTCCAGAAGAGATTAAAGCAAGCTTTGGTATT
TCAAAAGGCCAGTTTAAAAAAGCCTTGGGTGGATTGATGAAAGCTAAACGTATCAAACAAGACGCCACAGGAACTGAATTAATAGGA

SEQ ID 90

MNDLLATVITGLIKEENANDYFIHKEGFTFTLSKAEGERQIGDMVTGFAYTDIEQKARLTTKEIRSTRTSYGWGEVTEVRRDLGVFVDTGIPNKEI
VVSLDVLPEMKELWPKKGDKLYIRLDVDKKDRIWGLPAEPEVFQKMASPAYNNMQNQHWPAIVYRLKLTGTFVYLPENNMLGFIHSSERYAEPRLG
QVLDARVIGFREVDRTLNLSLKPRSFEMLENDAQMIVTYLEANGGFMTLNDKSSPEEIKASFGISKGQFKKALGGLMKAKRIKQDATGTELIG

SEQ ID 91

TTGGCTTTTTTTGTTATAATGTATCTATTAAAAAGAATGGAGAACGATATGGAACGTGCGATTTTTGCTGGAGGTTGTTTTTGGTGTATGGTACAA
CCATTTGAAGAATTAGATGGTATTGAATCTGTTTTATCTGGATACACTGGAGGACATGTTGAGAATCCAACTTATAAAGAAGTTTGTAGTAAAACT
ACTGGACATACAGAAGCTGTTGAAATTATTTTTAATCCTGAAAAAATCTCTTATGCAGATTTAGTTGAGTTATATTGGGCACAAACAGATCCAACA
GACGCTTTTGGTCAGTTTGAAGATCGTGGGGATAATTATCGTCCTGTCATCTTTTATGAGAATGAAGAGCAACGTCAGATTGCTCAAAAATCAAAA
GATAAGCTACAAGCTTCGGGTAGATTTGATAGACCAATTGTAACCAGCATTGAGCCTGCTGATACTTTTTACCCAGCAGAAGACTATCATCAAGCA
TTCTATCGGACTAACCCTGCTCGTTACGCCTTGAGTAGTGCCAGAAGACATGCATTTCTAGAGGAGAACTGGCAT

SEQ ID 92

MAFFVIMYLLKRMENDMERAIFAGGCFWCMVQPFEELDGIESVLSGYTGGHVENPTYKEVCSKTTGHTEAVEIIFNPEKISYADLVELYWAQTDPT
DAFGQFEDRGDNYRPVIFYENEEQRQIAQKSKDKLQASGRFDRPIVTSIEPADTFYPAEDYHQAFYRTNPARYALSSARRHAFLEENWH

SEQ ID 93

ATGGAAAGAGCCATTTTTGCAGGAGGTTGTTTCTGGTGTATGGTGCAACCTTTTGAGGAGCAAGCAGGTATTTTGTCAGTCAGAAGTGGCTACACA
GGTGGGCATCTCCCAAATCCTAGCTATGAACAAGTTTGTGCCAAAACAACAGGACATACAGAAGCTGTTGAAATTATTTTTGACCCTAAGCAAATC
GCTTATAAAGATTTGGTAGAGCTCTATTGGACGCAGACGGATCCAACAGACGCCTTTGGGCAATTTGAAGATCGTGGGGACAACTACCGTCCTGTC
ATTTACTACACAACGGAAAGACAAAAAGAAATTGCAGAGCAATCAAAAGCAAACTTGCAAGCTTCAGGACGTTTTGACCAACCCATTGTCACCACT
ATTGAACCAGCAGAGCCATTTTATCTCGCAGAGGATTATCACCAAGGATTTTATAAAAAGAATCCCAAGCGGTATGCACAAAGCAGTGCTATTCGT
CATCAGTTTTTAGAGGAGAATTGGTCA

SEQ ID 94

MERAIFAGGCFWCMVQPFEEQAGILSVRSGYTGGHLPNPSYEQVCAKTTGHTEAVEIIFDPKQIAYKDLVELYWTQTDPTDAFGQFEDRGDNYRPV
IYYTTERQKEIAEQSKANLQASGRFDQPIVTTIEPAEPFYLAEDYHQGFYKKNPKRYAQSSAIRHQFLEENWS

SEQ ID 95

TTGAGAAAATCATTTTACAGTTGGTTGATGACACAAAGAAATCCAAAATCAAATGAACCAGTAGCAATCCTAGCAGATTACGCTTTTGATGAAACC
ACTTTTCCAAAACATAGTTCGGATTTTGAAACAGTTAGTCGCTATTTAGAAGATGAGGCCAGTTTTTCCTTTAATTTAACAGATTTTGATGATATT
TGGGAAGATTATCTCAATCAT

SEQ ID 96

MRKSFYSWLMTQRNPKSNEPVAILADYAFDETTFPKHSSDFETVSRYLEDEASFSFNLTDFDDIWEDYLNH

SEQ ID 97

TTGGTCATGAGAAAATCATTTTACAGCTGGCTGATGACACAACGTAACCCTAAATCAAATGAACCTGTGGCGATTTTAGCAGATTTGGTGTTTGAT
GACACCACTTTTCCAAAGCATACCAATGATTTTGAACTCATTAGTCGGTATCTAGAAGATCAAGCTAGTTTTTCCTTTAATTTAGGTCAATTTGAT
GAAATCTGGGAAGATTATCTAGCACAT

SEQ ID 98

LVMRKSFYSWLMTQRNPKSNEPVAILADLVFDDTTFPKHTNDFELISRYLEDQASFSFNLGQFDEIWEDYLAH

SEQ ID 99

TTGTTTATGAGATATACAAATGGAAATTTTGAAGCCTTTGCAAGACCTCGAAAACCTGAAGGTGTGGATAAAAAATCCGCTTATATTGTTGGTTCT
GGTTTAGCAGGATTAGCTGCCGCTGTCTTTTTAATACGTGACGGTCAAATGGATGGTCAACGTATTCATATTTTTGAAGAACTACCTCTTTCTGGA
GGATCACTTGACGGTGTCAAACGACCTGATATCGGTTTTGTAACGCGTGGTGGTCGTGAAATGGAAAATCACTTCGAATGTATGTGGGATATGTAC
CGTTCCATCCCCTCTCTCGAAGTTCCAGATGCTTCTTATCTAGATGAATTTTATTGGCTTGACAAGGATGATCCCAATTCATCTAACTGTCGCCTC
ATTCATAAACAGGGGAATCGCTTAGAATCTGATGGTGATTTTACACTCGGAACACATTCCAAAGAGTTAGTTAAGCTAGTCATGGAGACTGAAGAG
TCTTTAGGTGCTAAGACGATTGAAGAAGTTTTTTCAAAAGAATTTTTTGAAAGTAATTTTTGGACTTATTGGGGTACTATGTTTGCCTTTGAGAAA
TGGCATTCAGCGATTGAAATGCGTCGATATGCTATGCGCTTTATCCATCATATTGGTGGTCTGCCTGATTTCACTTCATTAAAATTTAATAAATAT
AATCAATATGATTCTATGGTGAAACCAATCATCAGTTATTTAGAGTCTCATAATGTAGATGTTCAATTTGATAGCAAGGTAACTAATATCTCCGTA
GACTTTAAGAACGGTCAGAAGCTTGCAAAAGCTATTCATCTCACAGTTGGTGGTGAAGCAAAAACAATTGATCTTACTCCAAATGATTTTGTTTTT
GTAACGAATGGTTCTATCACTGAAAGTACGAACTATGGTAGTCATGATACTGTAGCTAAACCTAATACCGATTTGGGAGGTTCTTGGAATCTTTGG
GAAAACTTAGCTGCTCAATCTGATGAATTTGGACATCCTAAAGTCTTCTACAAAGATATTCCAAAAGAGTCATGGTTTGTTTCTGCTACTGCAACA
ATAAAAGATCCAGCTATTGAACCTTATATAGAGCGTTTAACACATCGTGACCTCCATGATGGTAAAGTAAATACCGGAGGCATTGTTACAGTTACA

GATTCTAATTGGATGATGAGTTTTGCTATCCATCGCCAACCGCATTTCAAAGAGCAAAAGGAAAATGAAACAATTGTTTGGATTTATGGACTCTAT
TCAAATGTGGAAGGTAATTATATTATAAAAAACCAATTGAAGAATGTACTGGTCGAGAAATCACAGAAGAGTGGTTATATCACTTAGGTGTTCCTGAA
ATGAAGATTCATGATTTATCTGATAAACAATATGTAAGTACAGTTCCTGTTTATATGCCTTACATTACTAGTTATTTCATGCCTCGAGTTAAAGGT
GACCGACCAGATGTTATCCCACAAGGATCTGTTAACCTAGCCTTCATTGGTAATTTTGCAGAATCTCCATCCAGAGATACAGTATTTACAACGGAA
TATTCTATTAGAACTGCTATGGAAGCTGTTTATACTTTCTTAAATATTGAACGTGGTGTTCCAGAAGTCTTTAATTCAGCATTTGATATTCGTGTC
TTGTTGCAATCTTTATACTATCTCAATGATAAGAAATCTGTTGAAGATATGGATTTACCAATACCTGCCTTAATGCGTAAAGTAGGCATGAAAAAA
ATTAGAGGAACTTATTTAGAAGAATTACTTCGAGAAGCTCATCTTTTA

SEQ ID 100

MFMRYTNGNFEAFARPRKPEGVDKKSAYIVGSGLAGLAAAVFLIRDGQMDGQRIHIFEELPLSGGSLDGVKRPDIGFVTRGGREMENHFECMWDMY
RSIPSLEVPDASYLDEFYWLDKDDPNSSNCRLIHKQGNRLESDGDFTLGTHSKELVKLVMETEESLGAKTIEEVFSKEFFESNFWTYWGTMFAFEK
WHSAIEMRRYAMRFIHHIGGLPDFTSLKFNKYNQYDSMVKPIISYLESHNVDVQFDSKVTNISVDFKNGQKLAKAIHLTVGGEAKTIDLTPNDFVF
VTNGSITESTNYGSHDTVAKPNTDLGGSWNLWENLAAQSDEFGHPKVFYKDIPKESWFVSATATIKDPAIEPYIERLTHRDLHDGKVNTGGIVTVT
DSNWMMSFAIHRQPHFKEQKENETIVWIYGLYSNVEGNYIKKPIEECTGREITEEWLYHLGVPEMKIHDLSDKQYVSTVPVYMPYITSYFMPRVKG
DRPDVIPQGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVYTFLNIERGVPEVFNSAFDIRVLLQSLYYLNDKKSVEDMDLPIPALMRKVGMKK
IRGTYLEELLREAHLL

SEQ ID 101

GTGATGATATCACTTTGCTTGACTATTCAAGGAGGTCTTGAAATGTATTATACTAGTGGTAATTACGAAGCTTTTGCAACACCTCGAAAACCCGAA
GGGGTAGATCAGAAATCAGCTTATATTGTTGGTACTGGTTTAGCTGGTTTAGCAGCAGCTGTTTTCCTTATTCGCGATGGGCATATGGCTGGGGAA
CGCATTCATCTGTTTGAGGAATTGCCTTTAGCAGGTGGTTCTTTAGATGGTATTGAAAAGCCTCATCTTGGTTTTGTGACCCGTGGTGGTCGTGAG
ATGGAAAATCATTTTGAGTGTATGTGGGACATGTATCGGTCTATTCCCTCACTGGAAATTCCCGGTGCGTCTTATTTAGATGAATTTTATTGGTTG
GATAAGGATGATCCTAACTCATCCAACTGTCGTTTGATTCACAAGAGAGGAAATCGTGTGGATGATGACGGCCAGTATACGCTCGGTAAACAGTCA
AAAGAATTAATCCATTTAATCATGAAGACAGAAGAATCTCTAGGAGACCAAACCATTGAAGAGTTCTTCTCAGAAGATTTCTTTAAGAGTAATTTT
TGGGTGTATTGGGCAACCATGTTTGCTTTTGAAAAATGGCATTCTGCTGTAGAAATGCGACGCTATGCGATGAGGTTTATCCACCATATTGATGGT
TTGCCAGATTTCACCTCCCTCAAGTTCAACAAATATAACCAATATGACTCTATGGTCAAACCGATTATTGCTTACCTAGAATCACACGACGTTGAC
ATCCAATTTGACACAAAAGTCACTGATATTCAGGTGGAGCAAACAGCTGGTAAAAAGGTAGCAAAAACCATCCATATGACGGTGTCTGGGGAGGCT
AAGGCGATTGAGCTAACACCTGATGATTTGGTTTTTGTGACCAATGGTTCTATTACTGAAAGCAGCACATACGGTAGTCATCACGAAGTGGCTAAG
CCAACCAAAGCGTTAGGTGGTTCTTGGAATTTATGGGAAAATCTAGCTGCTCAATCAGATGATTTTGGTCATCCTAAAGTGTTTTACCAGGACTTG
CCTGCTGAAAGCTGGTTTGTGTCTGCTACAGCAACCATAAAACACCCAGCTATCGAGCCTTATATAGAACGTTTGACCCACCGTGACTTGCACGAT
GGCAAAGTGAACACTGGCGGCATCATCACTATTACAGATTCTAACTGGATGATGAGCTTTGCCATTCACCGTCAACCTCATTTTAAAGAACAAAAA
GAAAATGAGACCACTGTCTGGATTTACGGTCTTTATTCCAATAGTGAGGGCAATTACGTCCACAAGAAAATTGAGGAGTGTACAGGTCAAGAAATC
ACAGAAGAATGGTTGTACCACCTTGGGGTACCTGTTGATAAAATCAAGGACTTAGCGAGTCAGGACTATATCAATACAGTTCCTGTTTACATGCCT
TATATTACGAGTTACTTTATGCCACGCGTCAAAGGAGACCGTCCGAAAGTTATCCCAGATGGTTCAGTCAACTTGGCCTTTATTGGTAACTTTGCG
GAATCTCCATCTCGAGATACGGTCTTTACGACTGAGTATTCTATTCGTACTGCCATGGAAGCAGTGTATAGCTTCTTGAATGTGGAACGAGGCATC
CCAGAAGTCTTTAATTCAGCCTATGATATTCGTGAATTGCTCAAAGCCTTTTATTACCTTAATGATAAAAAGGCAATCAAGGATATGGATTTGCCA
ATTCCTGCACTGATTGAGAAAATCGGACATAAAAAAATCAAGGATACCTTTATCGAAGAATTGCTCAAAGATGCTAATCTTATG

SEQ ID 102

VMISLCLTIQGGLEMYYTSGNYEAFATPRKPEGVDQKSAYIVGTGLAGLAAAVFLIRDGHMAGERIHLFEELPLAGGSLDGIEKPHLGFVTRGGRE
MENHFECMWDMYRSIPSLEIPGASYLDEFYWLDKDDPNSSNCRLIHKRGNRVDDDGQYTLGKQSKELIHLIMKTEESLGDQTIEEFFSEDFFKSNF
WVYWATMFAFEKWHSAVEMRRYAMRFIHHIDGLPDFTSLKFNKYNQYDSMVKPIIAYLESHDVDIQFDTKVTDIQVEQTAGKKVAKTIHMTVSGEA
KAIELTPDDLVFVTNGSITESSTYGSHHEVAKPTKALGGSWNLWENLAAQSDDFGHPKVFYQDLPAESWFVSATATIKHPAIEPYIERLTHRDLHD
GKVNTGGIITITDSNWMMSFAIHRQPHFKEQKENETTVWIYGLYSNSEGNYVHKKIEECTGQEITEEWLYHLGVPVDKIKDLASQDYINTVPVYMP
YITSYFMPRVKGDRPKVIPDGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVYSFLNVERGIPEVFNSAYDIRELLKAFYYLNDKKAIKDMDLP
IPALIEKIGHKKIKDTFIEELLKDANLM

SEQ ID 103

ATGAAATTTTGTTATAATGTAGTCACTTACTGTACGAAAAGGAAGAATAATTTGCAAGAATACTCTATCGAAATTACTTTACAACATCCAGATGAT
ATGATGTCACTCTTTGGCAGCAATGAGCGCCATTTAAAATTAATCGAAGAAAATTTAGATGTTATCATTCATGCTAGAACTGAACGTGTTCAGGTA
TTAGGTGACTCTGAAGAAGCAGTAGAAACCGCTCGGTTAACCATTGAAGCATTATTAGTGCTTGTTAACCGCGGGATGACTGTGAATACTTCAGAT
GTTGTAACAGCCTTATCCATGGCACAAAATGGTTCAATTGATAAATTCGTTGCCCTTTATGAGGAAGAAATTATTAAGGATAGCTATGGTAAGCCT
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TTTTTAGCAGTCACTCTAGCAGTAACGGCACTAAAGCGTGGTCAAGTTAAACGAATAATCTTAACGAGACCAGCGGTTGAAGCTGGTGAAAGCCTT
GGTTTCTTGCCTGGAGATCTCAAAGAGAAAGTTGATCCTTATTTGAGACCAGTTTATGATGCCCTATATCAAATTTTAGGTAAAGAGCAAACAAGT
CGCTTAATGGAGCGTGAAATCATCGAAATTGCTCCATTGGCTTACATGCGTGGTCGTACTTTAGATGATGCATTTGTCATATTAGATGAAGCGCAA
AACACCACTATAATGCAAATGAAAATGTTCCTAACACGTCTTGGCTTCAATTCTAAAATGATTGTAAATGGCGATGTTAGCCAAATTGACTTACCA
AAGAATGTTAAATCTGGTTTGATTGATGCTGTTGAGAAATTACGAAATATCAAAAAGATTGACTTTATTCATTTATCAGCAAAGGATGTTGTAAGA
CACCCTGTCGTTGCTGAAATAATAAATGCTTATTCAGATTCAGAAAGTAGTCACAAGCTACAATCTGATAAGGAC

SEQ ID 104

MKFCYNVVTYCTKRKNNLQEYSIEITLQHPDDMMSLFGSNERHLKLIEENLDVIIHARTERVQVLGDSEEAVETARLTIEALLVLVNRGMTVNTSD
VVTALSMAQNGSIDKFVALYEEEIIKDSYGKPIRVKTLGQKIYVDSVKNHDVVFGIGPAGTGKTFLAVTLAVTALKRGQVKRIILTRPAVEAGESL
GFLPGDLKEKVDPYLRPVYDALYQILGKEQTSRLMEREIIEIAPLAYMRGRTLDDAFVILDEAQNTTIMQMKMFLTRLGFNSKMIVNGDVSQIDLP
KNVKSGLIDAVEKLRNIKKIDFIHLSAKDVVRHPVVAEIINAYSDSESSHKLQSDKD

SEQ ID 105

TTGCAAGAGTATTCTATTGACATTACCTTAACCCATCCTGATGATGTTTTAGCTCTTTTTGGTAGCAACGAGCGTCATTTGAAGCTAATAGAAGCT
CATTTAGGAGTTATTGTTCACGCAAGAACCGAGCGAGTCCAAGTGATTGGTGATGATGAAGAAGCTGTGGAATTGGCTCGATTGACCATCAAAGCC
CTACTGGTTCTAGTGGGTCGTGGCATGGTGGTCAACACATCAGATGTGGTGACAGCTTTATCTATGGCAGAATCTCATCAGATTGACCAATTTATG
GCGCTTTATGAAGAAGAAATCATTAAAGATAACTATGGTAAGGCAATACGAGTCAAAACATTAGGTCAAAAAACCTATGTTGATAGTGTCAAACGT
CATGATGTGGTTTTTGGTGTAGGACCTGCAGGGACAGGTAAAACCTTCTTAGCTGTTACGCTTGCAGTCACTGCTCTGAAAAGAGGACAGGTAAAG
CGTATTATTTTGACGCGTCCTGCGGTAGAAGCTGGCGAAAGCCTAGGTTTTTTACCAGGCGATTTGAAAGAAAAGGTGGATCCTTACCTCAGACCT
GTTTACGATGCCCTTTATCACATTTTAGGCAAGGAACAAACCACACGCCTGATGGAACGAGATGTGATTGAGATTGCTCCGTTAGCTTATATGCGA
GGTCGTACTCTGGATGACGCTTTTGTTATCTTAGATGAGGCTCAAAACACGACCATCATGCAAATGAAGATGTTTTTGACCCGTCTTGGTTTTAAT
TCTAAAATGATTGTCAATGGAGATACGAGTCAGATTGACCTCCCTCGAAATGTCAAGTCTGGTTTGATTGATGCTACTCAGAAATTACAAGGCATT
AAACAGATTGATTTTGTCTATTTCTCTGCTAAGGATGTTGTCCGACATCCTGTTGTGGCTGATATTATCAAGGCTTATGAAACGTCCTCAGAGGAG
ATGAAGGACTTACTAAAACCTAAGGCTAGTGACGTTGAAGCTGATTACCAGCCAGGCTTGACAAAATACCCTGTGATCGGTCAAGAGCAC

SEQ ID 106

LQEYSIDITLTHPDDVLALFGSNERHLKLIEAHLGVIVHARTERVQVIGDDEEAVELARLTIKALLVLVGRGMVVNTSDVVTALSMAESHQIDQFM
ALYEEEIIKDNYGKAIRVKTLGQKTYVDSVKRHDVVFGVGPAGTGKTFLAVTLAVTALKRGQVKRIILTRPAVEAGESLGFLPGDLKEKVDPYLRP

VYDALYHILGKEQTTRLMERDVIEIAPLAYMRGRTLDDAFVILDEAQNTTIMQMKMFLTRLGFNSKMIVNGDTSQIDLPRNVKSGLIDATQKLQGI
KQIDFVYFSAKDVVRHPVVADIIKAYETSSEEMKDLLKPKASDVEADYQPGLTKYPVIGQEH

SEQ ID 107

ATGGACCATTTCACAAAACTCTGGCAAGATTTCTCTAAACTTCCAAATGTTGTTGCTATAGCACTCGGAGGCTCACGCTCTGGTGACAGTTTTGAC
CAATCTTCCGATTATGATTTGTATGTTTATTGTGCAGCAACTCCTGATATCACTAGTCGTAAACGTATCCTTAACAAGCACTGTCATTACATTGAA
CTTAACAATCATTACTGGGAGCTTGAAGATAATGGTACTTTAAACGACGGAACTGATATTGATATTCTCTATCGTAACATAGATAACTTTTTATCA
GACTTAGAAGATGTCGTTGAACACCACAATTCTCGAATTGGATACACTACTTGTTTTTGGCATAACCTCATCAATTGCCAAATACTCTATGATCCT
GAAAATCAATTACAATCACTCAAAGAGAGATTCGAAGTTTCTTATCCCAGTCAGTTACAAAAACAAATTATCATTCAAAATCGTAACTTATTAACT
GGCAAGCTTCCCTCTTACGATAAACAAATTATAAAAGCCCTTAAACGCCAAGACTTTGTTAGTACTCACCATAGAACTACTGCTTTCTTAGATTCC
TACTTTGATATTATTTTTGCACTTAATAAGTTGACACATCCTGGCGAAAAAAGAATGATTTCCTATGCTAAGAAGAATGCTACATTGCTTCCTAAA
CATTTCGAAGAAAATATCATTAAACTATGTCATCACAACTCCAACGAACACACTGTTAAAGAAACATTAAACGATATAATAATGCATCTCGACGTC
ATGCTTAAAGAAAATTTTCAACACTTTATAGGT

SEQ ID 108

MDHFTKLWQDFSKLPNVVAIALGGSRSGDSFDQSSDYDLYVYCAATPDITSRKRILNKHCHYIELNNHYWELEDNGTLNDGTDIDILYRNIDNFLS
DLEDVVEHHNSRIGYTTCFWHNLINCQILYDPENQLQSLKERFEVSYPSQLQKQIIIQNRNLLTGKLPSYDKQIIKALKRQDFVSTHHRTTAFLDS
YFDIIFALNKLTHPGEKRMISYAKKNATLLPKHFEENIIKLCHHNSNEHTVKETLNDIIMHLDVMLKENFQHFIG

SEQ ID 109

ATGAAACAAGATTATATTTCCTACATTAGGTCAAAAGTTGGACATGAGACTATCTTTTTAACATATTCTGGTGGTATTTTGACAGATGGTAAGGGA
CGTGTCTTACTCCAATTAAGAGCTGATAAGAATTCTTGGGGAATTATTGGTGGATGTATGGAGTTAGGTGAGTCATCAGTAGATACATTGAAAAGA
GAATTTTTCGAAGAAACTGGATTGAGAGTGGAACCAATCAGACTGTTAAATGTTTATACTAACTTTCAAGACTCTTATCCCAATGGCGATAAAGCA
CAAACCGTCGGTTTTATTTATGAAGTAAGCTGTCCAAAACCAGTTAATATAGAAGGTTTTCATAATGAGGAAACATTGCAATTGGACTATTTTTCT
AAAGAAGACGTCAAAAATATTACGATCGTAAATGAACAACACCAATTAATTTTAGATGAATATTTTTCACAAACATTCCAAATGGGGCGT

SEQ ID 110

MKQDYISYIRSKVGHETIFLTYSGGILTDGKGRVLLQLRADKNSWGIIGGCMELGESSVDTLKREFFEETGLRVEPIRLLNVYTNFQDSYPNGDKA
QTVGFIYEVSCPKPVNIEGFHNEETLQLDYFSKEDVKNITIVNEQHQLILDEYFSQTFQMGR

SEQ ID 111

TTGGCTATAATGAGAAAGAATACTAACATAGTAAAGCGAGATCATATGCCACAAGACTACATTTCTTATATCCGCTCCAAAGTTGGGCATGATAAG
ATTATTCTTAACTTTGCTGGTGGGATTTTGACCAATGATGACGGCAAGGTGCTGATGCAGCTGCGTGGTGATAAGAAAACCTGGACTATTCCTGGT
GGCACTATGGAACTGGGTGAGAGCTCTTTAGAGACTTGCAAACGTGAGTTCTTAGAGGAAACCGGAATTGAGGTTGAAGCTGTTCGCTTACTGAAT
GTTTACACTCATTTTGAGGAAGTTTATCCCAACGGTGATGCTGTTCAGACTATTGTCTTTATCTATGAACTAACGGCTGTTTCTGATATGGCTATT
GATAACTTTCATAATGAGGAAACGCTCAAGTTACAATTTTTCTCTCATGAGGAGATAGCAGAGTTAGAGAGTGTCTCAGCCAAACATCGCCTGATG
TTAGAGGAATATTTTAGTGATAGCTTTGCTATGGGGCAT

SEQ ID 112

LAIMRKNTNIVKRDHMPQDYISYIRSKVGHDKIILNFAGGILTNDDGKVLMQLRGDKKTWTIPGGTMELGESSLETCKREFLEETGIEVEAVRLLN
VYTHFEEVYPNGDAVQTIVFIYELTAVSDMAIDNFHNEETLKLQFFSHEEIAELESVSAKHRLMLEEYFSDSFAMGH

SEQ ID 113

GTGACTGTTTTTTTAGAAAGCATAAGAAGTACAGAAAAAGAAAATTATGGAATATTTGATGGTGGGGATATGCTTTACTTACGGTATTGGAATGAT
ATACTTAAAGAAATCCAGTTT

SEQ ID 114

MTVFLESIRSTEKENYGIFDGGDMLYLRYWNDILKEIQF

SEQ ID 115

ATGAAGATAACATTACACGGCGTTGCTGAAACGTTATTAATCACCTTATATATTAGGGCTAAAGATGCGATGGCTAAACATCCGATACTTAATGAT
CAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGAATTCGC
GTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTC
GATAATGGACAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGAGCATGAAAGAGTTACTAATATA
GCAAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAGAAGGTGTTTTAATGTTTCTAAAA
GAAGATGACGTAGAGACTTTTCTTCATATCCTGACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCATAAGGAAATGATTAATAAA
GGAAAGCAACATGATACAGTAAAGTATATGGATACAGAATTTCAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCCTAAATTAAAG
CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATAATTGT
TTAGGTGTGTACGAATATAAAGCATCTGAGAAAAAG

SEQ ID 116

MKITLHGVAETLLITLYIRAKDAMAKHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLDTRFERV
DNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQNAPFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINK
GKQHDTVKYMDTEFQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKASEKK

SEQ ID 117

ATGTACGTTGAAATGATTGATGAAACTGGACAAGTTTCAGAAGATATCAAAAAGCAAACTCTTGATTTGTTAGAGTTTGCAGCACAAAAAACAGGT
AAAGAGAATAAAGAAATGGCTGTAACGTTTGTCACTAATGAACGTAGCCATGAATTGAATTTAGAGTATCGAGATACCGATCGTCCGACTGATGTT
ATCAGTTTAGAATATAAGCCTGAGGTTGATATTTCTTTTGATGAAGAAGATCTGGCTGAAAATCCTGAACTTGCTGAGATGCTAGAAGATTTTGAT
TCTTATATTGGTGAACTTTTTATTTCTATTGATAAAGCTAAAGAACAAGCAGAAGAGTACGGTCACTCTTATGAACGTGAAATGGGTTTTTTAGCT
GTACATGGTTTTTTGCATATTAACGGTTATGATCATTATACACCCGAAGAAGAAAAAGAGATGTTCAGCTTACAGGAAGAAATTTTAACTGCTTAT
GGACTTAAACGACAA

SEQ ID 118

MYVEMIDETGQVSEDIKKQTLDLLEFAAQKTGKENKEMAVTFVTNERSHELNLEYRDTDRPTDVISLEYKPEVDISFDEEDLAENPELAEMLEDFD
SYIGELFISIDKAKEQAEEYGHSYEREMGFLAVHGFLHINGYDHYTPEEEKEMFSLQEEILTAYGLKRQ

SEQ ID 119

GTGCCCAACATACCAAATGAGGTGGGCAGCCCTTCCCTAACAATTAACCTTATGTATATCGAGATGATTGACGAAACGGGACAAGTTTCGCAAGAG
ATTATGGAGCAAACACTTGATTTGCTCAATTTTGCTGCTCAAAAGACGGGCAAAGAAGAAAAAGAAATGTCTGTGACCTTTGTGACCAATGAAAGA
AGTCATGAACTCAACTTAGAATACCGAGATACTGATCGTCCAACAGATGTGATTTCTCTAGAATATAAGCCAGAAACGCCTATTTTATTTAGTCAA
GAGGATTTGGCTGCTGATCCTAGTTTGGCAGAGATGATGGCAGAGTTTGATGCTTATATTGGCGAATTGTTTATTTCTATTGACAAGGCGCGTGAG
CAGTCCCAAGAATATGGGCACTCTTTTGAGCGTGAAATGGGATTTTTGGCTGTTCATGGATTCTTACATATTAATGGGTATGATCACTACACCCTT
GAAGAAGAAAAAGAGATGTTTACCTTACAGGAAGAGATTTTGACTGCTTATGGCCTTACACGACAA

SEQ ID 120

VPNIPNEVGSPSLTINLMYIEMIDETGQVSQEIMEQTLDLLNFAAQKTGKEEKEMSVTFVTNERSHELNLEYRDTDRPTDVISLEYKPETPILFSQ
EDLAADPSLAEMMAEFDAYIGELFISIDKAREQSQEYGHSFEREMGFLAVHGFLHINGYDHYTLEEEKEMFTLQEEILTAYGLTRQ

SEQ ID 121

ATGTCAGAAAATCCTGATGCCTATATTATTCGTAGTCAAAATTTGCATAATCAGGATTTCCCAAGTAACCTCAAAGCTATTGCTAGGGCGGGTGCA
GGAACAAATAATATTCCTATTGAAGAGGCAAGTGCACAGGGAATAGTCGTGTTTAATACCCCAGGTGCAAATGCTAATGCTGTAAAAGAAGCGGTC
ATTGCTGCCTTATTACTTTCAGCTCGTGATTATTTAGGAGCTAACCGATGGGTTAATACTCTAACTGGAACAGATATTCCCAAACAAATTGAAGCA
GGAAAGAAAGCTTTTGCTGGTAATGAAATTGCAGGAAAAAAATTGGGAGTTATCGGCCTTGGTGCCATTGGAGCTAGAATTGCGAATGATGCTAGA
CGCTTAGGAATGACAGTTCTTGGTTATGATCCCTATGTTTCAATTGAAACAGCTTGGAATATTTCAAGCCATGTTCAAAGGGTTAAAGAGATTAAG
GATATTTTTGAAACTTGTGACTATATCACAATTCATGTTCCCTTAACAAATGAAACTAAGCATACTTTTGATGCGAAAGCTTTTTCAATCATGAAA
AAAGGAACTACGATTATCAACTTTGCTCGTGCAGAATTAGTCAATAACCAAGAGCTATTTGAAGCGATAGAAACTGGTGTTGTCAAGCGCTATATT
ACTGATTTTGGAGACAAAGAATTATTAAACCAAAAG

SEQ ID 122

MSENPDAYIIRSQNLHNQDFPSNLKAIARAGAGTNNIPIEEASAQGIVVFNTPGANANAVKEAVIAALLLSARDYLGANRWVNTLTGTDIPKQIEA
GKKAFAGNEIAGKKLGVIGLGAIGARIANDARRLGMTVLGYDPYVSIETAWNISSHVQRVKEIKDIFETCDYITIHVPLTNETKHTFDAKAFSIMK
KGTTIINFARAELVNNQELFEAIETGVVKRYITDFGDKELLNQK

SEQ ID 123

TTGATGAAATTAAAATTATATAATGTTAGAGGCGAAGAAGCAGTCTTAGCAAAAAAATGGGCTGATGACAATGGGATTGAGATTTCCTTGACGGAG
TCTCCCTTAACTCCTGAAACGGTTAAAGAAGCTGAAGGCTTTGACGGGATTGCCAATGCCCAAATTGGTCCTTTAGATGATGCGATTTATCCTCTC
TTAAAGGAAATGGGGATTAAACAAATCGCTCAGCACAGTGCTAGTGTCGATATGTATAACCTTGATTTGGCCACCGAAAATGACATTATTATCACA
AATGTTCCTAGCTATTCTCCAGAATCCATTGCAGAATTTACGGTTACTATTGTCCTTAATTTAATTCGTCATGTGGAGTTGATTCGTGAAAATGTT
AAAAAACAAAATTTCACTTGGGGACTCCCTATCCGCGGCCGTGTTTTAGGTGATATGACAGTTGCGATTATCGGAACTGGACGTATTGGTCTAGCT
ACTGCTAAAATCTTTAAAGGTTTTGGCTGCAAGGTCGTTGGATATGATATTTACCAAAGCGATGCTGCCAAAGCTGTCTTGGACTATAAGGAATCT
GTAGAAGAAGCGATTAAAGATGCTGATCTTGTTTCCTTACACATGCCACCAACTGCAGAGAACACACACCTTTTCAATTCTGATTTATTTAAATCA
TTCAAAAAAGGGGCTATTTTGATGAATATGGCGCGTGGTGCCGTCATTGAGACGCAAGATTTACTGGATGCTTTGGATGCAGGCTTACTGAGCGGA
GCTGGTATTGACACTTACGAATTTGAAGGACCTTATATACCTAAGAATTTTGAAGGTCAAGAAATTACAGATTCACTATTTAAAGCTTTGATTAAC
CATCCTAAGGTTATTTATACACCTCATGCAGCTTATTATACTGATGAAGCCGTTAAAAACCTAGTTGAAGGTGCCCTTAATGCTACAGTAGAGATT
ATCAAAACTGGGACAACGACAACTCGTGTTAAC

SEQ ID 124

LMKLKLYNVRGEEAVLAKKWADDNGIEISLTESPLTPETVKEAEGFDGIANAQIGPLDDAIYPLLKEMGIKQIAQHSASVDMYNLDLATENDIIIT
NVPSYSPESIAEFTVTIVLNLIRHVELIRENVKKQNFTWGLPIRGRVLGDMTVAIIGTGRIGLATAKIFKGFGCKVVGYDIYQSDAAKAVLDYKES
VEEAIKDADLVSLHMPPTAENTHLFNSDLFKSFKKGAILMNMARGAVIETQDLLDALDAGLLSGAGIDTYEFEGPYIPKNFEGQEITDSLFKALIN
HPKVIYTPHAAYYTDEAVKNLVEGALNATVEIIKTGTTTTRVN

SEQ ID 125

ATGCTTTTCATGAGAGATAATTTAGATTCTTTGATTCAGCCTGTTATTGATGAGATGGCTAAACATTATCAATGGTCTGATCAAGACAAAACTTTC
TATGAAGAAGAATTACATGAGACTCTAAAAGACAATGACTTGGCAGCTTTGAANNNNNTTAAT

SEQ ID 126

MLFMRDNLDSLIQPVIDEMAKHYQWSDQDKTFYEEELHETLKDNDLAALXXXN

SEQ ID 127

ATGGAATTTTCAAGAGAAACAAGACGCTTAGCTCTCCAAAAAATGCAAGAAAGAGATTTAGACCTACTGATTATTGGGGGAGGTATTACGGGTGCT
GGTGTGGCACTTCAGGCGGCAGCTAGTGGCCTAGATACGGGTCTGATTGAGATGCAAGATTTTGCTCAAGGAACCTCTAGCCGTTCAACCAAATTG
GTTCACGGGGGGCTTCGTTACTTGAAACAATTTGATGTGGAGGTGGTTTCAGATACGGTGTCAGAGCGGGCTGTGGTGCAACAAATTGCACCCCAC
ATTCCAAAACCAGACCCTATGTTATTACCTGTTTATGACGAACCTGGCAGTACCTTTAGCATGTTCCGTTTGAAGGTCGCTATGGATTTGTATGAT
CTTTTAGCAGGCGTGTCCAATACGCCAGCGGCCAACAAGGTGTTAACCAAAGAAGAAGTCTTAAAACGAGAACCAGACTTAAAACAAGAAGGCTTG
CTTGGTGGTGGGGTTTACCTTGATTTCCGCAATAATGACGCAAGGCTTGTTATTGAAAATATCAAACGAGCTAATCGTGATGGGGCTCTTATTGCT
AGTCATGTGAAAGCAGAAGATTTCTTGCTAGATGACAATGGTAAGATTATTGGTGTGAAGGCGCGTGATCTGCTGTCAGATCAAGAAATCATTATC
AAGGCTAAATTAGTCATCAACACCACAGGTCCATGGAGTGATGAGATTCGTCAATTCTCTCATAAGGGACAACCGATTCATCAAATGCGCCCTACA
AAAGGGGTGCATCTGGTAGTGGACCGTCAAAAATTACCAGTGTCTCAACCTGTCTATGTTGACACAGGGTTAAATGATGGTCGTATGGTCTTTGTC
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TTGTTAGGCGTTGTCAATAACCGCTTTCCAAATGCCAACGTGACCATTGATGATATTGAAAGCAGTTGGGCTGGTCTTCGCCCCTTGTTATCAGGT
AATAGTGCTTCTGACTACAATGGTGGCAACAGCGGTAAAGTCAGTGATGATAGTTTTGATCACTTGGTTGATACTGTCAAAGCCTATATTAACCAC
GAAGATAGCCGAGAAGCTGTTGAAAAAGCTATTAAGCAGGTTGAAACCAGCACATCTGAAAAAGAATTGGATCCGTCTGCAGTGTCACGAGGTTCA
AGTTTTGAGCGTGATGAGAATGGACTCTTTACCTTGGCAGGTGGTAAGATTACCGACTATCGCAAAATGGCTGAAGGAGCATTGACAGGGATTATT
CAAATCCTCAAAGAAGAGTTTGGCAAATCCTTCAAGCTTATCAATTCAAAAACCTATCCTGTTTCAGGAGGTGAAATCAATCCAGCCAATGTAGAT
TCGGAAATAGAAGCCTATGCTCAATTAGGAACTCTTAGTGGTCTTTCGATGGATGATGCTAGGTATTTGGCAAACCTTTATGGTTCTAATGCGCCA
AAAGTCTTTGCCTTAACTCGTCAATTAACAGCAGCTGAAGGGTTAAGTTTAGCTGAAACCTTGTCCTTACATTATGCGATGGATTATGAAATGGCT
CTTAAACCGACAGATTATTTCTTGAGAAGAACAAATCACCTCTTATTTATGCGAGATAGCCTAGATGCTTTGATTGACCCAGTGATTAATGAAATG
GCTAAACATTTTGAATGGTCTGATCAGGAAAGAGTGGCACAAGAAGACGATCTTCGTCGCGTGATTGCAGACAATGATTTGAGTGCCTTAAAAGGC
CATCAGGAGGGT

SEQ ID 128

MEFSRETRRLALQKMQERDLDLLIIGGGITGAGVALQAAASGLDTGLIEMQDFAQGTSSRSTKLVHGGLRYLKQFDVEVVSDTVSERAVVQQIAPH
IPKPDPMLLPVYDEPGSTFSMFRLKVAMDLYDLLAGVSNTPAANKVLTKEEVLKREPDLKQEGLLGGGVYLDFRNNDARLVIENIKRANRDGALIA
SHVKAEDFLLDDNGKIIGVKARDLLSDQEIIIKAKLVINTTGPWSDEIRQFSHKGQPIHQMRPTKGVHLVVDRQKLPVSQPVYVDTGLNDGRMVFV
LPREEKTYFGTTDTDYTGDLEHPQVTQEDVDYLLGVVNNRFPNANVTIDDIESSWAGLRPLLSGNSASDYNGGNSGKVSDDSFDHLVDTVKAYINH
EDSREAVEKAIKQVETSTSEKELDPSAVSRGSSFERDENGLFTLAGGKITDYRKMAEGALTGIIQILKEEFGKSFKLINSKTYPVSGGEINPANVD
SEIEAYAQLGTLSGLSMDDARYLANLYGSNAPKVFALTRQLTAAEGLSLAETLSLHYAMDYEMALKPTDYFLRRTNHLLFMRDSLDALIDPVINEM
AKHFEWSDQERVAQEDDLRRVIADNDLSALKGHQEG

SEQ ID 129

ATGGTTCGTACAACTCGTCCAACAACTGATAAGGTTAAAGGCGCTATTTTTAATATGATTGGTCCTTTTTTTGAAGGTGGTCGTGTTTTAGACCTT
TTTTCTGGCAGTGGTAGCTTAGCTATTGAGGCGATCTCAAGGGGAATGGACCAAGCTGTCCTAGTTGAAAAAGATAGGCGTGCGCAGGTCGTTATT
CAAGAAAATATTGCAATGACTAAGAGTCCGGAGCAATTTCAATTATTAAAAATGGAAGCCAACCGTGCTTTAGAACAATTAACGGGACAATTTGAT
TTGGTCTTGTTGGACCCGCCATATGCTAAGGAAGAAATTGTAAAGCAAATCCAAATCATGGATAGCAAGGGTTTATTAGGCGATGATATCATGATT
GCTTGTGAAACGGACAAATCAGTTGATTTACCTGAAGAAATTGCTTCTTTTGGGATATGGAAACAGAAAATTTATGGCATTTCTAAAGTAACGGTC
TACGTTCGT

SEQ ID 130

MVRTTRPTTDKVKGAIFNMIGPFFEGGRVLDLFSGSGSLAIEAISRGMDQAVLVEKDRRAQVVIQENIAMTKSPEQFQLLKMEANRALEQLTGQFD
LVLLDPPYAKEEIVKQIQIMDSKGLLGDDIMIACETDKSVDLPEEIASFGIWKQKIYGISKVTVYVR

SEQ ID 131

ATGAGAGTTGTATCAGGTGAATTTGGTGGGCGTCCTTTAAAGACGCTCGATGGAAAGATAACACGCCCTACTTCAGACAAAGTTAGAGGTGCGATT
TTTAATATGATAGGACCTTACTTTAATGGTGGTCGTGTTTTAGATTTGTTTGCAGGTTCAGGTGGATTAGCCATTGAGGCTGTTTCTCGTGGGATG
TCTGCTGCAGTTTTGGTTGAGAAGAATCGTAAAGCGCAAGCTATTATTCAAGACAATATTATAATGACTAAAGCTGAGAATCGGTTTACCTTGTTA
AAAATGGAAGCTGAGCGAGCTATTGATTGCTTGACTGGTCGATTTGACTTAGTCTTTTTAGACCCTCCTTATGCCAAAGAAACAATTGTGGCAACT
ATTGAAGCTTTAGCAGCTAAAAACTTATTGAGTGAACAGGTTATGGTTGTCTGTGAGACAGATAAAACAGTCTTGTTGCCAAAAGAGATTGCAACG
TTAGGTATTTGGAAAGAAAAAATTTATGGAATTAGTAAGGTAACAGTTTATGTTAAC

SEQ ID 132

MRVVSGEFGGRPLKTLDGKITRPTSDKVRGAIFNMIGPYFNGGRVLDLFAGSGGLAIEAVSRGMSAAVLVEKNRKAQAIIQDNIIMTKAENRFTLL
KMEAERAIDCLTGRFDLVFLDPPYAKETIVATIEALAAKNLLSEQVMVVCETDKTVLLPKEIATLGIWKEKIYGISKVTVYVN

SEQ ID 133

ATGACAAAGAAAGCTTTATTTACAGGTTCATTTGATCCTGTTACTAATGGACATTTAGATATTATTGAGCGCGCCAGCTATCTATTTGATCATGTT
TACATTGGGTTATTTTATAACCTTGAGAAGCAAGGTTACTTTTCGATTGAGTGCCGTAAAAAAATGTTAGAAGAAGCTATCCGTCAGTTTAAGAAT
GTTTCAGTTTTAGTGGCGCAAGATAGACTGGCTGTTGACTTAGCAAGGGAAGTGGGAGCAAAATATTTTGTTCGAGGTCTGCGTAATAGCCAGGAT
TTTGATTATGAAGCCAATTTGGAGTTTTTTAATAAACAGTTGGCAGATGATATTGAGACAGTTTATTTATCAACGTCGCCATCTTTGAGTCCGATA
TCATCTAGTCGCATCCGTGAATTGATACATTTTAAGGCTTCTGTGAAGCCTTTTGTTCCAAAGAGTGTTGTTAGAGAAGTGGAGAAAATGAGTGAA
GAA

SEQ ID 134

MTKKALFTGSFDPVTNGHLDIIERASYLFDHVYIGLFYNLEKQGYFSIECRKKMLEEAIRQFKNVSVLVAQDRLAVDLAREVGAKYFVRGLRNSQD
FDYEANLEFFNKQLADDIETVYLSTSPSLSPISSSRIRELIHFKASVKPFVPKSVVREVEKMSEE

SEQ ID 135

ATGTTAACTAAAATAGGACTTTATACAGGGTCATTTGATCCTGTTACAAACGGTCATCTCGATATTGTTAAACGGGCAAGTGGCCTATTTGATCAA
ATATATGTTGGGATTTTTGATAATCCTACCAAAAAAAGCTATTTTAAACTAGAAGTTCGTAAAGCAATGCTTACTCAAGCTCTGGCTGATTTTACA
AATGTAATTGTAGTAACTTCGCACGAACGTTTAGCTATTGATGTAGCTAAAGAATTACGAGTAACTCACTTGATTAGAGGCTTGCGAAATGCAACT
GACTTTGAGTATGAAGAAAATTTGGAATATTTTAATCACCTTTTAGCTCCAAATATTGAAACCGTCTATTTGATATCAAGAAATAAATGGCAGGCC
CTTAGCTCTAGTCGTGTGAGAGAGCTAATTCATTTTCAGTCTTCCTTAGAAGGTTTGGTTCCTCAGTCGGTTATTGCTCAAGTGGAGAAAATGAAT
GAAAAGACT

SEQ ID 136

MLTKIGLYTGSFDPVTNGHLDIVKRASGLFDQIYVGIFDNPTKKSYFKLEVRKAMLTQALADFTNVIVVTSHERLAIDVAKELRVTHLIRGLRNAT
DFEYEENLEYFNHLLAPNIETVYLISRNKWQALSSSRVRELIHFQSSLEGLVPQSVIAQVEKMNEKT

SEQ ID 137

TTGGATCTCTATTCTTCACTCATTTTCTCCACTTCTCTAACAACACTCTTTGGAACAAAAGGCTTCACAGAAGCCTTAAAATGTATCAATTCACGG
ATGCGACTAGATGATATCGGACTCAAAGATGGCGACGTTGATAAA

SEQ ID 138

MDLYSSLIFSTSLTTLFGTKGFTEALKCINSRMRLDDIGLKDGDVDK

SEQ ID 139

GTGAAGAATAGAGATCCAAAAAGAAAACATAAAAGTTTACTAGGTCTGCTTAAATGGTGGATTATAGGTTTTGCTTTTTTATTGTTAGTATTAGCA
AGCCTTGTAGTGAGACTACCTTATTATTTGGAAATGCCAGGTGGAGCTTATGATATCCGTTCGGTATTGAAAGTGAATAAAAAGGCTGATAAAGCT
AAGGGTTCGTACAATTTTGTAGCGGTATCTGTCAGTCAAGCAACGCCAGCTCAGGTTCTTTATGCTTGGTTAACTCCTTTTACAGAATTATCTAGT
AAAGAGGAGACAACAGGTGGCTTTAGTAATGACGATTATCTCAGAATTAATCAATTCTACATGGAGACTTCTCAAAATGAGTCCATCTATCAAGCT
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GCTGATACAGTCACAGGAGTTAATGGCAAAAGTTTCAAAAATTCTTCTCAACTTATCAAATATGTTGCAGCTCTTCATCTAGGTGATAAAGTAAAG
GTACAATACACAAGTCAAGGTAAAAAGAAAGAATCAGTTGGTAAAGTTATTAAACTATCAAACGGTAAAAATGGTATTGGTATCGGTTTGACAGAC
CATACAGAAGTATTATCTGATGTTCCTGTGGACTTTAATACTGAAGGTGTTGGAGGACCAAGTGCAGGTTTAATGTTTACTTTAGCGATTTACGAC
CAATTGGTTAAAGAAGATTTACGTAAAGGACGTAAGATTGCAGGTACTGGTACTATTGAGCAAAATGGGCATGTTGGCGATATTGGTGGAGCAGGT
TTGAAAGTTGTTTCAGCGGCTAAAAAAGGAATGGATATTTTCTTTGTTCCTAATAATCCGATCGATAAAAATGCTAAAAAAGGCAAAACAAAGGTT
CAGACGAATTATCAAGAGGCAAAAGCAGCAGCTAAGCGATTAGGTACGAAGATGAAAATTGTACCAGTTCAAAATGTTCAGCAAGCTATTGATTAT
TTGAAAAAAACAAAA

SEQ ID 140

MKNRDPKRKHKSLLGLLKWWIIGFAFLLLVLASLVVRLPYYLEMPGGAYDIRSVLKVNKKADKAKGSYNFVAVSVSQATPAQVLYAWLTPFTELSS
KEETTGGFSNDDYLRINQFYMETSQNESIYQALKLANKQVSLTYKGVYVLNLAKNSTFKDRLHLADTVTGVNGKSFKNSSQLIKYVAALHLGDKVK
VQYTSQGKKKESVGKVIKLSNGKNGIGIGLTDHTEVLSDVPVDFNTEGVGGPSAGLMFTLAIYDQLVKEDLRKGRKIAGTGTIEQNGHVGDIGGAG
LKVVSAAKKGMDIFFVPNNPIDKNAKKGKTKVQTNYQEAKAAAKRLGTKMKIVPVQNVQQAIDYLKKTK

SEQ ID 141

ATGAAAAGACTTAAAAAAAATCAAATGGTGGTTAGTGGGTCTGCTAGCTTTAATCTCTTTGTTGCTAGCGTTATTTTTTCCGCTACCTTATTATATT
GAAATGCCTGGAGGCGCTTACGATATTCGGACTGTCTTACAAGTCAATGGCAAAGAAGACAAACGAAAAGGAGCTTACCAGTTTGTTGCAGTGGGC
ATTAGTCGTGCCAGCCTCGCTCAGCTATTATATGCTTGGCTGACACCGTTTACTGAAATTAGTACAGCAGAAGATACAACAGGCGGATACAGCGAT
GCTGATTTCCTTCGAATTAATCAATTTTACATGGAAACATCACAAAATGCAGCTATTTATCAAGCTTTATCCTTAGCTGGAAAACCAGTTACATTA
GATTATAAAGGCGTATATGTTTTAGACGTAAACAACGAATCTACTTTTAAAGGAACGCTACACTTAGCAGATACTGTAACAGGTGTAAATGGTAAA
CAGTTTACTAGTTCAGCAGAACTTATTGACTATGTTTCTCACCTAAAACTAGGGGATGAAGTTACGGTTCAGTTTACGAGTGATAATAAGCCTAAA
AAAGGAGTTGGCCGTATTATCAAACTGAAAAATGGGAAAAATGGGATTGGCATTGCCTTGACTGATCATACAAGTGTCAATTCAGAAGACACAGTG
ATCTTTAGTACTAAAGGAGTAGGAGGACCTAGTGCTGGTCTAATGTTTACTCTTGATATATATGATCAAATAACTAAAGAAGATTTACGCAAGGGC
CGTACAATTGCAGGTACAGGAACTATTGGCAAGGATGGCGAAGTAGGAGATATTGGTGGTGCAGGTCTTAAAGTAGTTGCAGCAGCTGAAGCTGGT
GCAGATATATTTTTTGTTCCGAATAATCCTGTTGATAAGGAAATTAAAAAAGTTAATCCAAATGCTATAAGTAATTACGAAGAAGCCAAACGGGCA
GCCAAACGACTAAAGACCAAAATGAAGATTGTTCCTGTTACGACTGTTCAAGAGGCACTGGTTTATCTTCGCAAA

SEQ ID 142

MKRLKKIKWWLVGLLALISLLLALFFPLPYYIEMPGGAYDIRTVLQVNGKEDKRKGAYQFVAVGISRASLAQLLYAWLTPFTEISTAEDTTGGYSD
ADFLRINQFYMETSQNAAIYQALSLAGKPVTLDYKGVYVLDVNNESTFKGTLHLADTVTGVNGKQFTSSAELIDYVSHLKLGDEVTVQFTSDNKPK
KGVGRIIKLKNGKNGIGIALTDHTSVNSEDTVIFSTKGVGGPSAGLMFTLDIYDQITKEDLRKGRTIAGTGTIGKDGEVGDIGGAGLKVVAAAEAG
ADIFFVPNNPVDKEIKKVNPNAISNYEEAKRAAKRLKTKMKIVPVTTVQEALVYLRK

SEQ ID 143

ATGACAGAGCTTATAAGAATACTACATTTAAATGATCTGCACTCTCATTTTGAGAATTTTCCTAAGGTAAAACGATTTTTTCATGACAATCAAGCG
CAGCCAATAGAGACGATTTCACTTGACTTGGGGGATAATATTGATAAAAGCCATCCTTTGACAGAAGCAAGCTCGGGAAAGGCTAATGTCCAATTG
ATGAATGAACTGGGTATTGAGCTTGCTACTATTGGTAATAATGAAGGAGTTGGTTTATCCAAAAAAGACTTGGACCAAGTCTACAAAGATTCAGAT
TTTACGGTTATTGTTGGCAATCTAAAAGATAACATAATCGAACCGAGTTGGGCAAAACCTTACATTATTTATGAGACGCAGCAAGGAACTAAGCTT
GCCTTTTTAGCTTATACTTTTCCTTATTATAAAACCTATGAACCTAATGGGTGGACGATAGAAGATCCAATTGACTGTCTTAAATGCCATTTACAA

ATAAATGAGATAAAAGAGGCAAATTGTCGCATTTTGATGAGTCATTTAGGTATTCGTTTTGATACAAGGATTGCTCAAGAATTTTCAGAAATTGAC
CTTATTATAGGTGCACATACACACCATTTATTTGAGGAAGGGGAGCTAATTAACGGTACATATCTTGCAGCAGCTGGTAAATATGGTCGCTTTGTT
GGGAGTATTGATATAACTTTTGATAATCATACACTAAAAGATATTTTAATCTCAACATGTGATACAAAACAACTAACTGGTTATCCTTCGGACAGT
GACTGGCTAAGAAGATTGAGTCAGAAGGTAAAGAACAGCTTAGAAAAGAAAGTT

SEQ ID 144

MTELIRILHLNDLHSHFENFPKVKRFFHDNQAQPIETISLDLGDNIDKSHPLTEASSGKANVQLMNELGIELATIGNNEGVGLSKKDLDQVYKDSD
FTVIVGNLKDNIIEPSWAKPYIIYETQQGTKLAFLAYTFPYYKTYEPNGWTIEDPIDCLKCHLQINEIKEANCRILMSHLGIRFDTRIAQEFSEID
LIIGAHTHHLFEEGELINGTYLAAAGKYGRFVGSIDITFDNHTLKDILISTCDTKQLTGYPSDSDWLRRLSQKVKNSLEKKV

SEQ ID 145

ATGGATGCGATGCTGTTTTACGCAGGTGCAGATGTTGCTATTATCAATTCTGGCTTAATTGTTCAGCCATTTGAAAAAGACTTTTCGAGGAAAAAT
CTCCACGAATCATTACCTCATCAAATGCGCCTCGCTAAATTGACAGTGAGTAGTCAAGAACTTTTAGAGATTTATGAAACTATTTATCAACAAGGT
CAATTTTTAGCGCAACAAAAGATTCATGGTATGGGCTTTCGTGGCAAGTGCTTTGGAGAAGTTTTACATTCGGGATTTGATTACAAAAATGGAAAA
ATAGTGTATAATGAGAAAGATATTGATGCCAAAGAAGAAGTGATTCTTGTAATCGTTGATCAGTATTATTTTGCATCGTATTTTGAGTGTTTAAAA
ACGAAAAAAGTAGACTTGCTTTTCCTGAATTACTCAGAGATGTGGCAGCAGATTATT

SEQ ID 146

MDAMLFYAGADVAIINSGLIVQPFEKDFSRKNLHESLPHQMRLAKLTVSSQELLEIYETIYQQGQFLAQQKIHGMGFRGKCFGEVLHSGFDYKNGK
IVYNEKDIDAKEEVILVIVDQYYFASYFECLKTKKVDLLFLNYSEMWQQII

SEQ ID 147

ATGCGAAAAGAAGTGACACCAGAGATGCTTAACTATAATAAGTATCCTGGCCCACAGTTCATTCACTTTGAAAATATCGTTAAAAGTGATGATATT
GAATTTCAACTTGTTATTAATGAAAAATCAGCTTTTGATGTGACTGTCTTTGGACAACGTTTTTCTGAGATTTTATTAAAATATGATTTTATCGTT
GGCGATTGGGGTAACGAGCAGTTGAGGCTAAGAGGCTTTTACAAAGATGCTAGTACAATTAGAAAAAATAGCCGGATTTCACGTTTAGAAGATTAT
ATTAAAGAGTATTGTAACTTTGGTTGTGCTTATTTTGTGTTGGAGAATCCAAATCCTAGAGATATTAAATTTGATGATGAAAGACCTCATAAGCGT
CGTAAGTCAAGATCCAAATCACAATCATCAAAGTCACAAACTAGAAATAATCGTTCCCAGTCAAATGCCAATGCTCATTTTACAAGTAAAAAGCGT
AAAGACACAAAACGCCGTCAAGAACGTCATATTAAAGAAGAGCAAGATAAGGAAATGACCTCTGCAAAGCAGCATTTTGTTATTCGTAAGAAAAAA

SEQ ID 148

MRKEVTPEMLNYNKYPGPQFIHFENIVKSDDIEFQLVINEKSAFDVTVFGQRFSEILLKYDFIVGDWGNEQLRLRGFYKDASTIRKNSRISRLEDY
IKEYCNFGCAYFVLENPNPRDIKFDDERPHKRRKSRSKSQSSKSQTRNNRSQSNANAHFTSKKRKDTKRRQERHIKEEQDKEMTSAKQHFVIRKKK

SEQ ID 149

ATGGATTTTTCAGAAAGGTGTCAAATGAAAAAAGAAATTTCGCCAGAAATGTACAACTATAATAAATTTCCAGGTCCCAAATTTATTCATTTTGAA
GAGCAAGTTAAGGCTGAAGGCATTGATTTGTTACTCTTAGAAGATGTTAAGAACGCTTTTGATACGACTAGCTTTGGTCAACGTTATACAGAAGTT
CTCCTAAAGTATGACTATATTGTTGGCGATTGGGGAAATGAACAGCTTCGTCTTAAAGGGTTTTATAAGGATAGTGACGATATCAAGAAAACGAAT
CGCATCTCACGTTTAGAAGATTATATTAAAGAATTTTGCAATTTTGGTTGTGCTTATTTTGTTTTAGAAAATCTTCATCCACAAGATATTAAATTT
GAAGAGGAGCGCCAACCAAGACGAAAGAAATCACCTAAATCAAAATCAAATCGTCGCAAGCCAAACTATTCAAATCAGCAGCCCGCAACACCTAAG
AGCAAATCGAAGCGGGCATCAAAAGAAAAGCAACCTGAAAACCAAGCGTTTACCAGTCAAAAACGTCGAAGTAATACTAAGCATAAAGAAAAGTCA
AAACGTAATCAGACTAGTCAACTTAATACCAAAATTAGTCATTTTATCATCAGAAAGAAAGATAAA

SEQ ID 150

MDFSERCQMKKEISPEMYNYNKFPGPKFIHFEEQVKAEGIDLLLLEDVKNAFDTTSFGQRYTEVLLKYDYIVGDWGNEQLRLKGFYKDSDDIKKTN
RISRLEDYIKEFCNFGCAYFVLENLHPQDIKFEEERQPRRKKSPKSKSNRRKPNYSNQQPATPKSKSKRASKEKQPENQAFTSQKRRSNTKHKEKS
KRNQTSQLNTKISHFIIRKKDK

SEQ ID 151

ATGAAGAAAGAAAATATTATGCCTAAAAAAACTGATACACCCGCCTATAAACCCTCTATTTATAGCTTAACTCGCGATGAACTAATAGCTTGGGCT
ATTGAACATGGAGAAAAGAAATTCCGTGCTTCACAAATCTGGGACTGGCTCTATAAAAAGCGTGTGCAAAGCTTCGATGAAATGACTAACATTTCC
AAAGATTTTATTGCACTTTTGAACGAGAATTTTGTTGTTAATCCTCTAAAACAACGTATTGTTCAAGAATCTGCTGATGGAACTGTTAAATACCTT
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GGTTGCACTTTCTGTGCAAGTGGTTTAATAAAGAAACAACGTGATCTTAACAATGGCGAAATCACTGCTCAAATTATGCTTGTTCAAAAATATTTT
GATGAACGTGGACAAGGTGAGCGCGTTAGTCACATTGTGGTCATGGGAATAGGTGAACCCTTTGATAACTATACCAATGTATTAAAATTCTTGCGT
ACAGTTAATGATGATAATGGATTAGCTATTGGTGCACGTCACATTACAGTGTCTACTTCAGGTTTAGCACATAAAATTCGTGAATTTGCAAATGAA
GGTGTACAAGTTAACTTAGCAGTATCTCTTCATGCTCCAAATAACGATTTACGATCAAGTATCATGCGTATTAATCGTTCTTTCCCTCTTGAAAAG
TTGTTTGCGGCTATTGAATATTATATTGAGACGACTAACCGTCGTGTAACATTTGAGTATATTATGTTAAATGGTGTCAACGATACCCCAGAAAAT
GCTCAAGAGTTAGCAGATTTAACGAAAAAGATTCGCAAATTATCTTATGTCAATTTAATTCCTTACAATCCTGTCTCAGAACATGACCAGTATAGT
CGTAGTCCTAAAGAGCGTGTAGAAGCTTTCTATGACGTTTTGAAGAAAAATGGAGTTAACTGTGTTGTTCGTCAAGAACATGGTACGGACATTGAT
GCAGCTTGCGGGCAATTACGTTCAAACACAATGAAACGCGATCGTCAAAAAGCGAAGGTAGGGCAG

SEQ ID 152

MKKENIMPKKTDTPAYKPSIYSLTRDELIAWAIEHGEKKFRASQIWDWLYKKRVQSFDEMTNISKDFIALLNENFVVNPLKQRIVQESADGTVKYL
FELPDGMLIETVLMRQHYGLSVCVTTQVGCNIGCTFCASGLIKKQRDLNNGEITAQIMLVQKYFDERGQGERVSHIVVMGIGEPFDNYTNVLKFLR
TVNDDNGLAIGARHITVSTSGLAHKIREFANEGVQVNLAVSLHAPNNDLRSSIMRINRSFPLEKLFAAIEYYIETTNRRVTFEYIMLNGVNDTPEN
AQELADLTKKIRKLSYVNLIPYNPVSEHDQYSRSPKERVEAFYDVLKKNGVNCVVRQEHGTDIDAACGQLRSNTMKRDRQKAKVGQ

SEQ ID 153

ATGAAACCATCGATTTATAGCTTAACACGCGATGAACTGATCGCGTGGGCAGTTGAACGCGGCCAAAAACAGTTTAGAGCTACTCAAATTTGGGAT
TGGCTCTATAAAAAAAGAGTTCAATCTTTTGAGGAGATGACGAATATTTCTAAAGATTTTGTTTCTATTTTAAATGATAGTTTCTGTGTCAATCCT
TTAAAACAGCGAGTTGTACAAGAGTCAGCTGATGGTACAGTAAAATATTTATTTGAACTGCCCGATGGTATGTTAATTGAAACAGTTTTAATGCGT
CAACATTATGGTCATTCTGTTTGTGTGACGACTCAAGTTGGCTGTAACATTGGCTGTACTTTTTGTGCTAGTGGATTGATCAAAAAGCAACGTGAT
CTAAACAGTGGGGAAATTACAGCTCAAATCATGTTAGTCCAAAAATATTTTGACGATAGAAAGCAAGGTGAGCGGGTTAGCCATGTTGTCGTAATG
GGCATTGGTGAACCTTTTGATAATTACAAAAATGTCATGTGCTTTCTTCGCGTCATCAACGATGATAATGGCTTAGCAATTGGTGCCCGTCATATT
ACAGTCTCTACCTCAGGGTTAGCTCACAAGATTCGGGATTTTGCAAACGAGGGAGTACAGGTTAACTTAGCAGTCTCGTTGCATGCACCAAATAAT
GATTTACGTTCAAGTATTATGCGAGTAAATCGCTCTTTTCCGCTTGAAAAGCTCTTTTCAGCTATAGAATACTATATTGAAAAAACGAATCGTCGT
GTCACTTTTGAATACATTATGCTAAATGAAGTTAACGATAGCATTAAGCAAGCTCAAGAATTAGCAGACTTAACTAAAACTATTCGTAAGTTATCT
TATGTTAACTTGATTCCGTATAATCCTGTTTCAGAACATGATCAGTATAGTAGAAGTCCTAAAGAGCGAGTTCTAGCGTTTTATGATGTGCTAAAG
AAAAATGGAGTTAACTGTGTGGTGCGTCAAGAGCACGGAACAGATATTGATGCAGCCTGTGGCCAGTTACGTTCTAAAACGATGAAAAAAGATCGC
GAAAAGGTTACAGCGACAAAA

SEQ ID 154

MKPSIYSLTRDELIAWAVERGQKQFRATQIWDWLYKKRVQSFEEMTNISKDFVSILNDSFCVNPLKQRVVQESADGTVKYLFELPDGMLIETVLMR
QHYGHSVCVTTQVGCNIGCTFCASGLIKKQRDLNSGEITAQIMLVQKYFDDRKQGERVSHVVVMGIGEPFDNYKNVMCFLRVINDDNGLAIGARHI
TVSTSGLAHKIRDFANEGVQVNLAVSLHAPNNDLRSSIMRVNRSFPLEKLFSAIEYYIEKTNRRVTFEYIMLNEVNDSIKQAQELADLTKTIRKLS
YVNLIPYNPVSEHDQYSRSPKERVLAFYDVLKKNGVNCVVRQEHGTDIDAACGQLRSKTMKKDREKVTATK

SEQ ID 155

ATGCTTAAAAGATTACTTACTGAAGATGGGGAATTGACAAAGATTAGTCGTCGTTTCGTTTGGATGTTAGTGATTATCTATTGTCTTATTATTGTC
AGGATGTGTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAACTCCGAATGTTCAGCGCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAAT
TCTTTTCGTAGTTTAGATCAGCTAACTAGCTTTAAAGAGATTTTTTGGGTTATTGGTCAAAATGTAGTGAATATTTTACTGCTGTTTCCTCTCATT
ATAGGGTTACTATCCCTAAAGCCAAGTTTACGGAAATATAAAAGCGTTATATTACTTGCTTTCTTGATGTCTATTTTCATAGAGTGTACTCAAGTT
GTTTTAGATATTTTAATAGATGCTAATCGGGTTTTTGAAATCGACGATCTATGGACAAATACCTTAGGCGGTCCTTTCGCCCTATGGACTTATCGA
AACATAAAAGGTTGGCTTCTAACTATTAGAAAA

SEQ ID 156

MLKRLLTEDGELTKISRRFVWMLVIIYCLIIVRMCFGPQIMIEGVSTPNVQRFGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVVNILLLFPLI
IGLLSLKPSLRKYKSVILLAFLMSIFIECTQVVLDILIDANRVFEIDDLWTNTLGGPFALWTYRNIKGWLLTIRK

SEQ ID 157

ATGTCTATTATAAAAAATTTGTGGTGGTTTTTTAAGGAAGAAAAGAAGCGCTATCTTATTGGAATTTTGTCATTAAGTTTGGTTGCGGTGTTAAAT
CTTATCCCTCCTAAAATCATGGGATCAGTTATTGATGCTATTACAACTGGAAAATTAACAAGACCACAATTGCTCTGGAATTTATTAGGTTTGGTT
TTGTCAGCTTTAGCTATGTATGGGCTGCGTTATATTTGGCGTATGTATATTTTAGGGACTTCTTACAAATTGGGTCAAGTTGTCAGATACCGTTTA
TTTGAACATTTTACAAAAATGTCTCCTTCTTTTTATCAGAAATATCGTACAGGTGATTTAATGGCGCACGCGACCAACGACATCAATTCTCTAACA
CGTCTTGCAGGAGGAGGAGTTATGTCAGCAGTGGATGCCTCTATCACAGCATTAGTAACGCTTATCACCATGTTCTTTACTATTTCGTGGCAAATG
ACATTAATTGCGGTTATCCCTTTGCCCTTAATGGCCTTAGCAACTAGTAAATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCC
TTTTCAGAATTAAATAATAAAGTGCAAGAAAGTGTCTCTGGCGTCAAAGTGACTAAATCATTTGGTTATCAAGAACAAGAAATTGCTTCTTTTCAA
GAGGTTAATCAGATGACTTTCGTGAAGAACATGCGGACCATGACTTATGATGTCATGTTTGATCCTTTAGTTCTTCTTTTTATAGGTGCCTCCTAC
GTATTAACATTGGCTATGGGAGCTTTTATGATTTCAAAAGGTCAAGTTACTGTTGGTGACTTGGTAACATTTGTGACGTATTTAGATATGTTGGTA
TGGCCCTTGATGGCGATTGGTTTCTTGTTCAATATGGTACAGCGTGGTAGTGTTTCTTATAACCGTATTAATAGCCTACTTGAGCAAGAATCGGAT
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CATGATGTGACTCAGGGAAAAATTACTTTAAATAAACATGATATACGTGATTATCGATTGTCTGAGTTACGTCAACTAATCGGTTATGTTCCTCAA
GATCAGTTTTTATTTGCTACCAGTATTTTAGAAAATGTTCGCTTTGGAAATCCAACTCTATCTATCAATGCTGTTAAAAAAGCAACTAAATTGGCT
CATGTTTACGATGACATTAAACAGATGCCAGCAGGATTTGAGACTCTAATTGGAGAAAAAGGAGTCTCATTATCTGGTGGACAAAAACAAAGGATT
GCGATGAGTCGTGCCATGATTTTAGATCCAGATATTCTTATTTTGGATGATTCTCTATCAGCAGTGGACGCTAAAACGGAACATGCCATTATTGAA
AATCTTAAAACGAATCGTCAAGGGAAATCGACTATTATTTCAGCACATCGATTATCAGCTGTTGTGCACGCAGACCTTATCTTAGTTATGCAAGAC
GGCAGAGTCATCGAGCGAGGTCAGCATCAAGAGTTGCTAAATAAAGGTGGTTGGTATGCTGAAACGTATGCCTCACAGCAATTAGAAATGGAGGAA
GCATTTGATGAAGTC

SEQ ID 158

MSIIKNLWWFFKEEKKRYLIGILSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYIWRMYILGTSYKLGQVVRYRL
FEHFTKMSPSFYQKYRTGDLMAHATNDINSLTRLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALATSKLGRKTHETFKESQAA
FSELNNKVQESVSGVKVTKSFGYQEQEIASFQEVNQMTFVKNMRTMTYDVMFDPLVLLFIGASYVLTLAMGAFMISKGQVTVGDLVTFVTYLDMLV
WPLMAIGFLFNMVQRGSVSYNRINSLLEQESDITDPLNPIRPVVNGTLRYDIDFFRYDNEETLADIHFTLEKGQTLGLVGQTGSGKTSLIKLLLRE
HDVTQGKITLNKHDIRDYRLSELRQLIGYVPQDQFLFATSILENVRFGNPTLSINAVKKATKLAHVYDDIKQMPAGFETLIGEKGVSLSGGQKQRI
AMSRAMILDPDILILDDSLSAVDAKTEHAIIENLKTNRQGKSTIISAHRLSAVVHADLILVMQDGRVIERGQHQELLNKGGWYAETYASQQLEMEE
AFDEV

SEQ ID 159

GTGATGAAAACAGCACGTTTTTTCTGGTTTTATTTTAAACGCTATCGTTTCTCATTTACTGTCATTGCTGTTGCCGTTATCTTAGCAACTTATTTA
CAAGTAAAAGCTCCTGTCTTCTTAGGAGAGTCCTTGACTGAGTTGGGAAAAATCGGTCAGGCTTATTACGTTGCTAAGATGAGTGGCCAGACACAT
TTTAGCCCTGATTTATCAGCTTTTAATGCCGTGATGTTTAAGCTTTTGATGACTTATTTCTTTACTGTTTTAGCTAATCTAATATATAGTTTCTTA
CTTACACGTGTTGTCTCACATTCGACTAACCGCATGCGCAAGGGCTTATTTGGTAAATTAGAACGTTTAACCGTCGCCTTTTTTGACCGCCATAAA
GATGGGGAGATTCTTTCTCGTTTCACGAGTGATTTGGATAATATTCAAAACTCGCTGAACCAATCCTTGATTCAAGTGGTGACTAATATTGCCCTT
TACATCGGCCTGGTCTGGATGATGTTTAGGCAAGATAGCCGTTTAGCTTTGTTAACCATCGCATCAACCCCAGTTGCTCTCATTTTTTTAGTGATT
AACATCCGTTTGGCAAGAAAATACACCAATATCCAACAGCAAGAAGTCAGTGCTTTAAATGCTTTTATGGATGAAACCATTTCAGGACAAAAGGCT
ATTATTGTACAAGGTGTCCAAGAAGATACGATGACAGCCTTTTTAAAGCATAATGAAAGGGTTCGACAAGCCACCTTCAAACGCCGTCTGTTCTCA
GGACAATTATTTCCAGTCATGAATGGAATGAGCCTTATTAACACGGCTATCGTGATTTTTGTCGGTTCAACAATTGTCCTCAGTGACAAATCTATG
CCAGCAGCGGCAGCGCTTGGTTTAGTGGTTACTTTTGTACAATATTCCCAGCAATATTACCAACCCATGATGCAAATCGCGTCTAGTTGGGGAGAA
TTGCAGCTGGCCTTTACCGGTGCTCACCGTATTCAAGAAATGTTTGATGAAACCGAAGAAGTTCGTCCACAAAATGCACCAGCGTTCACCAGCTTA
AAAGAAGCAGTGGCGATTAACCACGTCGATTTTGGGTATCTTCCTGGGCAAAAAGTTTATCAGATGTGTCAATCGTTGCACCCAAGGGCAAAATG
ATTGCCGTGGTTGGACCGACAGGTTCTGGAAAGACCACTATTATGAACTTGATTAACCGTTTCTACGATGTGGATGCAGGTTCGATTACCTTTGAT
GGCCGTGATATTCGTGACTACGATTTGGATAGTCTTCGTCAAAAGGTAGGGATTGTGTTGCAAGAGTCAGTTCTTTTTTCAGGAACCATTACGGAT
AATATTCGTTTTGGTGATCAGACCATTAGTCAAGACATGGTTGAAACTGCTGCGCGTGCGACCCATATTCATGACTTTATCATGTCCTTACCAAAA
GGGTACAATACCTATGTCTCAGATGATGACAATGTCTTTTCAACAGGTCAAAAGCAGTTGATTTCTATTGCTAGGACGCTACTGACTGACCCTGAA
GTGTTGATTTTGGATGAGGCCACTTCAAATGTTGATACGGTTACCGAAAGTAAAATTCAACGGGCCATGGAAGCTATCGTGGCAGGTCGAACTAGC
TTTGTCATTGCTCACCGCCTCAAAACCATTTTAAATGCCGATCACATTATTGTGTTGAAAGATGGCAAGGTCATTGAGCAAGGAAATCATCATGAG
CTATTGCATCAAAAAGGCTTTTATGCCGAATTGTATCACAATCAATTTGTCTTTGAA

SEQ ID 160

VMKTARFFWFYFKRYRFSFTVIAVAVILATYLQVKAPVFLGESLTELGKIGQAYYVAKMSGQTHFSPDLSAFNAVMFKLLMTYFFTVLANLIYSFL
LTRVVSHSTNRMRKGLFGKLERLTVAFFDRHKDGEILSRFTSDLDNIQNSLNQSLIQVVTNIALYIGLVWMMFRQDSRLALLTIASTPVALIFLVI
NIRLARKYTNIQQQEVSALNAFMDETISGQKAIIVQGVQEDTMTAFLKHNERVRQATFKRRLFSGQLFPVMNGMSLINTAIVIFVGSTIVLSDKSM
PAAAALGLVVTFVQYSQQYYQPMMQIASSWGELQLAFTGAHRIQEMFDETEEVRPQNAPAFTSLKEAVAINHVDFGYLPGQKVLSDVSIVAPKGKM
IAVVGPTGSGKTTIMNLINRFYDVDAGSITFDGRDIRDYDLDSLRQKVGIVLQESVLFSGTITDNIRFGDQTISQDMVETAARATHIHDFIMSLPK
GYNTYVSDDDNVFSTGQKQLISIARTLLTDPEVLILDEATSNVDTVTESKIQRAMEAIVAGRTSFVIAHRLKTILNADHIIVLKDGKVIEQGNHHE
LLHQKGFYAELYHNQFVFE

SEQ ID 161

TTGATGAAGTCTAATCAATGGCAAGTCTTTAAGAGATTAATCTCCTATTTACGCCCTTATAAATGGTTTACAGTATTAGCTCTATCTCTCTTATTG
TTGACGACTGTTGTTAAAAATATTATTCCTTTAATTGCTTCACATTTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCTTATTTTA
GTGGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATATTTTGGGAATCTCTTTTTTGCGCGTGTTTCTTATAGTATTGTTAGAGATATT
CGTAGAGATGCTTTTGCTAATATGGAAAGGCTTGGCATGTCTTATTTTGATAGGACACCGGCAGGATCTATAGTGTCACGTATTACTAATGATACT
GAAGCAATATCTGATATGTTTTCGGGTATTTTATCGAGTTTTATCTCGGCGATATTTATTTTTACAGTTACTCTGTACACTATGTTGATGCTAGAC
ATTAAACTAACAGGACTTGTCGCTCTTTTATTACCTGTTATCTTTATATTAGTGAATGTCTATCGGAAAAAATCAGTCACTGTCATTGCTAAAACG
AGAAGTTTACTTAGTGATATCAACAGTAAATTATCAGAAAGTATTGAAGGAATTCGCATTGTACAGGCTTTTGGTCAAGAAGAGCGCTTGAAGACT
GAATTTGAGGAAATTAACAAAGAGCATGTTGTGTATGCCAATCGTTCTATGGCTCTTGATAGTCTCTTCTTAAGACCGGCGATGTCTCTTTTAAAA
CTCCTAGCATATGCTGTTCTTATGGCTTATTTTGGATTTACAGGAGTTAAAGGAGGTCTTACGGCAGGATTGATGTATGCTTTTATTCAGTACGTT

AATCGTCTCTTTGACCCTTTAATTGAAGTAACGCAAAATTTTTCAACCTTACAAACATCAATGGTATCAGCAGGGCGTGTGTTTGATTTGATTGAT
GAAACAGGTTTTGAACCAAGCCAAAAAAATACAGAAGCTTTTGTGAGAGAAGGAAATATCGAATTTAAAAATGTATCATTCTCATATGATGGAAAA
AAACAAATCCTTGATAATGTTTCTTTTAGTGTTAAAAAAGGTGAAACGATTGCTTTTGTAGGAGCGACAGGTTCTGGAAAATCATCTATTATTAAT
GTCTTTATGAGGTTTTACGAATTTCAATCTGGACAAGTTTTATTAGATGGGAAGGATATTAGGGATTACTCACAAGAACAATTGCGAAAGAATATT
GGACTCGTCTTACAAGACCCCTTTTTATATCATGGCACTATTAAATCTAATATCAAAATGTACCAAGACATCACCGATCAAGAGGTACAGGACGCA
GCAGAGTTTGTTGATGCTGATCAATTTATTCAGAAGTTGCCAGATAAGTACGATGCAGCTGTTTCAGAACGTGGGTCAAGTTTTTCGACTGGACAA
CGCCAACTATTGGCGTTTGCCAGAACTGTGGCTAGTAAACCTAAAATTTTAATCTTAGATGAAGCGACAGCAAATATTGATTCGGAAACAGAGCAG
ATTGTACAAGATTCGTTAGCAAAAATGCGTCAAGGTCGAACAACAATTGCCATTGCTCACCGCTTATCAACCATTCAAGATGCTAATTGTATCTAT
GTTCTTGATAGAGGAAAGATAATTGAAAGTGGGAATCACGAGTCTTTATTAGACCTAAAAGGGACTTATTATCGTATGTACCAATTACAAGCTGGC
ATGATGGAGGTC

SEQ ID 162

MMKSNQWQVFKRLISYLRPYKWFTVLALSLLLLTTVVKNIIPLIASHFIDHYLTNVNQTAVLILVGYYSMYVLQTLIQYFGNLFFARVSYSIVRDI
RRDAFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFIFTVTLYTMLMLDIKLTGLVALLLPVIFILVNVYRKKSVTVIAKT
RSLLSDINSKLSESIEGIRIVQAFGQEERLKTEFEEINKEHVVYANRSMALDSLFLRPAMSLLKLLAYAVLMAYFGFTGVKGGLTAGLMYAFIQYV
NRLFDPLIEVTQNFSTLQTSMVSAGRVFDLIDETGFEPSQKNTEAFVREGNIEFKNVSFSYDGKKQILDNVSFSVKKGETIAFVGATGSGKSSIIN
VFMRFYEFQSGQVLLDGKDIRDYSQEQLRKNIGLVLQDPFLYHGTIKSNIKMYQDITDQEVQDAAEFVDADQFIQKLPDKYDAAVSERGSSFSTGQ
RQLLAFARTVASKPKILILDEATANIDSETEQIVQDSLAKMRQGRTTIAIAHRLSTIQDANCIYVLDRGKIIESGNHESLLDLKGTYYRMYQLQAG
MMEV

SEQ ID 163

GTGTATAATGAGGTCAAAGTGCAAGGAAAGGTCTATAAAATGTTACTATTGGTAGATAATTACGATTCTTTTACCTATAATTTAAAGCAATATTTA
AGTGTCTATAAAGAGGTATTCGTCATAAAAAATGATGTTCCTAACCTTTTTTTATTAGCTGAGAGCGCAGAAGCCATCGTCTTATCACCTGGACCA
GGACACCCAAAGGATGCTGGGAAAATGGTAGAATTAATCAATCAGTTTATAGGAAAGAAACCTATTCTAGGTATCTGTTTGGGGCATCAAGCGCTT
GCCGAGTGCTTGGGTGGGCGATTAAATTTAGCAAATCACGTTATGCATGGTAAACAAAGTTGGGTAACAATAAACGACCATACTAGTTTGTTTAAG
GGAATTGATAGTCCAACCCAAGTTATGCGTTATCATTCATTGGTAGTGACTGATTTACCAGAGAATATTGCTGTTATTGCACGATCAAATGAGGAT
AATGAAATCATGGCATTCCATTGCCCCAGCTTAAAGGTATATGCGATGCAGTTTCATCCTGAGTCAATCGGGAGTATTGATGGAATGAAAATGATT
GAAAACTTTTTGACGTTAATTAATGAC

SEQ ID 164

MYNEVKVQGKVYKMLLLVDNYDSFTYNLKQYLSVYKEVFVIKNDVPNLFLLAESAEAIVLSPGPGHPKDAGKMVELINQFIGKKPILGICLGHQAL
AECLGGRLNLANHVMHGKQSWVTINDHTSLFKGIDSPTQVMRYHSLVVTDLPENIAVIARSNEDNEIMAFHCPSLKVYAMQFHPESIGSIDGMKMI
ENFLTLIND

SEQ ID 165

ATGATACTCTTAATTGATAATTACGATTCATTTACCTACAACCTCGCCCAATATTTAAGTGAATTTGACGAGACGATTGTCTTGTATAACCAAGAC
CCAAACTTATATGACATGGCCAAAAAAGCTAACGCTCTAGTCCTCTCACCTGGTCCTGGTTGGCCCAAGGAAGCCAACCAAATGCCAAAACTCATT
CAAGACTTTTACCAAACAAAACCTATCTTAGGAGTGTGTCTGGGACACCAAGCTATCGCTGAAACTTTAGGGGGAACCTTACGCTTGGCCAAACGC
GTCATGCATGGGAGACAAAGCACCATTGAAACGCAAGGCCCTGCTAGTCTTTTTCGCTCCCTGCCACAAGAGATCACCGTCATGCGCTACCATTCC
ATCGTTGTGGATCAGTTACCAAAAGGTTTTAGCGTAACCGCTAGAGACTGTGACGATCAAGAAATCATGGCATTTGAACACCACACCCTGCCACTT
TTTGGGCTACAATTTCACCCAGAAAGCATCGGAACTCCTGATGGCATGACCATGATTGCCAACTTCATCGCAGCCATTCCCCGT

SEQ ID 166

MILLIDNYDSFTYNLAQYLSEFDETIVLYNQDPNLYDMAKKANALVLSPGPGWPKEANQMPKLIQDFYQTKPILGVCLGHQAIAETLGGTLRLAKR
VMHGRQSTIETQGPASLFRSLPQEITVMRYHSIVVDQLPKGFSVTARDCDDQEIMAFEHHTLPLFGLQFHPESIGTPDGMTMIANFIAAIPR

SEQ ID 167

ATGAAAACAAGAACAACTACCTATATTGCACTCATGGTTGCACTACTTATTGTTTTAGGTTTTATCCCAGGGATCCCATTAGGTTTCATTCCAGTC
CCAATTGTTTTACAAAATCTTGGTGTTATGCTGGCAGGTGCTCTGCTTGGTAGTAGGAAGGGTTTCCTAGCTGTGGCTATTTTCTTGCTCTTAGTT
GCTATTGGTGCACCATTTTTACCAGGAGGACGGTCAGGTCTCGTAACGCTGTTTGGGCCAACAGCAGGCTATCTGCTGACTTATCCATTTGCAGCT
TTTTTTATCGGCCTAGGGCTTGAGAAAGTGAAAACAACAAAACTCTGGGTTCAATTCCTTATTATTTGGATATTTGGCGTACTATTGATTGATATT
TGTGGTAGCATCGTTCTTTCCTTTCAAACTTCTCTACCCTTAACTAAATCACTATTTTCTAACCTTATTTTTATTCCTGGGGATACCTTAAAAGCA
TCCATTTGCTTGATTATTTATCGTAAATTTGCAAACAGATTAACTCATCTATACAAC

SEQ ID 168

MKTRTTTYIALMVALLIVLGFIPGIPLGFIPVPIVLQNLGVMLAGALLGSRKGFLAVAIFLLLVAIGAPFLPGGRSGLVTLFGPTAGYLLTYPFAA
FFIGLGLEKVKTTKLWVQFLIIWIFGVLLIDICGSIVLSFQTSLPLTKSLFSNLIFIPGDTLKASICLIIYRKFANRLTHLYN

SEQ ID 169

ATGTTTACAACCAAAGAACTTGTTAAGGTGGCTATGATGACCACTTTGATTATTATTTTAGGCTTTATTCCTGCTATCCCGCTAGGCTTTATCCCA
GTCCCTATTGTTTTACAAAACTTAGGTGTCATGTTGGCTGGATTGATGCTGGGTGGTAAAAAGGGAACCTTATCTGTTTTCTTATTTTTAGTGATT
GGCCTTTTCTTACCTGTTTTCTCAGGCTCAAGAACAACCATTCCAGTATTGATGGGGCCATCTGCTGGCTATGTTATTGCCTACCTTCTTGTGCCT
ATTGTCTTTTCATTACTTTACCGCAATTGGTTCTCAAAAAGCACGCCATTAGCATTCCTAGCTCTTTTAATCTCAGGAGTTGTACTGGTTGATGTT
CTGGGTGCTATCTGGTTGTCAGCCTACACTGGCATGTCTCTTGTGACATCGCTTTTATCAAACTTGGTCTTTATTCCAGGAGATACCATCAAAGCA
ATCATTGCGACCATTATCGCTGTTAAATACAAAGATAGTTTTTTGAATACAAAACAG

SEQ ID 170

MFTTKELVKVAMMTTLIIILGFIPAIPLGFIPVPIVLQNLGVMLAGLMLGGKKGTLSVFLFLVIGLFLPVFSGSRTTIPVLMGPSAGYVIAYLLVP
IVFSLLYRNWFSKSTPLAFLALLISGVVLVDVLGAIWLSAYTGMSLVTSLLSNLVFIPGDTIKAIIATIIAVKYKDSFLNTKQ

SEQ ID 171

GTGACTAATGATTCAAAATTCTCAAAATGGACCTCTCGTCCAGCGCTTAATCTTAATTCCTTGAAAGGAAAAACAAAACGCAACATGGCCATAATT
TTTAAGCATTTAATGGGAGTCAAA

SEQ ID 172

MTNDSKFSKWTSRPALNLNSLKGKTKRNMAIIFKHLMGVK

SEQ ID 173

ATGCTATTATTAATTTCGTTAAAGGAGGCTATCATGTCATTTCAAACAAATTATATCCATTTGGCTGACGAAATATTATCTGGAAAGACTAGCATT
TCTTATGAACAAGCGCTGGAAATTCTAAATAGCGATGAGAACTGGTGGGAAATCTACGCTGCTGCCTTATACCTTAAAAATCAAGTTAGCCGAAAT
AATATTCGCCTTAACGTTTTATTAAGTGCTAAGCAAGGACTTTGTGCAGAAAATTGTGGTTACTGTTCTCAATCTAAAGAAAGCACTGCTGACATT
GATAAATTTGGTCTGCTTCCTCAAAATGTCATTCTAAAACAGGCTATTGTCGCTCATCAAAATGGTGCTAGCGTCTTTTGTATTGCGATGAGTGGA
ACTAAGCCTAGCAAGAGAGAAATTGAGCAGTTATGTCAAGTCATCCCTGAAATCAAAAAAAGCCTCCCTCTAGAAATATGCCTTACCGCTGGTTTT
TTGGATAGAGAACAACTTCATCAGCTAAAACAAGCAGGAATTGACCGTATCAATCATAATCTCAACACCCCCGAAGAAAACTACCCCAACATTGCA
ACGACGCATAGCTTCAAAGATCGTTGTGATACTTTAGAAAGAATTCACAATGAAGACATTGATGTTTGTTCTGGATTCATTTGTGGTATGGGAGAG
AGCGATGAGGGGCTCATCACATTAGCTTTCAGACTAAAAGAGCTGGACCCCTATTCTATCCCTGTCAATTTTTTACTTGCTGTTGAAGGAACACCT
CTTGGAAAATATAACTATTTGACTCCCATTAAATGCTTAAAAATTATGGCCATGTTGCGTTTTGTTTTTCCTTTCAAGGAATTAAGATTAAGCGCT

GGACGAGAGGTCCATTTTGAGAATTTTGAATCATTAGTCACCTTACTTGTTGACTCAACTTTTTTGGGAAATTACCTAACAGAGGGCGGTCGCAAT
CAACATACCGATATTGAATTCTTGGAAAAATTACAACTAAATCATACTAAAAAGGAATTAATT

SEQ ID 174

MLLLISLKEAIMSFQTNYIHLADEILSGKTSISYEQALEILNSDENWWEIYAAALYLKNQVSRNNIRLNVLLSAKQGLCAENCGYCSQSKESTADI
DKFGLLPQNVILKQAIVAHQNGASVFCIAMSGTKPSKREIEQLCQVIPEIKKSLPLEICLTAGFLDREQLHQLKQAGIDRINHNLNTPEENYPNIA
TTHSFKDRCDTLERIHNEDIDVCSGFICGMGESDEGLITLAFRLKELDPYSIPVNFLLAVEGTPLGKYNYLTPIKCLKIMAMLRFVFPFKELRLSA
GREVHFENFESLVTLLVDSTFLGNYLTEGGRNQHTDIEFLEKLQLNHTKKELI

SEQ ID 175

ATGATATACTGGTCTTATATTTTGACGGGAGATAAGATGAAAAAACTATTTAAAAAAGCGATAGCTATGTGCCGAGATTTGCCGCTTAATTTTGTA
ATTGTTGAACTTAGTTTGTATCAAAGAGAGGATGGCTCATCTGATAATATTAAATGGATTTCTAAGAGAATTCTTGAGGTAACGGTAACTGATCAG
CAATGGATTTACCATTTGAGGATGCTTAATTTACCAAAACTTAAGCCAATGTCACTAGCATCCAGTGACTGTCCTGCAAGGGAAGAGAAGGCTAGT
CTTATTTCAATAGAAGAATGTCAAAAATTCACTAGCTTAGTGCGAGATAAAAATCCTTTTCACCAAGGGGAAGCAGCTATTGTGCCTGCGGCTCTA
TTATTGGAAAAAATAATGGAAGTTAGAAAAGGAAAAATAAAGGAGATTCATTTGACTTTTTTATCTCCAGTAAGGGTGAATCAAGAATTCTCAGTG
CAAGTAGTGGATAACACAGTGATTATTTTTCAGCATCAAATATTATGG

SEQ ID 176

MIYWSYILTGDKMKKLFKKAIAMCRDLPLNFVIVELSLYQREDGSSDNIKWISKRILEVTVTDQQWIYHLRMLNLPKLKPMSLASSDCPAREEKAS
LISIEECQKFTSLVRDKNPFHQGEAAIVPAALLLEKIMEVRKGKIKEIHLTFLSPVRVNQEFSVQVVDNTVIIFQHQILW

SEQ ID 177

TTGTTTAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTCACATTGTAGAAGTAGCAGGAGATCCCAA
GCT

SEQ ID 178

MFNARCCCISNASESENRIPDCSHCRSSRRSQA

SEQ ID 179

ATGAAGAATAGAGATGTTTATATTGGTTTTGGGCTACGAACACCTATCGGTATAAAAGGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGA
GCACACCTTTTAAATCAAATAAAAAAAATAGAATCAGAATCTAACATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGT
CGTTTGATGACTCTTTTTTCTGATTATGAATCCTATATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTTTTTTGGT
TATCTAAAAATCAGTACCGGTATTAATGAAAAAGTTCTTGTTGGGGGGATTGAAAGTAGTTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGAT
AATCGTAACGGAGAATATACAGTTGCTCAGTTTTCTCCTGACTCTTATGCTGAAACTGTAATGTTAGAAGGGGCCCAGAGAGTCTGTCAAAAATAT
GGTTTTAGAAGAGAAATGTTAGATAAATTGGCATTCTTGAGCCATAAACGCGCCTTAACAGCTAAACAAGGTGGCTATTTAGAAGAGGTAATCTTA
CCAATGGAAGGGATGCGAGATCAAGGCGTTAGAAAACTAAAAGAAACATTTTTTCAAAAATTACCAAGATTGATGGAAAATTCACCTTTGCTCACT
ATTGGAAATGTTTGTTTAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTCACATTGTAGAAGTAGCA
GGAGATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAAACTATTAACAGAAACTCATACTAAAATATCGGATTATGATGCAATTGAA
TGGAATGAACCATTTGCAGCGATTGATGCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTTGGAGGGACATTAGCTTAC
GGACACCCTTATGCCTGCTCAGGAATTATTAATATCCTTCATCTTATGCAGGCATTAAAATATAAAAATAAACCTATGGGTCTAACTGCCATTGCA
GGGGCAGGAGGAGTCGGAATGGCCATATCAATAGAGTACTTAGGAGTTAAGAATGCT

SEQ ID 180

MKNRDVYIGFGLRTPIGIKGKQFKHYRPELLGAHLLNQIKKIESESNIDSIICGNTVGTGGNIGRLMTLFSDYESYIPVQTIDMQCASSSSALFFG
YLKISTGINEKVLVGGIESSSLQPMRRYAKEDNRNGEYTVAQFSPDSYAETVMLEGAQRVCQKYGFRREMLDKLAFLSHKRALTAKQGGYLEEVIL
PMEGMRDQGVRKLKETFFQKLPRLMENSPLLTIGNVCLMHDAAAFLTLQSQKTEFRIVHIVEVAGDPKLSPELVHTATEKLLTETHTKISDYDAIE
WNEPFAAIDALFNHYYPEEREKFNIFGGTLAYGHPYACSGIINILHLMQALKYKNKPMGLTAIAGAGGVGMAISIEYLGVKNA

SEQ ID 181

ATGACGGATGTTTATATTGCTGCAGGCCTTAGAACCCCTATCGGTTTAGTAGGGAAACAATTTGCTAAAGAACAACCAGAAATCCTTGGAGCAAAG
CTCATCAACGCTTTACAAAATAAGTATCCAGTTCCCATTGACCAAGTGATTTGTGGCAATACCGTCGGAACGGGTGGTAATATTGGGCGCTTGATG
ACCCTGTATTCTCATTTAGGAGAATCTGTCTCTGCTTTGACGGTTGATATGCAGTGTGCATCAGCTGGTGCAGCTCTTTCCGTGGGTTATGCTAAA
ATCAAGGCAGGTATGGCAAGCAACCTTTTAGTGGGAGGGATTGAAAGCAGCTCCTTACAACCTGAATCGGTATATGCTTCAGCTGATTGGCGCCAA
GGAGCCTACAAGGTAGCTCAGTTTTCTCCAGATAGTATCAGCCCTTTTGCGATGATTGAAGGGGCAGAACGAGTGGCAAGAGAGCATGGCTTTACA
AAGGAGTATTTGAATCACTGGACATTGAGAAGTCATCAAAAGGCTAGTTATTGCCAGGAGCAAGCCCTGTTAGCTGATCTTATTCTAGACCTGTCA
GGAGCCAGTGATCAAGGTATTCGACCGCGCTTGTCAAGTAAGGTGTTGTCAAAGGTACCCCCTATCTTAGGAGAAGGTCACGTGATTAGTGCAGCC
AATGCCTGCCTAACCCATGATGCTGCTGCCTTTTTACAGCTAAGTAGTCAGCCTTCAGCTTTTAAACTGATTGATGTGGTAGAAGTAGCAGGAGAC
CCACAGCGTAGCCCTTTAATGGTGATTAAGGCTAGTCAAGTCCTTTTGGAAAAACATGGTCTAGGGATGGCAGATATGACAGCGATTGAATGGAAC
GAAGCCTTTGCCGTTATTGATGGTCTATTTGAAACCCATTATCCAGATTTATTGGACCGCTATAATATATTTGGTGGTGCATTAGCTTATGGTCAT
CCCTATGGTGCCTCAGCAGCCATTATAATATTGCACTTAATGAGGGCTTTAGAGATTAAAAATGGACGCTATGGAATAGCTGCTATAGCAGCAGCT
GGTGGCCAAGGGTTTGCTGTTTTACTAAAATATCATAAGGAGTTTAGTCATGCTGACAAAGCTAGAATATTGGGCAAAGCAATGCCCAAA

SEQ ID 182

MTDVYIAAGLRTPIGLVGKQFAKEQPEILGAKLINALQNKYPVPIDQVICGNTVGTGGNIGRLMTLYSHLGESVSALTVDMQCASAGAALSVGYAK
IKAGMASNLLVGGIESSSLQPESVYASADWRQGAYKVAQFSPDSISPFAMIEGAERVAREHGFTKEYLNHWTLRSHQKASYCQEQALLADLILDLS
GASDQGIRPRLSSKVLSKVPPILGEGHVISAANACLTHDAAAFLQLSSQPSAFKLIDVVEVAGDPQRSPLMVIKASQVLLEKHGLGMADMTAIEWN
EAFAVIDGLFETHYPDLLDRYNIFGGALAYGHPYGASAAIIILHLMRALEIKNGRYGIAAIAAAGGQGFAVLLKYHKEFSHADKARILGKAMPK

SEQ ID 183

ATGCTTGAATCATTGAAAACGATAGTTAAAACCAATAGCGATAAAAAGTTATTTGATGGTGATTTACAGGTCAGTTATGGAGAATTTTATAACTTA
GTAAGACAAGATATGGCGTCACAAGACAATAGGAAACATGTGATTAGCACACACTCTCTGCTTAACCAATTAGTAAGATTTGTTTCAAAGTTATGT
CAAAAAGCTCTTCCTATTATTTGTAAACCTAACCTTACTCATAATGAAATAAGTCGATTAGAAAAAGAAGTGCAGTATGCTCCTCAACTAGCTGAT
TTTGGTGTTCTTTCTTCTCTGGGACTACAGCTGATGCTAAACTATTGTGGAGGAGCTTCACTTCGTGGTCTGATTTTTTTAGCATTCAGAATGCTTAT
TTTTCGGTCACTTCCAATAGCAAACTGTTTATTCAAGGTGATTTTTCATTTACTGGTAACTTAAATTTAGCGCTATCCCTTTTATTACTGGGGGGA
ACACTTGTTGTCACACAGAAAAATTCTGTAAAATACTGGCAGACTTTATGGGAAAAAACTGGTGTAACGCATCTATATCTGCTCCCTAGTTATCTC
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TATAGAAAGCATCCTAAAGTGTCAGTGAAAATCTTCTATGGTGCTAGTGAGCTCAATTATGTGTCATGGTACGATGGTCGTGATATCCGAGATAAG
CCACAGTATGTTGGAGAAATCGTTCCAAATGTAGCTGTTAGGATTAAAGAGGGAAGAATTTTTGTAAAAACACCGTATAGTATCTGTGGCCTTTCA
AGTGAATATTGTGCTGGTGATTATGGTGAACTGATAGATGGCAAATTATATCTATTTGGCCGTGGTGGTGATTGGTGCAATCAATCGGGCATTAAG
CTCTATTTACCTAGATTAATCGAAAAAATAAAAACATGCCCTTATATCAAGGATGCAGTAGCATTTACAAAAGAGAGTCAAAGTCATGGACAAGAG
TCACATTGCTGTATTGTTTTAATTGAAAATCAGATGCAACAAGAGTGTTTGAAGTGGTTATCGGAACATTTTGAAAAGAAGTATGGGTTTAAGCAT
TATCATATTGTATCTAAAATTCCTTTGATGCCATCTGGAAAAATTGATTATCAACAACTCAAAAGACAGTTAGCA

SEQ ID 184

MLESLKTIVKTNSDKKLFDGDLQVSYGEFYNLVRQDMASQDNRKHVISTHSLLNQLVRFVSKLCQKALPIICKPNLTHNEISRLEKEVQYAPQLAD
FGVLSSGTTADAKLLWRSFTSWSDFFSIQNAYFSVTSNSKLFIQGDFSFTGNLNLALSLLLLGGTLVVTQKNSVKYWQTLWEKTGVTHLYLLPSYL

KLVEQYSKETALDNKTIITSSQYVSDSLLEGLYRKHPKVSVKIFYGASELNYVSWYDGRDIRDKPQYVGEIVPNVAVRIKEGRIFVKTPYSICGLS
SEYCAGDYGELIDGKLYLFGRGGDWCNQSGIKLYLPRLIEKIKTCPYIKDAVAFTKESQSHGQESHCCIVLIENQMQQECLKWLSEHFEKKYGFKH
YHIVSKIPLMPSGKIDYQQLKRQLA

SEQ ID 185

ATGCTGACAAAGCTAGAATATTGGGCAAAGCAATGCCCAAATAAAAAAGCTATCGTAGCCGATCAGATAAGCTTGACTTATCAAGAGCTATGGCAA
GCGGTTTTAATAAAGGATCAGACAATAAAAGACAGTGTACCATATATCATCAGTCATAGTCGCTATCTTAATCAGTTACTCTCTTTTTTACGAGGA
TTAAAAGAAGGCAGTTGTCCTATCATTTTACACCCTAATATCTCAGGTACATTTCAGCAGCAAATAAAACACGTCGATGGTGAGCTTCTTAAAAAA
GCTGATTTTGCTGTTTTGAGTTCGGGAACAACTGGCAAAGCAAAATTATTTTGGCGTCGTCTATCAACTTGGACGAGACTTTTTGATTATCAAAAT
AAGGTGTTTGGTATGACTGGTAATAGTTGTCTATTCTTACATGGTAGTTTTAGTTTTACTGGCAATCTTAACTTAGCATTAGCTCAACTATGGGCC
GGGGGATGTCTGGTTTTAAGCCAAAAGCTGTCTTTGAAAACGTGGTTAAGCTTATGGCAAGCAAAAAAGGTGAGTCACCTTTACCTTTTACCGACC
TACCTAAATCGCTTGCTACCTTATTTGACTAAGAACAACATGACTGCGACTCACTTATTGACCTCTTCGCAAATGATATCACAAGAATTACTAAGA
CATTATTACAAAAAATTTCCTCAGCTTGAAATTGTCATTTTCTACGGGGCTAGTGAATTATCTTTTATAACGTGGTGTAATGGCAGAGCTGCTGTC
AAAATTAATGGTTTGGTAGGACAGCCCTTTCCTGATGTGTCTATCAGTTTCAAAGATAAGGAAATTTTTGTAGAGACTCCTTATAGTGTAGAAGGA
ATGTCACAACCATACAGTGTTTCAGACTTAGGAAAAATGAGCCCAGCGGGTTTAATTTTAGAAGGGCGACAAGATGACTGGGTTAATCAACGAGGA
GTGAAATGCCACCTGCCTAGCCTAGTTGAACTCGCTCACCAAGCGCCAAACGTCAAAGAAGCGCACGCTTTAAAGATAGGAAAAGGAGAAAACGAA
ACCCTAATATTAGTATTAGTTTTGACTAAGAAGGATTGCCTAGCACCTATTAAAGACTTTTTAGCTCTTTATTTAAACTCTGGACAACTTCCCAAG
TACTATCTTGTGATTGATTGTTTGCCTTTAAAAGATAATGGTAAAATTAATCGAGAAGTTCTTTTAAATAAAATACCCAAACAGTGGCTTAGT

SEQ ID 186

MLTKLEYWAKQCPNKKAIVADQISLTYQELWQAVLIKDQTIKDSVPYIISHSRYLNQLLSFLRGLKEGSCPIILHPNISGTFQQQIKHVDGELLKK
ADFAVLSSGTTGKAKLFWRRLSTWTRLFDYQNKVFGMTGNSCLFLHGSFSFTGNLNLALAQLWAGGCLVLSQKLSLKTWLSLWQAKKVSHLYLLPT
YLNRLLPYLTKNNMTATHLLTSSQMISQELLRHYYKKFPQLEIVIFYGASELSFITWCNGRAAVKINGLVGQPFPDVSISFKDKEIFVETPYSVEG
MSQPYSVSDLGKMSPAGLILEGRQDDWVNQRGVKCHLPSLVELAHQAPNVKEAHALKIGKGENETLILVLVLTKKDCLAPIKDFLALYLNSGQLPK
YYLVIDCLPLKDNGKINREVLLNKIPKQWLS

SEQ ID 187

ATGTTATCAAAAGCAAAATCACGATATATTATCCGTGAGATTATTAAGTTATTTCCAGATGCTAAACCTAGCTTAGACTTTACTAATGTCTTTGAG
CTTTTGGTAGCTGTAATGCTATCAGCTCAAACAACTGATGCAGCTGTTAATAAAGTTACACCCGCCCTTTTTGAACGCTTTCCAAATCCTTTAGTT
TTGGCACAAGCTGATCCCAAAGAGATTGAACCCTATATTTCTAAAATTGGGCTTTACCGTAATAAAGCTCGATTCTTAAATCAATGCGCTAAACAA
TTGATAGAGCATTTTGATGGAAAAGTCCCCCGAACTCGTCAAGAGCTAGAAAGTTTGGCTGGCGTTGGAAGGAAAACGGCTAACGTGGTCATGAGT
GTTGGATTTGGTATTCCGGCTTTTGCCGTAGATACTCATGTCACTCGGATTTGTAAACACCACCAGATTTGCAAACAGTCGGCTTCTCCACTGGAA
ATTGAGAAACGAGTCATGGAGGTTTTACCACCAGAAGAGTGGCTAGCTGCACATCAATCCATGATTTATTTTGGTCGTGCAATTTGTCATCCTAAA
AATCCAAAATGCGACCAGTACCCACAACTTTATCACTTTCCTGATAATTTAAAG

SEQ ID 188

MLSKAKSRYIIREIIKLFPDAKPSLDFTNVFELLVAVMLSAQTTDAAVNKVTPALFERFPNPLVLAQADPKEIEPYISKIGLYRNKARFLNQCAKQ
LIEHFDGKVPRTRQELESLAGVGRKTANVVMSVGFGIPAFAVDTHVTRICKHHQICKQSASPLEIEKRVMEVLPPEEWLAAHQSMIYFGRAICHPK
NPKCDQYPQLYHFPDNLK

SEQ ID 189

ATGAGAATTGGAAAAGCAAGATTAGCAAAAGTCCTGACCATCATTGGTCAAATGTTTCCTGAGGCTAAGGGAGAGTTAGACTGGGAAACACCTTTT
CAATTGTTGATTGCGGTGATTTTATCAGCTCAAACGACAGATAAGGCCGTCAATAAGGTAACTCCTGGACTATGGCAGTCTTATCCAGAAATAGAA
GACTTAGCTTTTGCTGAACTTTCTGATGTTGAAAATGCTCTGAGAACGATTGGACTCTATAAAAATAAGGCCAAAAATATCATTAAAACTGCTCAG
GCTATTCGTGATGATTTTAAGGGTCAAGTGCCAAAAACCCACAAAGAGCTTGAAAGTTTACCGGGTGTTGGCCGAAAAACAGCCAATGTGGTGCTG
GCAGAGGTTTATGGTGTTCCAGCTATTGCGGTTGATACTCATGTGGCTAGAGTCTCAAAGAGGCTCAATATTTCATCGCCAGATGCCGATGTCAAG
CAGATTGAAGCAGATTTGATGGCTAAAATTCCAAAGAAAGATTGGATTATTACTCACCATCGATTGATTTTTTTTGGACGCTACCATTGTTTAGCC
AAAAAACCAAAATGTGAGATTTGTCCCGTTCAGTCTTACTGCAAGTACTATCAAGATACTTATGGAAAATCGAAAGCC

SEQ ID 190

MRIGKARLAKVLTIIGQMFPEAKGELDWETPFQLLIAVILSAQTTDKAVNKVTPGLWQSYPEIEDLAFAELSDVENALRTIGLYKNKAKNIIKTAQ
AIRDDFKGQVPKTHKELESLPGVGRKTANVVLAEVYGVPAIAVDTHVARVSKRLNISSPDADVKQIEADLMAKIPKKDWIITHHRLIFFGRYHCLA
KKPKCEICPVQSYCKYYQDTYGKSKA

SEQ ID 191

ATGAAAGTTTTATTCGATGTGCAGAATCTTTTGAAAAAATTTGGTATTTATGTTTATATTGGTAAACGTCTTTATGATATCGAAGTTATGAAGATT
GAATTGCAACGTCTCTACGATAATGGTCTGATAAGTAGAGATGATTATTTAAAAGCAGAACTGATTTTAAGAAGAGAGCACAGACTAGAATTGGAG
AAGGAAAATAAAAAA

SEQ ID 192

MKVLFDVQNLLKKFGIYVYIGKRLYDIEVMKIELQRLYDNGLISRDDYLKAELILRREHRLELEKENKK

SEQ ID 193

TTGCTAAAATCTACTTATATGAAAACACTATATGATGTGCAACAATTGCTAAAAAACTTTGGCATTTTTGTTTACCTTGGCAAACGTCTTTATGAT
ATTGAAATGATGAAGATTGAACTTCAGCGTCTCTATGATAGCGGCTTATTGGATAAGAGGGATTACTTAAATGCGGAGTTAATTTTGCGACGTGAG
CATAGATTAGAATTGGAAAAAGAAGGA

SEQ ID 194

LLKSTYMKTLYDVQQLLKNFGIFVYLGKRLYDIEMMKIELQRLYDSGLLDKRDYLNAELILRREHRLELEKEG

SEQ ID 195

ATGAGTAAGAAATTATTGGGAATTGACCTCGGAGGAACGACCATTAAATTTGGTATCTTGACGCTTGAGGGAGAAGTACAAGAAAAATGGGCAATT
GAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAAACATCGTTTGAGCCTCTATGGATTAACAAAAGATGAC
TTTCTCGGTATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAACAGTAACAGGTGCTTTTAATCTAAATTGGGCTGATACTCAAGAA
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GCCAATAATCCCGACGTTGTTTTCGTAACCCTCGGAACAGGAGTAGGTGGAGGTGTTATCGCAGATGGTAACCTCATCCATGGTGTTGCAGGAGCA
GGTGGAGAAATTGGGCATATGATTGTTGATCCAGAAAATGGATTTACGTGCACATGTGGTAACAAAGGCTGCCTTGAGACAGTTGCATCAGCGACA
GGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAATATGAGGGTTCGTCTGCCATTAAAGCAGCGATTGACAACGGTGATACTGTTACAAGTAAA
GATATTTTTATAGCAGCAGAAGATGGGGATAAATTTGCTAATTCTGTTGTTGAACGTGTATCACGTTACCTTGGACTGGCAGCAGCTAATATTTCA
AATATTTTAAACCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTTACGTAGTCGCGTTGAGAAATACTTTGTCACATTT
GCTTTCCCACAAGTTAAAAAGTCAACTAAAATTAAGATTGCTGAACTAGGTAATGATGCTGGTATTATTGGTGCAGCAAGCTTAGCCAATCAACAA
GCAAGT

SEQ ID 196

MSKKLLGIDLGGTTIKFGILTLEGEVQEKWAIETNTLENGRHIVSDIVESLKHRLSLYGLTKDDFLGIGMGSPGAVDRTSKTVTGAFNLNWADTQE
VGSVIEKEVGIPFFIDNDANVAALGERWVGAGANNPDVVFVTLGTGVGGGVIADGNLIHGVAGAGGEIGHMIVDPENGFTCTCGNKGCLETVASAT

GVVRVARQLAEQYEGSSAIKAAIDNGDTVTSKDIFIAAEDGDKFANSVVERVSRYLGLAAANISNILNPDSVVIGGGVSAAGEFLRSRVEKYFVTF
AFPQVKKSTKIKIAELGNDAGIIGAASLANQQAS

SEQ ID 197

ATGAGTCAAAAATTACTGGGGATTGATTTAGGTGGTACCACCATTAAATTTGGAATTTTAACAGCAGCAGGAGAAGTCCAAGAAAAATGGGCAATT
GAGACTAATATTTTAGAAGGAGGCAAACATATTGTCCCTGATATCATCGCTTCCATCAAACATCGCTTAGACTTGTATGGTCTAAGCAGTGCTGAC
TTTGTGGGAATTGGTATGGGATCACCAGGAGCGGTTGACCGTGATACTAATACAGTTACTGGGGCATTCAACCTTAATTGGAAAGAAACCCAAGAA
GTCGGTTCCGTTGTTGAAAAAGAATTGGGCATTCCTTTTGCCATTGACAATGATGCCAATGTGGCTGCCCTTGGTGAACGTTGGGTAGGTGCTGGT
GAAAATAACCCAGATGTCGTCTTCATGACACTTGGAACAGGTGTCGGTGGAGGCATTATTGCTGATGGTAACTTGATTCATGGTGTTGCAGGAGCA
GGTGGTGAAATCGGCCACATGATTGTTGAGCCAGAAAATGGCTTTGCTTGTACTTGTGGCTCACACGGCTGTTTGGAAACAGTAGCTTCAGCAACA
GGAGTTGTCAAAGTGGCACGTTTACTGGCAGAAGCCTACGAAGGGGATTCAGCCATCAAAGCAGCTATTGACAATGGTGAAGGTGTTACCAGTAAA
GACATTTTCATGGCGGCTGAAGCAGGGGATTCCTTTGCTGATTCTGTTGTGGAAAAGGTTGGTTACTACCTTGGCCTTGCTTCAGCAAATATTTCC
AATATCTTGAATCCAGACTCAGTGGTTATCGGTGGGGGTGTGTCAGCAGCAGGAGAATTTCTACGCTCACGTATTGAAAAATACTTTGTGACCTTC
ACTTTCCCACAAGTGAGGTATTCAACTAAAATTAAGATTGCAGAACTTGGCAATGATGCTGGAATTATCGGTGCAGCTAGCCTTGCTCGACAATTT
ATCACAAAA

SEQ ID 198

MSQKLLGIDLGGTTIKFGILTAAGEVQEKWAIETNILEGGKHIVPDIIASIKHRLDLYGLSSADFVGIGMGSPGAVDRDTNTVTGAFNLNWKETQE
VGSVVEKELGIPFAIDNDANVAALGERWVGAGENNPDVVFMTLGTGVGGGIIADGNLIHGVAGAGGEIGHMIVEPENGFACTCGSHGCLETVASAT
GVVKVARLLAEAYEGDSAIKAAIDNGEGVTSKDIFMAAEAGDSFADSVVEKVGYYLGLASANISNILNPDSVVIGGGVSAAGEFLRSRIEKYFVTF
TFPQVRYSTKIKIAELGNDAGIIGAASLARQFITK

SEQ ID 199

ATGGATATGTCTGTTATTTTAATTATTGTTATTCTTCTGGCTTTTGTTGCTTGGGCATCTTGGAATTATTGGAGGGTTCGTAGGGCAGCTAAATTT
TTAGATAACGAGTCTTTTCAAAAAGAAATGTCACGAGGACAGTTAATTGATATCCGAGAAGCTGGTGCTTTTCATAGAAAGCATATTCTCGGAGCA
CGTAACATTCCAGCAAGTCAATTTAAAGTTGCCTTATCGGCTTTGCGCAAAGATAAACCTGTCCTCTTATATGACGCAAGCCGTGGTCAATCTATT
CCAAGGATTGTTTTGTTACTCAGAAAAGAAGGTTTTAATCAACTTTACGTGTTAAAGGACGGTTTCAATTACTGGACGGGTAGAGTTAAG

SEQ ID 200

MDMSVILIIVILLAFVAWASWNYWRVRRAAKFLDNESFQKEMSRGQLIDIREAGAFHRKHILGARNIPASQFKVALSALRKDKPVLLYDASRGQSI
PRIVLLLRKEGFNQLYVLKDGFNYWTGRVK

SEQ ID 201

ATGTCTCCAATCACACTTATCTTATGGTTACTTCTTGTCGGCATTGTTGGTTATTATACATGGAACTATTTCTCTTTTCGAAAAATGGCAAAGCAG
GTTGATAACGAGACTTTTAAAGACGTGATGCGTCAAGGTCAATTGATTGATTTACGAGAGCCAGCGGCTTTTAGAACTAAGCATATTTTAGGAGCT
CGAAATTTTCCAGCGCAACAATTTGATGCTGCTATTAAGGGACTACGCAAGGACAAACCTGTTCTTATTTACGAAAATATGCGTCCCCAGTACCGT
GTGCCTGCGGTCAAAAAACTTAAAAAAGCTGGCTTTGAAGACGTTTATGTCTTAAAAGACGGTATTGATTATTGGGATGGCAAAGTTAAACAAACA
ACC

SEQ ID 202

MSPITLILWLLLVGIVGYYTWNYFSFRKMAKQVDNETFKDVMRQGQLIDLREPAAFRTKHILGARNFPAQQFDAAIKGLRKDKPVLIYENMRPQYR
VPAVKKLKKAGFEDVYVLKDGIDYWDGKVKQTT

SEQ ID 203

ATGACAAATTTAAGAACAGATATCCGTAACGTTGCGATCATTGCCCACGTTGACCACGGTAAAACAACTCTCGTTGATGAATTATTAAAACAATCA
CATACTCTTGATGAGCGTAAAGAGCTTGAAGAACGTGCAATGGATTCAAATGATATCGAAAAAGAACGTGGTATCACCATTCTTGCAAAAAATACA
GCCGTAGCATACAACGATGTTCGTATCAATATTATGGACACACCTGGTCACGCGGACTTTGGTGGTGAAGTTGAGCGTATTATGAAAATGGTTGAT
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CTAGATTTCCCTGTTGTTTATGCTTCAGCTATCAATGGAACATCTTCAATGTCAGATGATCCTTCAGATCAAGAAAAAACAATGGCACCGATTTTT
GATACTATCATTGATCACATTCCAGCCCCAGTTGACAACTCGGAAGAACCACTTCAATTCCAAGTTTCTCTTCTTGATTACAATGATTTTGTAGGA
CGTATTGGTATTGGACGTGTTTTCCGCGGGACTGTCAAAGTTGGAGATCAAGTTACTCTTTCAAAACTTGATGGTACAACTAAAAACTTCCGCGTA
ACAAAACTTTTTGGTTTCTTTGGACTTGAACGTAAAGAAATCCAAGAGGCTAAAGCGGGTGATTTAATCGCTGTTTCTGGTATGGAAGATATCTTC
GTTGGTGAGACAGTAACTCCGACAGATGCTATTGAACCACTACCAGTTTTACGTATTGACGAGCCAACACTTCAAATGACTTTCTTGGTGAATAAT
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GACCCAACAGATTCGCCAGATAAATGGACGGTTTCAGGGCGTGGAGAATTACATTTATCTATCCTTATTGAAACAATGCGTCGTGAGGGATATGAA
CTTCAAGTATCACGTCCAGAAGTTATCATCAAAGAAATTGATGGTGTTCAATGCGAGCCGTTTGAGCGTGTTCAAATTGATACTCCAGAAGAATAT
CAGGGTGCTATTATCCAAAGTTTGTCAGAGCGTAAAGGTGATATGCTTGATATGCAGATGGTTGGTAATGGTCAAACGCGTTTGATTTCTTGATT
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GGGACTATCTTTGTAAATCCAGGTATAGAAGTTTATGAAGGAATGATTGTTGGTGAGAATTCTCGTGATAATGACCTCGGAGTCAATATTACAACT
GCTAAACAAATGACAAATGTCCGTTCAGCAACTAAAGATCAAACTGCAGTCATCAAGACGCCTCGTATCCTTACTTTAGAAGAGTCACTTGAATTT
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AAAAAATCAGCTGAA

SEQ ID 204

MTNLRTDIRNVAIIAHVDHGKTTLVDELLKQSHTLDERKELEERAMDSNDIEKERGITILAKNTAVAYNDVRINIMDTPGHADFGGEVERIMKMVD
GVVLVVDAYEGTMPQTRFVLKKALEQNLIPIVVVNKIDKPSARPSEVVDEVLELFIELGADDDQLDFPVVYASAINGTSSMSDDPSDQEKTMAPIF
DTIIDHIPAPVDNSEEPLQFQVSLLDYNDFVGRIGIGRVFRGTVKVGDQVTLSKLDGTTKNFRVTKLFGFFGLERKEIQEAKAGDLIAVSGMEDIF
VGETVTPTDAIEPLPVLRIDEPTLQMTFLVNNSPFAGREGKWITSRKVEERLLAELQTDVSLRVDPTDSPDKWTVSGRGELHLSILIETMRREGYE
LQVSRPEVIIKEIDGVQCEPFERVQIDTPEEYQGAIIQSLSERKGDMLDMQMVGNGQTRLIFLIPARGLIGYSTEFLSMTRGYGIMNHTFDQYLPV
VQGEIGGRHRGALVSIENGKATTYSIMRIEERGTIFVNPGIEVYEGMIVGENSRDNDLGVNITTAKQMTNVRSATKDQTAVIKTPRILTLEEESLEF
LADDEYMEVTPESIRLRKQILNKAARDKANKKKKSAE

SEQ ID 205

ATGACTAACTTAAGAAACGATATCCGTAACGTAGCGATTATTGCCCACGTTGACCACGGAAAAACAACACTTGTAGATGAATTATTAAAACAATCC
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GCAGTAGCCTATAACGATGTTCGTATTAACATCATGGATACCCCAGGACACGCGGACTTCGGTGGTGAAGTTGAACGTATCATGAAAATGGTTGAC
GGGGTTGTTCTTGTTGTGGATGCCTACGAAGGAACAATGCCCCAGACGCGTTTCGTATTGAAAAAAGCACTTGAGCAAAACCTTATCCCGATCGTT
GTGGTGAACAAGATTGACAAACCTTCAGCTCGTCCAGCAGAAGTTGTAGATGAAGTGCTTGAATTATTCATCGAACTTGGTGCCGATGATGAGCAA
TTGGAATTCCCAGTTGTTTACGCATCAGCTATTAATGGAACATCATCATTATCAGATGACCCTGCTGACCAAGAGCATACTATGGCACCGATCTTT
GATACGATTATTGATCATATTCCAGCGCCAGTTGATAATTCAGATGAGCCTTTGCAATTCCAAGTGTCACTTTTGGACTACAACGATTTCGTAGGT
CGTATCGGTATCGGTCGTGTTTTCCGTGGTACTGTTAAAGTGGGTGACCAAGTAACTCTTTCAAAACTTGATGGTACCACTAAAAACTTCCGTGTT
ACAAAACTGTTTGGTTTCTTCGGTTTGGAACGTCGTGAAATTCAAGAAGCTAAAGCAGGTGACTTGATTGCTGTTTCAGGTATGGAAGATATCTTT

GTTGGAGAAACCATTACACCAACTGACTGTGTGGAAGCTCTGCCAATTCTTCGTATTGATGAGCCAACACTTCAGATGACTTTCTTGGTCAATAAC
TCTCCTTTTGCAGGTCGTGAAGGTAAATGGATCACGTCACGTAAGGTTGAAGAACGTCTTTTAGCAGAATTGCAAACAGACGTGTCACTTCGTGTT
GACCCAACAGATTCGCCAGATAAATGGACGGTTTCAGGGCGTGGAGAATTGCATTTATCTATCCTCATTGAAACCATGCGCCGTGAAGGCTATGAA
CTTCAAGTATCACGTCCAGAAGTTATCATCAAAGAAATTGATGGTGTCAAATGTGAACCGTTTGAGCGTGTTCAAATTGATACACCAGAAGAATAT
CAGGGTGCAATCATCCAGTCTCTTTCAGAACGTAAAGGGGATATGCTTGATATGCAGATGGTTGGTAATGGTCAAACGCGTTTGATTTTCTTGATT
CCTGCACGTGGTTTGATTGGTTATTCAACAGAGTTTCTTTCAATGACACGTGGATATGGTATCATGAATCATACTTTTGATCAGTATCTACCGGTT
GTTCAAGGAGAAATCGGTGGCCGTCATCGTGGTGCCTTGGTTTCTATTGAAAATGGGAAAGCAACGACATATTCAATCATGCGTATTGAAGAACGT
GGAACTATCTTTGTCAATCCAGGTACAGAAGTTTACGAAGGGATGATTGTTGGTGAAAACTCACGTGATAACGACCTTGGTGTTAACATTACAACA
GCTAAGCAAATGACAAATGTCCGTTCAGCGACTAAAGATCAAACTGCAGTTATCAAGACGCCTCGTATCCTAACGCTTGAAGAATCATTAGAGTTC
TTGAATGACGACGAATACATGGAAGTAACGCCAGAATCTATCCGCTTGCGTAAACAAATCTTGAATAAAGCTGCGCGTGATAAAGCTAATAAAAAG
AAAAAATCAGCCGAA

SEQ ID 206

MTNLRNDIRNVAIIAHVDHGKTTLVDELLKQSHTLDERKELQERAMDSNDLEKERGITILAKNTAVAYNDVRINIMDTPGHADFGGEVERIMKMVD
GVVLVVDAYEGTMPQTRFVLKKALEQNLIPIVVVNKIDKPSARPAEVVDEVLELFIELGADDEQLEFPVVYASAINGTSSLSDDPADQEHTMAPIF
DTIIDHIPAPVDNSDEPLQFQVSLLDYNDFVGRIGIGRVFRGTVKVGDQVTLSKLDGTTKNFRVTKLFGFFGLERREIQEAKAGDLIAVSGMEDIF
VGETITPTDCVEALPILRIDEPTLQMTFLVNNSPFAGREGKWITSRKVEERLLAELQTDVSLRVDPTDSPDKWTVSGRGELHLSILIETMRREGYE
LQVSRPEVIIKEIDGVKCEPFERVQIDTPEEYQGAIIQSLSERKGDMLDMQMVGNGQTRLIFLIPARGLIGYSTEFLSMTRGYGIMNHTFDQYLPV
VQGEIGGRHRGALVSIENGKATTYSIMRIEERGTIFVNPGTEVYEGMIVGENSRDNDLGVNITTAKQMTNVRSATKDQTAVIKTPRILTLEESLEF
LNDDEYMEVTPESIRLRKQILNKAARDKANKKKKSAE

SEQ ID 207

ATGGGACGAGTAATGAAAACAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACGTTTGTTA
GCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAGTGGTT
TGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGCA
TTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACG
ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAG
GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAAT
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GTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCT
TACGTACAAGACAAGCAACTTTTCTATAAAGGGGAGAATATTATGTCAGTAGATGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTA
GCAACTATTGCGGTTGCTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCA
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GTTATCCTAATTGCAGGAGGTCTTGATCGCGGTAATGAGTTTGATGAATTGATACCAGATATCACTGGACTTAAACATATGGTTGTTTTAGGGGAA
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GCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAATTCATTGATACT
TTCGAAAGTCTTAGAGGAGAG

SEQ ID 208

MGRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKA
LEKQIPVLTEVELAYLVSESQLIGITGSNGKTTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHIAVITN
LMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTKATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENAL
ATIAVAKLAGISNQVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFDELIPDITGLKHMVVLGE
SASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID 209

ATGAAAGTGATAAGTAATTTTCAAAACAAAAAAATATTAATATTGGGGTTAGCCAAATCGGGCGAAGCAGCAGCAAAATTATTGACCAAACTTGGT
GCTTTAGTGACTGTTAATGATAGTAAACCATTTGACCAAAATCCAGCGGCACAAGCCTTGTTGGAAGAGGGGATTAAGGTCATTTGTGGTAGCCAC
CCAGTAGAATTATTAGATGAGAACTTTGAGTACATGGTTAAAAACCCTGGGATTCCTTATGATAATCCTATGGTTAAACGCGCCCTTGCAAAGGAA
ATTCCCATCTTGACTGAAGTAGAATTGGCTTATTTCGTATCTGAAGCGCCTATTATCGGGATTACAGGATCAAACGGGAAGACAACCACAACGACA
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GGTGATACTTTGGTGATGGAATTGTCCTCTTTTCAATTAGTGGGAGTGAATGCTTTTCGCCCTCATATTGCTGTCATCACTAATTTAATGCCGACT
CACCTGGACTATCATGGCAGTTTTGAGGATTATGTTGCTGCTAAATGGATGATTCAAGCTCAGATGACAGAATCAGACTACCTTATTTTAAATGCT
AATCAAGAGATTTCAGCAACTCTAGCTAAGACCACCAAAGCAACAGTGATTCCTTTTTCAACTCAAAAAGTGGTTGATGGAGCTTATCTGAAGGAT
GGAATACTCTATTTTAAAGAACAGGCGATTATAGCTGCAACTGACTTAGGTGTCCCAGGTAGCCACAACATTGAAAATGCCCTAGCAACTATTGCA
GTTGCCAAGTTATCTGGTATTGCTGATGATATTATTGCCCAGTGCCTTTCACATTTTGGAGGCGTTAAACATCGTTTGCAACGGGTTGGTCAAATC
AAAGATATTACCTTCTACAATGACAGTAAGTCAACCAATATTTTAGCCACTCAAAAAGCTTTATCAGGTTTTGATAACAGTCGCTTGATTTTGATT
GCTGGCGGTCTAGATCGTGGCAATGAATTTGACGATTTGGTGCCAGACCTTTTAGGACTTAAGCAGATGATTATTTTGGGAGAATCCGCAGAGCGT
ATGAAGCGAGCTGCTAACAAAGCAGAGGTCTCTTATCTTGAAGCTAGAAATGTGGCAGAAGCAACAGAGCTTGCTTTTAAGCTGGCCCAAACAGGC
GATACTATCTTGCTTAGCCCAGCCAATGCTAGCTGGGATATGTATCCTAATTTTGAGGTTCGTGGGGATGAATTTTTGGCAACCTTTGATTGTTTA
AGAGGAGATGCC

SEQ ID 210

MKVISNFQNKKILILGLAKSGEAAAKLLTKLGALVTVNDSKPFDQNPAAQALLEEGIKVICGSHPVELLDENFEYMVKNPGIPYDNPMVKRALAKE
IPILTEVELAYFVSEAPIIGITGSNGKTTTTTMIADVLNAGGQSALLSGNIGYPASKVVQKAIAGDTLVMELSSFQLVGVNAFRPHIAVITNLMPT
HLDYHGSFEDYVAAKWMIQAQMTESDYLILNANQEISATLAKTTKATVIPFSTQKVVDGAYLKDGILYFKEQAIIAATDLGVPGSHNIENALATIA
VAKLSGIADDIIAQCLSHFGGVKHRLQRVGQIKDITFYNDSKSTNILATQKALSGFDNSRLILIAGGLDRGNEFDDLVPDLLGLKQMIILGESAER
MKRAANKAEVSYLEARNVAEATELAFKLAQTGDTILLSPANASWDMYPNFEVRGDEFLATFDCLRGDA

SEQ ID 211

ATGGGGAAAAAAATTGTTTTTACAGGTGGTGGTACGGTAGGTCATGTAACACTAAACCTAATATTAATCCCCAAATTTATCAAAGATGGTTGGGAA
GTACATTATATTGGTGATAAAAATGGCATAGAACATGAACAAATTAATCAGTCTGGACTTGATATCACATTTCACTCTATAGCTACTGGGAAACTA
CGTCGCTATTTTTCATGGCAAAATATGTTAGATGTCTTTAAAGTAGGGGTTGGCGTTCTTCAATCGATTGCTATTATTGCTAAACTTAGACCCCAA
GCCTTATTTTCAAAAGGGGGATTTGTTTCAGTACCTCCTGTAGTAGCTGCACGCCTATTAAAAGTTCCTGTTTTTGTTCATGAATCAGATTTATCA
ATGGGGTTAGCAAATAAGATTGCTTATAAATTTGCGACTATTATGTATACGACTTTTGAACAATCTAAAGATTTAATCAAAACTAAGCATATTGGT
GCTGTAACAAAAGTCATGGATTGTAAAAAGTCGTTTGAAAATACTGACTTAACTAGTATAAAAGAAGCCTTCGATCCAAACCTAAAGACCTTACTA
TTTATTGGAGGATCAGCAGGTGCAAAAGTATTCAATGATTTTATTACTCAAACACCTGAGCTGGAAGAAAAATATAATGTTATCAATATTTCAGGC
GATTCTTCTCTCAATCGATTGAAGAAGAACCTTTATCGCGTGGATTATGTTACAGACCTTTATCAGCCTTTAATGAATTTAGCAGATGTGGTTGTT
ACACGAGGTGGCTCTAATACTATTTTTGAATTAGTAGCTATGAAAAAACTTCATCTTATTATCCCTCTTGGACGTGAAGCGAGCCGAGGTGACCAA
TTAGAGAATGCTGCTTATTTTGAAGAAAAGGGCTACGCATTGCAGTTACCAGAATCTGAATTAAACATAAATACACTTGAGAAACAGATAAATTTA
TTAATTTCTAACAGTGAGAGTTACGAAAAAAACATGTCACAATCATCTGAAATAAAATCTCAAGATGAATTTTATCAATTATTAATTGATGATATG
GCAAAAGTAACAAAAGGA

SEQ ID 212

MGKKIVFTGGGTVGHVTLNLILIPKFIKDGWEVHYIGDKNGIEHEQINQSGLDITFHSIATGKLRRYFSWQNMLDVFKVGVGVLQSIAIIAKLRPQ
ALFSKGGFVSVPPVVAARLLKVPVFVHESDLSMGLANKIAYKFATIMYTTFEQSKDLIKTKHIGAVTKVMDCKKSFENTDLTSIKEAFDPNLKTLL
FIGGSAGAKVFNDFITQTPELEEKYNVINISGDSSLNRLKKNLYRVDYVTDLYQPLMNLADVVVTRGGSNTIFELVAMKKLHLIIPLGREASRGDQ
LENAAYFEEKGYALQLPESELNINTLEKQINLLISNSESYEKNMSQSSEIKSQDEFYQLLIDDMAKVTKG

SEQ ID 213

TTGTTTAAGAGGAGATGCCTAATGCCTAAGAAGATTTTATTTACAGGTGGTGGAACTGTAGGTCATGTCACCTTGAACCTCATTCTCATACCAAAA
TTTATCAAGGACGGTTGGGAAGTACATTATATTGGTGATAAAAATGGCATTGAACATACAGAAATTGAAAAGTCAGGCCTTGACGTGACCTTTCAT
GCTATCGCGACAGGCAAGCTTAGACGCTATTTTTCATGGCAAAATCTAGCTGATGTTTTTAAGGTTGCACTTGGCCTCCTACAGTCTCTCTTTATT
GTTGCCAAGCTTCGCCCTCAAGCCCTTTTTTCCAAAGGTGGTTTTGTCTCAGTACCGCCAGTTGTGGCTGCTAAATTGCTTGGTAAACCAGTCTTT
ATTCATGAATCAGATCGGTCAATGGGACTAGCAAACAAGATTGCCTACAAATTTGCAACTACCATGTATACCACTTTTGAGCAGGAAGACCAGTTG
TCTAAAGTTAAACACCTTGGAGCGGTGACAAAGGTTTTCAAAGATGCCAACCAAATGCCTGAATCAACTCAGTTAGAGGCGGTGAAAGAGTATTTT
AGTAGAGACCTAAAAACCCTCTTGTTTATTGGTGGTTCGGCAGGGGCGCATGTGTTTAATCAGTTTATTAGTGATCATCCAGAATTGAAGCAACGT
TATAATATCATCAATATTACAGGAGACCCTCACCTTAATGAATTGAGTTCTCATCTGTATCGAGTAGATTATGTTACCGATCTCTACCAACCTTTG
ATGGCGATGGCTGACCTTGTAGTGACAAGAGGGGGCTCTAATACACTTTTTGAGCTACTGGCAATGGCTAAGCTACACCTCATCGTTCCTCTTGGT
AAAGAAGCTAGCCGTGGCGATCAGTTAGAAAATGCCACTTATTTTGAGAAGAGGGGCTACGCTAAACAATTACAGGAACCTGATTTAACTTTGCAT
AATTTTGATCAGGCAATGGCTGATTTGTTTGAACATCAGGCTGATTATGAGGCTACTATGTTGGCAACTAAGGAGATTCAGTCACCGGACTTCTTT
TATGACCTTTTGAGAGCTGATATTAGCTCCGCGATTAAGGAGAAG

SEQ ID 214

LFKRRCLMPKKILFTGGGTVGHVTLNLILIPKFIKDGWEVHYIGDKNGIEHTEIEKSGLDVTFHAIATGKLRRYFSWQNLADVFKVALGLLQSLFI
VAKLRPQALFSKGGFVSVPPVVAAKLLGKPVFIHESDRSMGLANKIAYKFATTMYTTFEQEDQLSKVKHLGAVTKVFKDANQMPESTQLEAVKEYF
SRDLKTLLFIGGSAGAHVFNQFISDHPELKQRYNIINITGDPHLNELSSHLYRVDYVTDLYQPLMAMADLVVTRGGSNTLFELLAMAKLHLIVPLG
KEASRGDQLENATYFEKRGYAKQLQEPDLTLHNFDQAMADLFEHQADYEATMLATKEIQSPDFFYDLLRADISSAIKEK

SEQ ID 215

ATGCCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAAAGAA
GATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAAT
CGCATTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCCGTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACA
GTTAGTGGAAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAAAAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAA
GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAA
AATAAGATTATTGCATATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAGGCTGATCCTGTAAATAGTTCAGAGCTACCA
AAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTTTAGACCCTGATTTAATAAGTGAGATT
CAGGTGATAAGTTTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAGAATACCATTATCTAAATTT
AAAGAAAGACTTCCTTTTTACAAACAAATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAAATACC
ATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGGA
CAAACAAATAACTCAAATACTAATCAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT

SEQ ID 216

MPKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQNTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTN
RIRTAPIFVVAFLVILVSVFLLTPFSKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQFPNKFHIQVQE
NKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLLIKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKF
KERLPFYKQIKKNLKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQQGQQIATEQAPNPQNVN

SEQ ID 217

ATGGCAAAAGATAAAGAGAAACAAAGTGATGACAAGCTCGTTTTGACAGAGTGGCAAAAGCGTAACATTGAATTTTTAAAGAAAAAGAAGCAGCAA
GCTGAGGAAGAAAAAAAACTCAAAGAGAAATTATTGAGTGATAAAAAAGCGCAGCAGCAAGCTCAAAATGCTTCTGAAGCGGTTGAGCTTAAAACT
GATGAGAAAACTGATAGTCAGGAAATTGAGTCAGAAACGACGTCAAAACCTAAAAAAACCAAAAAAGTTAGACAACCCAAGGAAAAAAGCGCGACA
CAAATCGCTTTTCAAAAATCCTTGCCTGTTCTTTTGGGGGCGCTCTTACTCATGGCGGTGTCTATTTTTATGATCACTCCTTATAGCAAAAAGAAA
GAGTTTTCTGTAAGAGGAAACCATCAAACGAACCTTGACGAATTAATCAAAGCTAGCAAAGTCAAAGCATCTGACTATTGGTTAACGCTGTTAACT
TCGCCTGGTCAGTATGAACGACCGATTCTTCGTACTATTCCATGGGTGAAATCTGTACATCTCTCTTACCAATTTCCTAATCACTTTCTATTTAAC
GTTATTGAATTTGAAATCATCGCTTATGCACAAGTTGAAAACGGTTTTCAGCCTATTTTGGAGAATGGAAAACGTGTGGACAAGGTCAGGGCATCA
GAACTACCGAAATCTTTCTTGATTCTTAATTTAAAAGATGAGAAAGCGATCCAACAGTTAGTTAAGCAATTAACGACATTACCTAAAAAATTAGTC
AAGAATATCAAGTCAGTGTCTCTTGCAAATTCCAAAACGACAGCGGATTTACTACTTATTGAAATGCATGACGGTAATGTAGTTAGAGTACCGCAG
TCACAACTCACATTGAAACTTCCCTATTATCAAAAATTGAAAAAAAACCTTGAAAATGATAGTATAGTGGATATGGAAGTGGGAATTTATACTACA
ACACAGGAGATTGAAAATCAACCTGAAGTTCCTCTTACGCCTGAACAAAACGCAGCTGATAAAGAAGGAGATAAGCCTGGTGAACATCAGGAACAG
ACAGACAATGATTCAGAAACGCCAGCAAATCAGAGTAGTCCTCAGCAAACACCACCATCCCCAGAAACGGTCCTCGAACAGGCCCATGGC

SEQ ID 218

MAKDKEKQSDDKLVLTEWQKRNIEFLKKKKQQAEEEKKLKEKLLSDKKAQQQAQNASEAVELKTDEKTDSQEIESETTSKPKKTKKVRQPKEKSAT
QIAFQKSLPVLLGALLLMAVSIFMITPYSKKKEFSVRGNHQTNLDELIKASKVKASDYWLTLLTSPGQYERPILRTIPWVKSVHLSYQFPNHFLFN
VIEFEIIAYAQVENGFQPILENGKRVDKVRASELPKSFLILNLKDEKAIQQLVKQLTTLPKKLVKNIKSVSLANSKTTADLLLLIEMHDGNVVRVPQ
SQLTLKLPYYQKLKKNLENDSIVDMEVGIYTTTQEIENQPEVPLTPEQNAADKEGDKPGEHQEQTDNDSETPANQSSPQQTPPSPETVLEQAHG

SEQ ID 219

ATGGCTAGAAATGGCTTTTTTACTGGTTTGGATATAGGAACAAGCTCGATTAAAGTTTTAGTTGCAGAATTTATTGCAAATGAAATGAATGTAATT
GGGGTTAGCAACGTCCCTAGTTCCGGTGTAAAAGATGGTATAATTATTGATATTGAGGCAGCAGCAACTGCAATCAAAGAGGCGGTAAAACAAGCT
GAGGAGAAAGCAGGCATCACCATTGACAAAATCAATGTTGGATTACCAGCAAATCTTCTCCAAATTGAACCAACTCAAGGAATGATTCCTGTTCCT
AATGAATCAAAAGAAATTAAGGATGAAGATGTCGAAAGTGTTGTTAAATCAGCATTGACTAAAAGCATTACTCCTGAAAGAGAAGTTATTTCATTG
ATTCCGCTTGAATTCATTGTAGATGGTTTCCAAGGGATTAGAGACCCTAGAGGGATGATGGGGATTCGCCTTGAGATGCGTGGTCTTATCTATACT
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TCAGTTCTAAACGAAGGTGAACGTGAGTTTGGTGCAACTGTGATTGATATGGGAGGCGGACAAACAACAGTCGCTTCTATGCGTAATCAAGAATTG
CAATATACTAATATTTATTCTGAAGGTAGCGATTATGTTACCAAAGATATTTCTAAAGTGCTACGTACAACAGTAGAAATCGCCGAAGCATTGAAA
TTCAACTTTGGACAAGCTAATGTTGAAGAAGCAAGTACTTCTGATACAGTTCAAGTTAATGTTGTTGGTAACGAGGAACCTGTTGAAATTACAGAA
AGCTATCTTTCGCAAATTATTTCAGGACGTATTCGTCAAATTTTAGAACATGTCAAACAAGACTTGGGTAGAGGTCGTTTACTTGATTTACCTGGT
GGTATTATTCTTGTTGGAGGTGGTGCAATTATGCCAGGAGTTGTCGAGGTTGCTCAACAAATTTTTGGAACTAGAGTTAAATTGCACGTTCCAAAC
CAAGTAGGTATTCGCAATCCAATGTTTGCTAATGTTATTAGTATCGTTGATTATGTAGGAATGATGTCAGAAGTTGACATTATCGCACAACATGCT
GTAACTGGCGACGAAATGCTAAGACATAAACCAGTCGACTTTGATTATAAAGAAAAAACAAATACAATGTCGACAATGCCTTATTCTGAGCCGTTA
ACCTCTTCTATGGAAGATTCTAATTTAGAACCAATCCGAGCAAGAGAAAACGCTCAAGAGCCTACTGAGCCTAAAGCTAATATTGGTGAGCGCATC
AGAGGAATTTTTGGAAGTATGTTTGAC

SEQ ID 220

MARNGFFTGLDIGTSSIKVLVAEFIANEMNVIGVSNVPSSGVKDGIIIDIEAAATAIKEAVKQAEEKAGITIDKINVGLPANLLQIEPTQGMIPVP
NESKEIKDEDVESVVKSALTKSITPEREVISLIPLEFIVDGFQGIRDPRGMMGIRLEMRGLIYTGPTTILHNLRKTVERAGIKVEHVVIAPLALAK
SVLNEGEREFGATVIDMGGGQTTVASMRNQELQYTNIYSEGSDYVTKDISKVLRTTVEIAEALKFNFGQANVEEASTSDTVQVNVVGNEEPVEITE
SYLSQIISGRIRQILEHVKQDLGRGRLLDLPGGIILVGGGAIMPGVVEVAQQIFGTRVKLHVPNQVGIRNPMFANVISIVDYVGMMSEVDIIAQHA
VTGDEMLRHKPVDFDYKEKTNTMSTMPYSEPLTSSMEDSNLEPIRARENAQEPTEPKANIGERIRGIFGSMFD

SEQ ID 221

TTGGACATTGGAACAAGCTCGATAAAAGTTTTAGTAGCAGAATTTATTTCTGGTGAGATGAACGTCATTGGTGTTAGTAATGTTCCAAGTACCGGC
GTAAAAGATGGCATAATAATCGATATAGAGGCAGCTGCGACTGCCATCAAAACTGCGGTAGAACAAGCAGAAGAAAAAGCAGGGATGACAATTGAA
AAGGTTAATGTTGGGCTACCGGCAAACCTTCTTCAAATTGAACCAACACAAGGAATGATTCCTGTCCCAAGTGAGTCTAAAGAGATAAAAGATGAG
GATGTTGATAGCGTTGTTAAATCGGCTTTAACAAAAAGTATCACACCAGAACGAGAGGTTATCTCTTTAGTTCCAGAAGAGTTCATTGTGGATGGC
TTTCAGGGCATTCGAGATCCACGTGGTATGATGGGGATTAGATTAGAGATGCGCGGGCTTATTTATACTGGACCAAGCACCATTTTACATAATCTG
CGTAAAACGGTAGAAAGAGCAGGCATTAAAGTTGAAAACATCATTATTTCTCCGTTAGCTATGGCTAAAACCATTTTAAACGAAGGTGAGCGCGAG
TTTGGAGCTACTGTAATTGATATGGGAGGTGGACAGACAACTGTCGCTTCTATGCGAGCACAAGAATTGCAGTATACCAATATATATGCCGAAGGC
GGCGAATACATTACTAAAGATATATCAAAAGTATTAAAAACGTCTTTGGCTATTGCAGAAGCACTTAAGTTTAATTTTGGTCAAGCGGAGATATCA
GAAGCTAGTATAACTGAAACAGTAAAAGTTGATGTGGTAGGTAGTGAAGAGCCTGTTGAGGTAACTGAACGTTATTTATCTGAAATTATTTCAGCG
CGTATTCGTCATATTTTAGATCGTGTGAAGCAAGATTTGGAAAGAGGTCGTTTACTAGACTTACCAGGAGGCATTGTTTTGATTGGTGGCGGTGCA
ATCATGCCTGGAGTGGTAGAAATTGCACAAGAAATCTTTGGAGTAACTGTAAAGCTCCATGTTCCAAACCAAGTCGGTATTAGAAATCCAATGTTT
TCAAACGTTATCAGTTTGGTAGAATATGTTGGTATGATGTCTGAAGTAGACGTTTTAGCACAAACTGCAGTTTCAGGAGAAGAACTTTTGCGACGC
AAGCCTATCGATTTCAGTGGCCAAGAATCTTATTTACCAGATTATGATGATTCAAGAAGACCAGAATCGACCATTGGCTATGAACAACAAGCGTCA
CAAACAGCATATGATTCACAAGTTCCGAGTGATCCTAAACAAAAAATTTCAGAACGTGTTCGTGGCATATTTGGGAGTATGTTTGAT

SEQ ID 222

LDIGTSSIKVLVAEFISGEMNVIGVSNVPSTGVKDGIIIDIEAAATAIKTAVEQAEEKAGMTIEKVNVGLPANLLQIEPTQGMIPVPSESKEIKDE
DVDSVVKSALTKSITPEREVISLVPEEFIVDGFQGIRDPRGMMGIRLEMRGLIYTGPSTILHNLRKTVERAGIKVENIIISPLAMAKTILNEGERE
FGATVIDMGGGQTTVASMRAQELQYTNIYAEGGEYITKDISKVLKTSLAIAEALKFNFGQAEISEASITETVKVDVVGSEEPVEVTERYLSEIISA
RIRHILDRVKQDLERGRLLDLPGGIVLIGGGAIMPGVVEIAQEIFGVTVKLHVPNQVGIRNPMFSNVISLVEYVGMMSEVDVLAQTAVSGEELLRR
KPIDFSGQESYLPDYDDSRRPESTIGYEQQASQTAYDSQVPSDPKQKISERVRGIFGSMFD

SEQ ID 223

ATGGTATTTTCATTTGATACAGCATCAGTACAAGGTGCAGTTATTAAAGTTATTGGTGTTGGAGGCGGTGGCGGTAACGCTATTAACCGCATGATT
GACGAAGGTGTCGCTGGCGTTGAGTTTATTGCAGCAAATACTGATATTCAAGCCTTAAGTAGCTCAAAAGCTGAAACTGTCATTCAACTTGGTCCA
AAATTAACTCGCGGACTTGGTGCAGGAGGACAACCTGAAGTTGGTCGTAAAGCAGCTGAAGAAAGTGAAGAAGTTTTAACAGAAGCACTTACTGGC
GCTGATATGGTATTTATCACAGCAGGTATGGGGGGCGGATCTGGTACAGGTGCGGCTCCAGTTATTGCACGTATTGCAAAGAGTTTAGGAGCACTT
ACAGTAGCGGTCATCACACGTCCTTTTGGCTTTGAGGGTAATAAACGTTCTAACTTCGCTATCGAAGGTATTCAAGAATTAAGAGAACAAGTTGAT
ACACTGCTTATCATTTCAAATAATAATCTTCTTGAAATTGTAGATAAGAAGACACCATTGCTTGAAGCTCTTAGTGAAGCAGATAATGTTTTACGT
CAAGGTGTTCAAGGTATTACGGATTTGATTACTAACCCAGGTTTAATTAACCTTGACTTTGCAGATGTTAAAACAGTTATGGCAAATAAAGGTAAT
GCACTGATGGGAATTGGTATCGGTTCTGGTGAGGAACGTATTACTGAAGCTGCTCGAAAAGCAATTTATTCACCACTTCTTGAAACAACGATTGAT
GGAGCAGAAGACGTTATTGTCAATGTTACCGGCGGTATGGATATGACACTTACTGAAGCAGAGGAAGCATCAGAGATTGTTAGCCAAGCAGCAGGT
AAAGGTGTCAATATTTGGTTAGGTACTTCAATTGACATGGATATGAAAGACGAAATCCGCGTAACAGTTGTTGCAACAGGTGTACGTAAAGATAAA
ACTAATCAAGTATCTGGTTTTACAACATCAGCTCCAACTAATCAAGCACCTTCAGAACGTCAAAGTACTTCAAATTCAAACTTTGATCGTCGTGGC
AACTTTGATATGACAGAGTCTCGCGAAATGCCAACTCAACAAAATCAGCCTCATGCACAAAATCAGCAACAAAGTTCTGCTTTTGGTAATTGGGAC
CTTCGTCGTGATAATATTTCACGTCCGACAGAAGGTGAACTTGATAGCAAGTTGTCTATGTCAACGTTTTCAGAAAATGATGATATGGATGATGAA
CTTGAAACACCTCCATTCTTTAAAAACCGT

SEQ ID 224

MVFSFDTASVQGAVIKVIGVGGGGGNAINRMIDEGVAGVEFIAANTDIQALSSSKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEEVLTEALTG
ADMVFITAGMGGGSGTGAAPVIARIAKSLGALTVAVITRPFGFEGNKRSNFAIEGIQELREQVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLR
QGVQGITDLITNPGLINLDFADVKTVMANKGNALMGIGIGSGEERITEAARKAIYSPLLETTIDGAEDVIVNVTGGMDMTLTEAEEASEIVSQAAG
KGVNIWLGTSIDMDMKDEIRVTVVATGVRKDKTNQVSGFTTSAPTNQAPSERQSTSNSNFDRRGNFDMTESREMPTQQNQPHAQNQQQSSAFGNWD
LRRDNISRPTEGELDSKLSMSTFSENDDMDDELETPPFFKNR

SEQ ID 225

ATGGCATTTTCATTTGATACTGCATCAATTCAAGGTGCAATTATAAAAGTAATTGGAGTCGGCGGAGGTGGCGGAAATGCCATTAATCGTATGATT
GATGAAGGTGTTGCTGGTGTCGAGTTCATCGCAGCAAACACAGACATTCAGGCATTAAGCTCATCAAAAGCTGAAACGGTTATTCAACTAGGCCCT
AAATTAACTCGTGGACTTGGTGCTGGAGGACAACCTGAAGTAGGACGTAAAGCTGCTGAAGAAAGCGAAGAAATTTTAACAGAAGCTCTTACAGGA
GCGGACATGGTATTTATTACTGCCGGTATGGGTGGTGGCTCTGGGACAGGGGCTGCACCGGTTATTGCTCGTATCGCTAAAAGTTTGGGAGCCTTG
ACAGTAGCTGTTGTTACTCGCCCGTTTGGTTTTGAAGGTAACAAACGTGGTAATTTTGCTATTGAAGGTATCGAAGAACTACGTGAACAAGTTGAT
ACTTTGTTAATTATTTCAAATAATAACCTTCTTGAGATTGTTGATAAAAAGACACCTTTATTAGAAGCACTTAGTGAAGCTGATAATGTTTTACGC
CAGGGAGTTCAAGGGATAACCGACTTAATTACTAGTCCTGGCCTTATCAATCTCGATTTTGCCGACGTGAAAACAGTTATGGCAAATAAAGGGAAT
GCCTTGATGGGGATTGGGATTGGCTCTGGAGAAGAGCGCATTGTTGAGGCGGCGCGTAAGGCAATCTATTCACCCCTATTAGAAACGACTATTGAT
GGTGCACAAGACGTTATTGTGAACGTTACAGGAGGTCTCGACATGACACTTACAGAAGCTGAAGAAGCCTCTGAAATTGTTGGGCAAGCTGCTGGT
CAAGGCGTTAACATTTGGTTAGGAACATCTATTGATGATACTATGAAAGATGACATCCGTGTGACTGTTGTAGCAACTGGAGTGCGCCAAGAAAAA
GCCGAACAAGTTTCAGGTTTTCGTCAGCCTAGGACTTTTACCCAAACCAACGCGCAGCAAGTAGCGGGTGCACAATATGCATCAGATCAAGCAAAA
CAGTCGGTTCAACCAGGGTTTGATCGTCGCTCAAATTTTGATTTTGACATGGGGGAGTCTCGCGAGATACCAAGTGCACAAAAGGTAATTTCTAAT
CATAATCAAAATCAAGGTTCTGCTTTTGGAAATTGGGATTTGAGACGTGATAATATTTCTCGTCCAACAGAAGGTGAATTGGATAACCATCTTAAT
ATGTCAACGTTCTCAGCTAACGATGACAGTGATGATGAATTAGAAACGCCTCCATTCTTTAAAAACCGT

SEQ ID 226

MAFSFDTASIQGAIIKVIGVGGGGGNAINRMIDEGVAGVEFIAANTDIQALSSSKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEEILTEALTG
ADMVFITAGMGGGSGTGAAPVIARIAKSLGALTVAVVTRPFGFEGNKRGNFAIEGIEELREQVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLR
QGVQGITDLITSPGLINLDFADVKTVMANKGNALMGIGIGSGEERIVEAARKAIYSPLLETTIDGAQDVIVNVTGGLDMTLTEAEEASEIVGQAAG
QGVNIWLGTSIDDTMKDDIRVTVVATGVRQEKAEQVSGFRQPRTFTQTNAQQVAGAQYASDQAKQSVQPGFDRRSNFDFDMGESREIPSAQKVISN
HNQNQGSAFGNWDLRRDNISRPTEGELDNHLNMSTFSANDDSDDELETPPFFKNR

SEQ ID 227

ATGATGAATTTACAAGAAAATAAAACAGCGATTTTTGACAATGTTAGTAAATTAGCACTAAAAGCAGGTCGCGCTCATGAATCAGTTCATATCGTA
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AAATATCAAGCATTAAAAGATGAAAAGCTTACATGGCATCTCATTGGTAGTTTACAACGTCGAAAAGTTAAAGATGTCATTAATTATGTTGATTAT
TTTCATGCTTTAGATTCTGTTAAGTTAGCAGCTGAGATTCAAAAACATGCTCAAAAACTAATTAAATGTTTTCTACAAGTTAATATATCACGAGAA
GACAGTAAGCATGGTTTTACTATTGAGCAAATAGATGATGCACTGAACTTAATTTCTCGGTACGATAAAATTGAACTTATCGGCATCATGACTATG

GCTCCCTTAAAAGCAACTAAAGAGGAAATATCATCAATTTTTGAAGAGACTGAGAGTCTTAGGAAAAGGCTTCAAGCTAGGAACATAGAACGAATG
CCGTTTACAGAATTAAGCATGGGCATGAGTAGAGATTATGATATTGCTATTCAAAATGGATCAACATTTGTAAGGATAGGAACTTCATTCTTTAAA

SEQ ID 228

MMNLQENKTAIFDNVSKLALKAGRAHESVHIVAVTKYVNCQTTEALIRTGVNHIGENRVDKFLEKYQALKDEKLTWHLIGSLQRRKVKDVINYVDY
FHALDSVKLAAEIQKHAQKLIKCFLQVNISREDSKHGFTIEQIDDALNLISRYDKIELIGIMTMAPLKATKEEISSIFEETESLRKRLQARNIERM
PFTELSMGMSRDYDIAIQNGSTFVRIGTSFFK

SEQ ID 229

ATGGATTTACTGACAAATAAAAAGAAAATTTTTGAGACTATCCGCTTATCTACAGAGGCAGCAAATAGGACTAATGATAGTGTTTCAGTTATTGCT
GTAACAAAATATGTGGATAGTACAATTGCAGGTCAGCTTATCGAAGCAGGAATTGAGCACATTGCCGAAAACCGTGTTGATAAATTTCTTGAAAAG
TATGATGCGTTAAAGTATATGCCAGTAAAGTGGCATTTAATTGGTACCTTACAACGTCGTAAAGTCAAGGAAGTTATCAATTATGTTGATTATTTT
CACGCTCTAGATTCTGTGAGATTAGCTTTGGAAATCAACAAGAGAGCTGACCATCCTGTGAAGTGTTTTCTACAAGTTAATATTTCTAAAGAAGAG
AGTAAACATGGTTTTAACATTTCTGAGATTGATGAAGCGATTGGAGAAATAGGTAAGATGGAGAAGATACAGTTAGTTGGTTTAATGACTATGGCA
CCAGCAAATGCCAGTAAAGAAAGTATTATAACTATTTTTCGACAAGCAAATCAATTAAGAAAAAACTTGCAGTTAAAAAAAAGAAAGAATATGCCT
TTTACAGAATTGAGCATGGGCATGAGTAACGATTATCCAATTGCTATTCAAGAAGGCTCAACTTTTATTCGGATTGGTAGAGCTTTCTTTCAC

SEQ ID 230

MDLLTNKKKIFETIRLSTEAANRTNDSVSVIAVTKYVDSTIAGQLIEAGIEHIAENRVDKFLEKYDALKYMPVKWHLIGTLQRRKVKEVINYVDYF
HALDSVRLALEINKRADHPVKCFLQVNISKEESKHGFNISEIDEAIGEIGKMEKIQLVGLMTMAPANASKESIITIFRQANQLRKNLQLKKRKNMP
FTELSMGMSNDYPIAIQEGSTFIRIGRAFFH

SEQ ID 231

ATGGAGGGGAATATGGCATTAAAAGATAGATTTGACAAAATTATTTCTTATTTTGACACTGACGATGTAAGTGAAAATGAAGTACACGAAGTACAA
GAGAGAACTTCAGTGCAAAGAGATTCCAGAGCAGCTACAGCACAGGAAGCTTCTCAGCGTAGTCATATGACTAACTCCGCAGAGGAAGAGATGATT
GGTAGTCGTCCGAGAACTTATACCTATGATCCTAATCGTCAGGAGAGACAAAGGGTACAGAGAGACAATGCTTATCAGCAAGCTACTCCTAGGGTT
CAAAATAAAGACTCAGTTCGACAACAGAGAGAACAAGTAACAATTGCTCTGAAGTATCCCCGTAAGTATGAGGATGCACAAGAAATTGTTGATTTA
CTTATCGTTAATGAATGTGTCTTGATTGATTTTCAATATATGCTTGATGCGCAAGCACGACGTTGCTTGGATTATATTGATGGTGCAAGTAGAGTA
TTATATGGTTCATTACAAAAGGTTGGGAGTTCAATGTTTCTATTAACACCAGCCAATGTTATGGTTGATATTGAGGAGATGAATATTCCAAAGACT
GGTCAAGAGACGAGTTTTGATTTTGATATGAAGAGACGA

SEQ ID 232

MEGNMALKDRFDKIISYFDTDDVSENEVHEVQERTSVQRDSRAATAQEASQRSHMTNSAEEEMIGSRPRTYTYDPNRQERQRVQRDNAYQQATPRV
QNKDSVRQQREQVTIALKYPRKYEDAQEIVDLLIVNECVLIDFQYMLDAQARRCLDYIDGASRVLYGSLQKVGSSMFLLTPANVMVDIEEMNIPKT
GQETSFDFDMKRR

SEQ ID 233

ATGGAGAATAAGATGGCTTTTAAAGATACATTTAACAAGATGATTTCTTATTTTGACACGGATGAGGTTAACGAAGTTGAAGAAGATGTTGCAGCA
TCAACTGATAACGTTATTCCAAGATCACAACAATCAGTCAGAGCAAGTAGTCATCCAAAACAAGAACCTAGAAACAATCACGTACAACAAGATCAT
CAAGCGAGATCCCAAGAACAGACAAGGTCACAAATGCATCCAAAACATGGCACTTCTGAACGCTATTATCAGCAGTCTCAGCCAAAAGAAGGCCAT
GAAATGGTTGACAGAAGAAAACGGATGAGCACTTCTAGTATTGCAAATCGCCGTGAGCAGTATCAACAATCAACTTGTTCAGATCAAACAACTATT
GCCTTAAAGTATCCTCGTAAATATGAGGATGCTCAAGAAATTGTGGATCTTTTAATAGTTAATGAATGCGTTTTGATTGATTTTCAGTTTATGCTA
GATGCTCAGGCTAGACGGTGTTTAGATTTTATTGATGGTGCTAGTAAAGTGCTCTATGGTAGCTTACAAAAGGTCGGCTCTTCAATGTACTTACTG
GCTCCGTCAAATGTATCCGTCAATATAGAAGAAATGACTATCCCACATACTACACAAGATATTGGCTTTGATTTTGATATGAAAAGGCGG

SEQ ID 234

MENKMAFKDTFNKMISYFDTDEVNEVEEDVAASTDNVIPRSQQSVRASSHPKQEPRNNHVQQDHQARSQEQTRSQMHPKHGTSERYYQQSQPKEGH
EMVDRRKRMSTSSIANRREQYQQSTCSDQTTIALKYPRKYEDAQEIVDLLIVNECVLIDFQFMLDAQARRCLDFIDGASKVLYGSLQKVGSSMYLL
APSNVSVNIEEMTIPHTTQDIGFDFDMKRR

SEQ ID 235

ATGACGTTAGATGATATTTATCAGCATTTTCGACCAGAAGAGTATGCGTTTATCCATAAAATAGACCATTTAGCTCAATATGTCGAAAACACCTAT
TCGTTTATTACCACTGAATTTCTAAATCCTAGGGAATTTAAAATACTCGAAAGTGTTCTAGAGAGGCGAGGTAGTCATTATTACACTTCTGGTCAG
TATTTTCAAACAGAATATGTTAAAGTAATAATAGCACCGGAATACTATCAGTTAGATATGGCTGATTTTAACCTTAGCCTAATTGAAATAAAGTAT
AATGCTAAATTTAATCACCTTACCCATGCTAAAATTATGGGAACTTTACTGAATTACTTAGGTGTAAAACGATCAATTTTAGGGGATATCCTAGTT
GAAGAAGGCTGTGCTCAGGTTTTGGTCGATAGTCAAATGACAAATCACCTTGTTCATTCAGTTACAAAAATTGGAACTGCTAGTGTACAATTAGCT
GAAGTTCCCTTGTCCAAACTTCTAACTCCCAAACAAGATATTCAAAAACTAACTGTTATTGCTTCCAGTTTACGTCTTGATAAAATTTTAGCAACG
ATTTTAAAGATTTCACGAACACAGTCGACGAAATTGATTGAGGCAGATAAAGTCAAGGTCAATTATGCAACCGTCAATCGAGTTTCTGAACAATTA
GTAGAGGGGGATTTGATTAGTGTTAGAGGATATGGTCGATTTACGTTGAACCATAACCTAGGGTTAACTAAAAATCAAAAATATAAGTTAGAAGTA
GACAAAATGATACATAAC

SEQ ID 236

MTLDDIYQHFRPEEYAFIHKIDHLAQYVENTYSFITTEFLNPREFKILESVLERRGSHYYTSGQYFQTEYVKVIIAPEYYQLDMADFNLSLIEIKY
NAKFNHLTHAKIMGTLLNYLGVKRSILGDILVEEGCAQVLVDSQMTNHLVHSVTKIGTASVQLAEVPLSKLLTPKQDIQKLTVIASSLRLDKILAT
ILKISRTQSTKLIEADKVKVNYATVNRVSEQLVEGDLISVRGYGRFTLNHNLGLTKNQKYKLEVDKMIHN

SEQ ID 237

ATGGTTAGTCATAGTAAGATTTATCAGCATTTTCACCAAGAAGAATATCCTTTTATTGATAGAATGTCTGATATGATTAATAGAGTTGAAGATTAC
TATCTTTTAGAAGTTACTGAGTTTTTAAATCCTAGAGAAGTGATGATTTTAAAAAGTTTGATTGCTTTAACAGATCTAAAAATGTTCGTATCAACA
GATTACTACCCAAGCGAATATGGTCGTGTCATTATTGCACCTGGTTACTATGACTTAGAACAAAGTGATTTTCAAATAGCTTTAGTAGAGATAAGT
TATCAGGCAAAGTTTAATCAGTTGACACATAGTCAAATTTTAGGAACTTTAATTAATGAATTAGGAGTAAAGCGAAATTTATTTGGAGATGTTTTT
GTTGAAATGGGATATGCCCAGCTCATGATTAAGCGGGAGTTATTGGATTATTTTTTAGGAACAATTACTAAAATAGCTAAAACTAGTGTGAAATTA
AGAGAAGTTAACTTTGATCAGTTAATTAGGTCTATTGATAACAGCCAGACCCTGGATATTCTAGTTTCTAGTTTTCGATTAGATGGTGTAGTTGCT
ACTATCTTAAAAAAATCTCGAACGCAAGTTATAGCATTAATTGAAGCAAATAAGATTAAGGTAAACTATCGAGTTGCTAATAAAGCTTCAGATAAT
CTAGTCATAGGGGATATGGTGAGTATCAGAGGTCACGGGCGTTTTACTCTTTTAGCAGATAATGGAGTGACCAAACATGGCAAACAAAAAATAACA
CTAAGTAAAATGATACATAAA

SEQ ID 238

MVSHSKIYQHFHQEEYPFIDRMSDMINRVEDYYLLEVTEFLNPREVMILKSLIALTDLKMFVSTDYYPSEYGRVIIAPGYYDLEQSDFQIALVEIS
YQAKFNQLTHSQILGTLINELGVKRNLFGDVFVEMGYAQLMIKRELLDYFLGTITKIAKTSVKLREVNFDQLIRSIDNSQTLDILVSSFRLDGVVA
TILKKSRTQVIALIEANKIKVNYRVANKASDNLVIGDMVSIRGHGRFTLLADNGVTKHGKQKITLSKMIHK

SEQ ID 239

ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTTCATCAAAATTTCGCGGTTATAGCGAAGAAGAAGTTAATGAATTTTTAGAGATTGTT
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GAATCGTTAAGTCAATCAGTTATTTTAGCTCAAGAAACTGCTGAGCGTGTGAAAATTTCAGCACAGGATGAAGCATCTAACCTAATGGGGAAAGCT
ACATTTGATGCTCAACATTTAATTGATGAGGCTAAATTAAAAGCAAATCAAATCCTTCGAGATGCGACAGATGATGCTAAGCGTGTTGCTATAGAA

ACAGAAGATTTGAAACGTCAATCACGTGTTTTCCACCAACGTTTGCTTTCTGAGTTAGAAGGGCAGCTAAAATTAGCTAACTCATCTGCTTGGGAA
GAATTGTTGAAACCAACAGCTATTTATCTTCAAAATTCTGATGCTTCTTTCAAAGAAGTTGTTGAAAAAGTTCTTGATGAAGATGATGCTTTACCA
GTGGTGGATGACACTGAGTCATTTGATGCTACTCGTCAATTCTCACCAGATGAAATGGAAGAATTACAGCGTCGTGTTGAAGAAAGTAACAAACAA
CTTGAAGAGTCAGGTTTATTAGATACTAATAATTTCCAAATGGAAGAACCGATCAATTTAGGTGAAACTCAAACTTTTAAATTAAATATTGAAGAT

SEQ ID 240

MPLTALEIKDKTFSSKFRGYSEEEVNEFLEIVVDDYEDLIRRNREQEQYIKDLEEKIAYFNEMKESLSQSVILAQETAERVKISAQDEASNLMGKA
TFDAQHLIDEAKLKANQILRDATDDAKRVAIETEDLKRQSRVFHQRLLSELEGQLKLANSSAWEELLKPTAIYLQNSDASFKEVVEKVLDEDDALP
VVDDTESFDATRQFSPDEMEELQRRVEESNKQLEESGLLDTNNFQMEEPINLGETQTFKLNIED

SEQ ID 241

ATGGCACTTACAACGCTAGAAATTAAAGATAAAACTTTTAAGACAAAATTCCGAGGATACTGTGAAGAAGAAGTCAATGAATTCCTTGATATTGTT
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GAGTCACTTAGCCAGTCTGTAATCTTAGCTCAAGAAACAGCTGAAAAAGTGAAAGCAACGGCTAATGCGGAAGCAACAAACTTGGTTAGTAAAGCG
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ACAGAAGAACTAAAGCGTCAAACACGTGTGTTCCACCAACGTTTAATCTCATCTATTGAGTCACAATTAAGCTTATCAAATTCACCTGAATGGGAT
GAACTGCTACAACCGACTGCAATCTATCTTCAAAATTCTGACGATGCTTTTAAGGAAGTCGTGAAGACCGTTCTTAATGAAGACATTCCTGAATCT
GATGATAGTGCCTCTTTTGATGCAACACGTCAGTTTACTCCAGAAGAGTTAGAAGAATTGCAACGTCGTGTTGATGAAAGCAATAAGGAGTTAGAG
GCTTACCAACTTGACTCTCAATCTGATTCTACGACTGAGCCAGAGGTAAATCTCAGTGAAACACAAACGTTTAAATTAAATATC

SEQ ID 242

MALTTLEIKDKTFKTKFRGYCEEEVNEFLDIVVDDYEALVRKNRDNEARIKDLEEKLSYFDEMKESLSQSVILAQETAEKVKATANAEATNLVSKA
TYDAQHLLDESKAKANQMLRDATDEAKRVAIETEELKRQTRVFHQRLISSIESQLSLSNSPEWDELLQPTAIYLQNSDDAFKEVVKTVLNEDIPES
DDSASFDATRQFTPEELEELQRRVDESNKELEAYQLDSQSDSTTEPEVNLSETQTFKLNI

SEQ ID 243

ATGAAATTAAAAGAAACCTTGAATTTAGGACAAACAGCTTTTCCAATGCGTGCAGGGCTTCCAAATAAGGAACCTCAATGGCAAGAAGCATGGGAT
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GCAGACAAACCAGCTGACTCAGTATCATTTGAAGGTGTTGCATTTACTGTTGAACACGCTGAAGGTGAAGTCTGCGAACGCTCACGCCGTATTGAT
CCAACCACAAAGATGCGTTCGTATGGTGTAGCTGTTTGTGATGCTAGTGCAGCAATTATTGAGCAATATTATCCTGAAGCAGTAGCTCAAGGTTTT
GAAGCT

SEQ ID 244

MKLKETLNLGQTAFPMRAGLPNKEPQWQEAWDQADIYKKRQALNEGKPAFHLHDGPPYANGNIHVGHALNKISKDIIVRSKSMSGFRAPYVPGWDT
HGLPIEQVLAKKGVKRKEMDLAEYLEMCRDYALSQVDKQRDDFKRLGVSADWENPYITLTPDYEADQVRVFGAMADKGYIYRGAKPVYWSWSSESA
LAEAEIEYHDIDSTSLYYANKVKDGKGILDTDTYIVVWTTTPFTVTASRGLTVGPDMEYVVVVPVGSERKYLLAEVLVDSLAAKFGWENFEIVTHH
TGKELNHIVTEHPWDTEVEELVILGDHVTTDSGTGIVHTAPGFGEDDYNVGIANGLDVVVTVDSRGLMMENAGPDFEGQFYDKVTPLVKEKLGDLL
LASEVINHSYPFDWRTKKPIIWRAVPQWFASVSKFRQEILDEIEKTNFQPEWGKKRLYNMIRDRGDWVISRQRAWGVPLPIFYAEDGTAIMTKEVT
DHVADLFAEYGSIVWWQRDAKDLLPAGYTHPGSPNGLFEKETDIMDVWFDSGSSWNGVMNARENLSYPADLYLEGSDQYRGWFNSSLITSVAVNGH
APYKAVLSQGFVLDGKGEKMSKSLGNTILPSDVEKQFGAEILRLWVTSVDSSNDVRISMDILKQTSETYRKIRNTLRFLIANTSDFNPKQDAVAYE
NLGAVDRYMTIKFNQVVDTINKAYAAYDFMAIYKAVVNFVTVDLSAFYLDFAKDVVYIEAANSPERRRMQTVFYDILVKLTKLLTPILPHTAEEIW
SYLEHEEEEFVQLAEMPVAQTFSGQEEILEEWSAFMTLRTQAQKALEEARNAKVIGKSLEAHLTIYASQEVKTLLTALNSDIALLMIVSQLTIADE
ADKPADSVSFEGVAFTVEHAEGEVCERSRRIDPTTKMRSYGVAVCDASAAIIEQYYPEAVAQGFEA

SEQ ID 245

ATGAAATTAAAAGAGACACTTAATCTAGGAAAAACAGCCTTTCCAATGCGCGCAGGTCTTCCTAATAAAGAGCCACAATGGCAAGCAGCTTGGGAA
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GTTGGGCATGCCCTTAATAAAATTTCAAAAGATATCATTGTGCGTTCTAAGTCCATGTCTGGCTTTCAAGCGCCTTATGTACCTGGTTGGGACACA
CACGGCCTTCCAATCGAACAAGTCTTGGCTAAGCAAGGAATCAAACGTAAGGAGATGGATTTAGCAGAATACCTTGAGATGTGTCGTCAATACGCT
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GCTGATCAAATTCGTGTTTTTGGAGCGATGGCTGAAAAAGGTTACATCTATCGTGGTGCTAAACCTGTTTATTGGTCATGGTCTTCAGAATCGGCC
TTGGCAGAGGCTGAAATTGAATACCATGACATCGATTCAACCTCTTTATACTACGCCAATAAAGTTAAAGATGGTAAAGGTATCCTTGATACTAAT
ACGTATATCGTTGTTTGGACCACAACACCATTTACCGTTACAGCATCACGCGGTTTGACTGTTGGTCCTGATATGGATTATCTTGTGGTGAAACCT
GCTGGTTCAGACCGTCAATATGTTGTGGCAGAAGGTCTTTTGGATAGCCTTGCTGGAAAATTTGGCTGGGAATCTTTTGAAACTTTAGCTAGCCAT
AAAGGAGCTGATTTAGAGTACATTGTGACAGAACACCCATGGGATACTGACGTAGAAGAATTGGTTATCCTTGGTGACCATGTTACCCTTGAGTCA
GGGACAGGGATTGTCCACACAGCACCAGGTTTTGGTGAGGATGACTACAATGTTGGGACAAAATACAAACTGGAAGTTGCTGTGACTGTTGATGAA
CGTGGCCTAATGATGGAAAATGCAGGTCCAGATTTCCACGGACAATTTTATAACAAGGTAACGCCGATTGTCATTGATAAACTTGGTGATCTTTTA

TTGGCACAAGAAGTGATCAATCACTCTTACCCATTTGACTGGCGGACGAAAAAACCAATCATCTGGCGTGCTGTACCGCAATGGTTTGCTTCTGTT
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GGCGACTGGGTTATTTCTCGTCAACGTGCTTGGGGAGTTCCGCTTCCTATCTTCTATGCCGAAGATGGCACAGCTATTATGACTAAAGAAGTGACA
GATCATGTGGCTGATTTGTTCCAAGAAAATGGATCAATCATTTGGTGGCAAAAAGAAGCTAAAGACCTATTACCAGAGGGCTTCACTCATCCAGGG
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CTTTCCTATCCAGCGGATCTATACTTAGAAGGCTCTGACCAGTATCGTGGTTGGTTCAATTCATCCTTAATTACATCTGTGGCTGTTAATGGGCAT
GCTCCATATAAGGCTATTTTATCGCAAGGCTTTGTTCTTGATGGTAAGGGCGAAAAAATGTCTAAATCAAAAGGCAATATCATTTCTCCTAATGAT
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GATTTAGGAACTGTTGATAAGTACATGACAATTGTCTTTAATCAGTTGGTAGCAACGATTACTGACGCTTATGAGCGTTATGACTTTATGGCTATT
TACAAAGCAGTGGTGAACTTTGTTACGGTTGATTTATCAGCCTTCTATCTTGATTTTGCTAAAGACGTTGTCTATATTGAAGCTGCCAATAGCTTA
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ATCTACGCTAGTGAAGAAGTGAAAACCTTATTGACTGCTTTAGACAGCGATATTGCTTTGCTTTTGATCGTGTCTCAATTAACCATTGCTGACTTG
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GAAGAGAGTGGCAAA

SEQ ID 246

MKLKETLNLGKTAFPMRAGLPNKEPQWQAAWEQAELYKKRQELNAGKPAFHLHDGPPYANGNIHVGHALNKISKDIIVRSKSMSGFQAPYVPGWDT
HGLPIEQVLAKQGIKRKEMDLAEYLEMCRQYALSQVDKQRDDFKRLGVSADWENPYVTLDPQFEADQIRVFGAMAEKGYIYRGAKPVYWSWSSESA
LAEAEIEYHDIDSTSLYYANKVKDGKGILDTNTYIVVWTTTPFTVTASRGLTVGPDMDYLVVKPAGSDRQYVVAEGLLDSLAGKFGWESFETLASH
KGADLEYIVTEHPWDTDVEELVILGDHVTLESGTGIVHTAPGFGEDDYNVGTKYKLEVAVTVDERGLMMENAGPDFHGQFYNKVTPIVIDKLGDLL
LAQEVINHSYPFDWRTKKPIIWRAVPQWFASVSDFRQDILDEIEKTTFHPSWGETRLYNMIRDRGDWVISRQRAWGVPLPIFYAEDGTAIMTKEVT
DHVADLFQENGSIIWWQKEAKDLLPEGFTHPGSPNGEFTKETDIMDVWFDSGSSWNGVMNTKENLSYPADLYLEGSDQYRGWFNSSLITSVAVNGH
APYKAILSQGFVLDGKGEKMSKSKGNIISPNDVAKQYGADILRLWVASVDTDNDVRVSMEILGQVSETYRKIRNTLRFLIANTSDFNPATDTVAYA
DLGTVDKYMTIVFNQLVATITDAYERYDFMAIYKAVVNFVTVDLSAFYLDFAKDVVYIEAANSLERRRMQTVFYDILVKITKLLTPILPHTTEEIW
SYLEHESEAFVQLAEMPVAETFSAQEDILEAWSAFMTLRTQAQKALEEARNAKIIGKSLEAHLTIYASEEVKTLLTALDSDIALLLIVSQLTIADL
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SEQ ID 247

ATGAGACTAATTAATACAACCAGTAGTCATCCTGAACTAGTTCGAAATCAACTCCAAAATACAGATGCAAAATTAGTGGAAGTCTATTCAGCTGGC
AACACCGATGTCGTTTTTACAAAAGCACCTAAACATTATGAATTATTAATTTCAAACAAATATCGTGCTATCAAAGATGAAGAATTAGAAGCTATT
CGTGAGTTCTTCTTAAAGCGTAAAATAGATCAATCTATTATTATTCAAGAGCAGATGAAATCACTCCATACTGCCAAGTTAATTGAAATTTCATAT
CCAACAACAGCA

SEQ ID 248

MRLINTTSSHPELVRNQLQNTDAKLVEVYSAGNTDVVFTKAPKHYELLISNKYRAIKDEELEAIREFFLKRKIDQSIIIQEQMKSLHTAKLIEISY
PTTA

SEQ ID 249

ATGAGACTCATCAATACCACTAGCAGTCACCCAGAACTCATCAAAAATCAGCTAAAAAACACCGATGCCTATTTAGTCGAAGTATACTCAGCAGGA
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CGCGAATTTTTTTTAAAACGTAAAATTGATCCTAAAATTGTTATTCCTGGACAATCAAAAACACTTCACACGAATAACCTTATTGAAATTTCATTT
CAAACTTCTGTA

SEQ ID 250

MRLINTTSSHPELIKNQLKNTDAYLVEVYSAGNTDVIFTQAPKHYELLISNKYRAIKEDELDIIREFFLKRKIDPKIVIPGQSKTLHTNNLIEISF
QTSV

SEQ ID 251

ATGACTAATCCTACTTTCGGTGAAAAAATAGATAATGTAAACTATAGGTCACGATTTGGTGTCTATGCTATTATTCCAAATCCAACTCATGATAAA
ATTATTTTAGTACAGGCACCTAATGGTGCTTGGTTTCTTCCAGGTGGGGAAATTGAAGAAAATGAAAATCACCTAGAAGCTTTAACTCGTGAGTTA
ATTGAAGAATTAGGTTATTCCGCAACAATTGGCCATTACTATGGTCAAGCTGATGAATATTTTTACTCTAGACACCGTGATACTTACTACTATAAT
CCCGCCTATATTTATGAAGTTACTGCCTATCATAAGGATCAAGCGCCACTAGAAGATTTCAACCATCTAGCCTGGTTTCCTATCCAAGAAGCTAAA
GAAAAGCTAAAACGAGGAAGCCATAGATGGGGTGTCCAAGCTTGGGAAAAAAATCACCATTCTAGGAAA

SEQ ID 252

MTNPTFGEKIDNVNYRSRFGVYAIIPNPTHDKIILVQAPNGAWFLPGGEIEENENHLEALTRELIEELGYSATIGHYYGQADEYFYSRHRDTYYYN
PAYIYEVTAYHKDQAPLEDFNHLAWFPIQEAKEKLKRGSHRWGVQAWEKNHHSRK

SEQ ID 253

ATGATGATTCCAACATTTGGACATAAAAATGCACATAAAGACTATGTCACACGTTACGGTGTCTATGCTATCATTCCCAATCACGAACAAACAAAA
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ATTGAAGAACTTGGTTTTTCTGCTACTATTGGTTCATATTACGGTCAGGCAGATGAATATTTCTACTCTCGCCATCGTGATACCCACTTCTACCAT
CCTGCCTATCTTTATGAAGTAACTGCATTTCAAGCCGTTTCTAAGCCCTTAGAAGATTTTAATAACTTAGGTTGGTTTTCTCCTATCGAGGCAATT
GCTAAATTAAAACGAGAGAGCCATCAATGGGGAGTCAAGGAATGGCAAAAAAAGCATCATTCTACTAAC

SEQ ID 254

MMIPTFGHKNAHKDYVTRYGVYAIIPNHEQTKIILVQAPNGSWFLPGGEIEAGEGQLQALERELIEELGFSATIGSYYGQADEYFYSRHRDTHFYH
PAYLYEVTAFQAVSKPLEDFNNLGWFSPIEAIAKLKRESHQWGVKEWQKKHHSTN

SEQ ID 255

ATGCTCTGTCAAAACTGCAAACTAAACGAATCAACTATTCATTTGTATACAAATGTTAATGGAAAACAAAAGCAAGTTGATCTTTGTCAAAATTGC
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GGTTCTAAAATGAACCTAACACTAAATTTTGTTGATCCAAAAGAAATTGATCAACGTCTCATTGAAGCAGAAAATTTAAAAGCGCAAGCGACTCGT
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GCTGGACAATTAACTGAAAAGGTTCGTCGAAATCCTTACTCGCTCATCCTTCTAGATGAAATTGAAAAAGCTCATCCTGATGTCATGCATATGTTC
TTGCAGGTCCTTGATGACGGTCGATTAACAGATGGACAAGGAAGAACTGTTAGTTTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTTCT
GGTAAAACTGAAGCAAGCGTTGGCTTTGGTGCCTCACGAGAAGGTAGAACGAATTCCGTACTAGGTCAACTAGGTAACTTCTTCAGCCCTGAATTT
ATGAACCGCTTTGACGGTATTATTGAATTCAAGGCTTTAGATAAAGAGAATCTCCTCAATATCGTTGATATTATGTTATCTGACGTTAATGCACGT
CTCGCCATCAATGGTATTCATCTAGATGTCACTGATAAAGTGAAAGAAAAATTGGTTGATTTAGGTTACGATCCCAAAATGGGAGCACGTCCATTA
CGTCGTACCATTCAAGAACATATTGAAGATGCTATCACAGATTACTATCTTGAGAATCCAAGCGAAAAAGAACTTCGTGCTATTATGACTAGCAAT
GGAAATATCATAATAAAATCTTCTAAAAAAACTGAAGAAAGTACAAAAGGT

SEQ ID 256

MLCQNCKLNESTIHLYTNVNGKQKQVDLCQNCYQIIKTDPNNPLFSGLNHVSHAPGGINPFFDDFFGDLNNFRAFNGQDLPNTPPTQSGGNRGGGN
GNGRNNNRNQTATPSQAKGILEEFGINVTEIARHGDIDPVIGRDSEIIRVIEILNRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGNVPHKLQGKQ
VIRLDVVSLVQGTGIRGQFEERMQKLMEEIRQRQDVILFIDEIHEIVGAGTAGEGSMDAGNILKPALARGELQLVGATTLNEYRIIEKDAALERRM
QPVKVDEPSVEETITILKGIQKKYEDYHHVKYNNDAIEAAAVLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFVDPKEIDQRLIEAENLKAQATR
EEDYERAAYFRDQIAKYKEMQQQKVDDQDTPIITEKTIEHIIEEKTNIPVGDLKEKEQSQLINLADDLKQHVIGQDDAVVKIAKAIRRNRVGLGSP
*NRPIGSFLFVGPTGVGKTELSKQLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRRNPYSLILLDEIEKAHPDVMHMF*
LQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGSGKTEASVGFGASREGRTNSVLGQLGNFFSPEFMNRFDGIIEFKALDKENLLNIVDIMLSDVNAR
LAINGIHLDVTDKVKEKLVDLGYDPKMGARPLRRTIQEHIEDAITDYYLENPSEKELRAIMTSNGNIIIKSSKKTEESTKG

SEQ ID 257

ATGCTGTGTCAAAATTGTAATTTAAACGAATCTACTATTCATCTTTATACAAGTGTTAATGGAAAACAAAGACAGGTTGATCTCTGTCAAAATTGT
TATCAAATCATGAAATCCGATCCTGCCAATTCTATTTTAAATGGCCTAACCCCAGGATATAGAGCACAAGATAGATCCACAAGTCCTTTCTTTGAT
GACTTTTTTGGTGATTTGAATAATTTTAGAGCTTTTGGTAATCTTCCAAATACCCCACCTACTCAGGCAGGGCAAAATGGAAATGGCGGAGGACGC
TATGGTGGTAACTACAACGGACAACGACCTGCTCAGCCACAAACACCAAATCAGCAAGCAAAGGGCTTGTTAGAAGAGTTTGGGATTAATGTCACA
GATATTGCAAGAAATGGTAATATTGATCCTGTTATTGGTCGTGACGAAGAGATTACACGCGTTATCGAGATCCTCAACCGCCGTACTAAAAATAAT
CCTGTGCTAATTGGTGAGCCTGGAGTTGGTAAAACTGCTGTTGTAGAAGGTTTGGCTCAAAAAATTATTGATGGTACTGTTCCTCAAAAACTCCAA
GGCAAGCAAGTGATTCGTCTTGATGTGGTTAGCCTCGTTCAGGGAACAGGTATCCGTGGTCAGTTTGAAGAGCGCATGCAAAAATTAATGGAAGAA
ATTCGCAATCGCAAGGATGTGATTCTCTTTATTGATGAAATTCATGAGATTGTCGGTGCTGGTTCTGCAGGAGACGGCAATATGGATGCTGGTAAT
ATTTTAAAACCAGCCTTGGCCCGTGGTGAGTTGCAACTCGTTGGTGCTACTACATTAAATGAATACCGTATTATTGAAAAAGACGCTGCCTTAGAA
CGACGTATGCAACCCGTTAAAGTTGATGAACCTTCTGTTGAGGAAACCATCACGATTTTAAAAGGTATCCAACCGAAATACGAAGACTATCATCAT
GTCAAATATAGCCCAGCCGCTATTGAAGCTGCCGCTCATTTATCTAACCGCTATATTCAAGACCGTTTTCTTCCTGATAAGGCTATTGACCTTCTG
GACGAAGCTGGTTCCAAAATGAATCTAACCCTCAACTTTGTTGATCCTAAAGAAATTGACAAACGTCTTATTGAAGCTGAGAATCTCAAGGCGCAA
GCTACTCGAGACGAAGACTATGAACGCGCAGCTTATTTCCGCGATCAAATTACAAAATACAAAGAAATGCAGGCTCAAAAAGTCGATGAGCAAGAT
ATTCCCATCATTACTGAAAAAACCATTGAAGCTATTGTAGAGCAAAAAACTAATATTCCAGTTGGGGACTTAAAAGAAAAGGAACAGTCTCAACTC
GTAAACTTAGCCAATGATCTGAAAGCACACGTGATCGGGCAAGACGATGCTGTTGATAAAATCGCTAAGGCTATTCGTCGTAACCGTGTGGGATTA
GGAACTCCAAATCGCCCTATTGGTTCTTTCTTATTCGTTGGACCGACTGGGGTTGGTAAAACTGAATTGTCTAAACAACTAGCCATTGAACTCTTT
GGTTCGACAAACAATATGATTCGCTTTGACATGTCCGAATACATGGAAAAACACGCTGTCGCCAAATTAGTCGGGGCTCCTCCAGGTTATATCGGC
*TATGAAGAAGCTGGACAGCTAACCGAACAAGTTCGTCGCAATCCATATTCACTTATTCTCTTAGATGAGGTGGAAAAAGCCCATCCTGACGTCATG*
CACATGTTCTTACAAGTTCTTGATGATGGCCGTTTAACAGATGGTCAAGGACGAACAGTCAGCTTCAAGGACACCATTATTATCATGACCTCTAAT
GCCGGAACAGGTAAAAGCGAAGCTTCTGTCGGATTTGGTGCTGCTAGAGAAGGACGGACAAGTTCTGTCCTTGGTGAATTAAGCAACTTCTTCAGC
CCAGAGTTTATGAATCGTTTCGATGGTATTATTGAATTCAAAGCTTTATCTAAAGAGCATTTGCTGCATATCGTTGATTTAATGCTGGAAGATGTT
AATGAGCGCTTAGGCTATAATGGGATTCATCTTGATGTGACACAAAAGGTCAAAGAAAAATTAGTAGATTTAGGCTATGATCCTAAAATGGGCGCT
CGGCCGCTCCGTCGTACTATTCAAGATTATATCGAAGATGCCATTACAGACTATTATTTAGAACACCCAACTGAAAAACAGTTACGTGCACTGATG
ACAAACAGTGAAAATATCACGATTAAAGCTGTTAAAGAGGGAGATTCTTTTCTTAACGAAGAGTCTCTCGAT

SEQ ID 258

*MLCQNCNLNESTIHLYTSVNGKQRQVDLCQNCYQIMKSDPANSILNGLTPGYRAQDRSTSPFFDDFFGDLNNFRAFGNLPNTPPTQAGQNGNGGGR*
YGGNYNGQRPAQPQTPNQQAKGLLEEFGINVTDIARNGNIDPVIGRDEEITRVIEILNRRTKNNPVLIGEPGVGKTAVVEGLAQKIIDGTVPQKLQ
GKQVIRLDVVSLVQGTGIRGQFEERMQKLMEEIRNRKDVILFIDEIHEIVGAGSAGDGNMDAGNILKPALARGELQLVGATTLNEYRIIEKDAALE
RRMQPVKVDEPSVEETITILKGIQPKYEDYHHVKYSPAAIEAAAHLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFVDPKEIDKRLIEAENLKAQ
ATRDEDYERAAYFRDQITKYKEMQAQKVDEQDIPIITEKTIEAIVEQKTNIPVGDLKEKEQSQLVNLANDLKAHVIGQDDAVDKIAKAIRRNRVGL
GTPNRPIGSFLFVGPTGVGKTELSKQLAIELFGSTNNMIRFDMSEYMEKHAVAKLVGAPPGYIGYEEAGQLTEQVRRNPYSLILLDEVEKAHPDVM
HMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGKSEASVGFGAAREGRTSSVLGELSNFFSPEFMNRFDGIIEFKALSKEHLLHIVDLMLEDV
NERLGYNGIHLDVTQKVKEKLVDLGYDPKMGARPLRRTIQDYIEDAITDYYLEHPTEKQLRALMTNSENITIKAVKEGDSFLNEESLD

SEQ ID 259

ATGTCAATGAATTTTTCATTTTTACCACAATATTGGTCCTATTTTAATTATGGTGTGATGGTAACCATTATGATTTCAACATGTGTTGTTTTTTTTT
GGAACTATTATAGGTGTGTTAATTGCTTTAGTAAAGCGTACTAATTTACATTTTCTCACAATATTAGCTAATTTCTATGTATGGGTATTTCGTGGG
ACACCGATGGTAGTTCAAATTATGATTGCTTTCGCATGGATGCATTTTAACAATTTACCAACGATTAGCTTTGGTGTTTTAGATTTAGATTTTACA
CGACTTTTACCTGGTATCATTATCATTTCCTTAAATAGTGGTGCCTATATTTCGGAAATTGTACGTGCAGGGATTGAGGCTGTACCATCTGGACAA
ATAGAAGCAGCTTACTCGTTGGGGATTCGACCTAAAAATACACTTCGCTATGTTATCTTACCCCAAGCTTTTAAAAATATTTTACCTGCTCTAGGG
AATGAATTTATTACAATTATTAAAGATAGTGCTCTCCTTCAAACTATTGGTGTCATGGAATTATGGAACGGAGCACAATCAGTTGTAACGGCTACT
TACTCACCAGTTGCACCGTTATTATTTGCAGCATTTTACTATTTAATGTTGACAACGATTCTCTCAGCTTTGTTAAAACAAATGGAGAAATATCTT
GGGAAAGGGGTAAAAATAGATGGT

SEQ ID 260

MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTILANFYVWVFRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFT
RLLPGIIIISLNSGAYISEIVRAGIEAVPSGQIEAAYSLGIRPKNTLRYVILPQAFKNILPALGNEFITIIKDSALLQTIGVMELWNGAQSVVTAT
YSPVAPLLFAAFYYLMLTTILSALLKQMEKYLGKGVKIDG

SEQ ID 261

ATGGATTTGTCATTTTTGCCCAAATACTGGGCCTACTTTAACTACGGTGTACTTGTCACCATTATGATTTCAGTCAGCGTTGTCTTTTTTGGAACC
CTTATTGGTGTCTTGGTAACCCTGATTAAGCGTAGTCATGTGAAGCCGTTGACCTGGGTCGTTAATCTTTACGTTTGGATCTTTCGGGGAACACCT
ATGGTGGTTCAAATCATGATTGCCTTTGCTTGGATGCATTTTAACAATATGCCTACTATTGGTTTTGGGGTTTTAGACTTGGACTTTTCAAGACTA
CTTCCTGGAATTATTATCATTTCATTGAATAGCGGTGCTTATATTTCAGAAATTGTTAGAGCAGGTATTGAGGCTGTACCAAAAGGGCAATTAGAA
GCAGCTTATTCACTAGGTATTCGTCCTCAAAATGCCATGCGTTATGTGATTTTGCCTCAGGCCTTTAAAAATATTTTGCCAGCCTTAGGAAATGAA
TTTATTACCATTATTAAGGATAGTGCTCTTTTACAAACCATTGGAGTGATGGAACTTTGGAATGGTGCCCAATCGGTGGTAACGGCTACTTATTCT

CCAATTTCCCCTTTACTGGTGGCTGCTTTTTACTACTTAATGGTCACAACAGTGATGGCACAGTTATTGGCAGTCTTAGAACGTCACATGGCGCAA
GGAGGTAATCAT

SEQ ID 262

MDLSFLPKYWAYFNYGVLVTIMISVSVVFFGTLIGVLVTLIKRSHVKPLTWVVNLYVWIFRGTPMVVQIMIAFAWMHFNNMPTIGFGVLDLDFSRL
LPGIIIISLNSGAYISEIVRAGIEAVPKGQLEAAYSLGIRPQNAMRYVILPQAFKNILPALGNEFITIIKDSALLQTIGVMELWNGAQSVVTATYS
PISPLLVAAFYYLMVTTVMAQLLAVLERHMAQGGNH

SEQ ID 263

ATGTCTCATATGAATTATAAAGAGATTTATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAAGATATTAAGTCAGATTTAGAAGCTATTAAAGGC
GATGAATCTGAAATTCAGGATCGTTTTTACAAAACATTAGAATTTGGAACGGCGGGATTGAGAGGTAAACTTGGAGCAGGAACCAATCGTATGAAT
ACTTATATGGTGGGGAAAGCAGCACAAGCATTAGCTAATACGATTATTGATCATGGCCCTGAAGCTATTGCACGTGGAATTGCAGTTAGTTATGAT
GTCCGTTATCAATCTAAGGAATTTGCAGAATTAACTTGTTCCATTATGGCAGCAAATGGTATTAAGTCTTATATTTATAAAGGGATTCGCCCAACA
CCAATGTGCTCATATGCTATTCGTGCTCTAGGATGTGTTTCGGGTGTGATGATTACTGCTAGTCATAATCCTCAAGCTTATAATGGTTATAAGGCA
TATTGGAAAGAAGGATCTCAGATTTTAGATGATATTGCTGATCAAATTGCCAATCATATGGATGCTATAACCGATTATCAGCAAATTAAGCAAATA
CCCTTTGAAGAGGCTCTGGCAAGTGGTTCGGCAAGTTATATCGATGAGAGTATTGAAGAAGCATATAAAAAAGAAGTGCTTGGTTTAACTATTAAT
GATACTAATATTGATAAGTCAGTCCGGGTAGTTTATACTCCTTTAAATGGCGTAGGAAATTTACCTGTGCGCGAAGTTTTAAGACGCCGTGGTTTT
GAAAATGTTTATGTGGTACCTGAGCAGGAAATGCCCGATCCTGATTTTACAACGGTTGGCTATCCAAACCCTGAAGTTCCTAAAGCATTTGCCTAT
TCAGAATCTCTAGGAAAGTCAGTTGATGCAGATATCTTACTTGCCACAGATCCAGATTGTGACCGAGTAGCATTGGAAGTCAAAGATAGTAAGGGA
GAATATATTTTCTTAAATGGTAATAAGATAGGGGCACTTCTTTCCTATTATATTTTTTCACAACGATGTGCCTTAGGGAATTTGCCACATCATCCT
GTATTGGTAAAATCCATTGTAACTGGTGATCTATCAAAAGTTATTGCAGATAAATATAATATTGAAACTGTTGAAACTTTAACAGGATTTAAAAAT
ATTTGTGGAAAAGCTAATGAATATGATATCTCAAAGGATAAAACTTATCTCTTTGGCTATGAAGAAAGTATTGGTTTTTGCTATGGCACTTTTGTA
CGTGATAAAGATGCTGTGAGTGCTTCAATGATGGTAGTAGAAATGACTGCCTATTATAAAGAACGAGGGCAAACACTTTTAGACGTTTTGCAAACC
ATTTACGATAAATTTGGCTATTACAACGAGCGCCAATTTTCTCTTGAGTTAGAGGGTGCTGAGGGGCAAGAACGTATTAGTCGTATTATGGAGGAT
TTTAGACAGGACCCAATATTACAAGTAGGTGAGATGACATTGGAGAATTCTATTGATTTCAAGGATGGTTATAAGGATTTTCCAAAGCAAAATTGT
TTAAAATATTATTTTAATGAGGGTTCATGGTATGCTTTAAGGCCGTCAGGGACGGAACCTAAGATAAAATGTTACCTTTATACGATTGGTTGTACA
GAAGCAGATAGTTTATCGAAACTTAATGCAATTGAGTCGGCTTGTCGTGCTAAAATGAATAGTACTAAA

SEQ ID 264

MSHMNYKEIYQEWLENDSLGKDIKSDLEAIKGDESEIQDRFYKTLEFGTAGLRGKLGAGTNRMNTYMVGKAAQALANTIIDHGPEAIARGIAVSYD
VRYQSKEFAELTCSIMAANGIKSYIYKGIRPTPMCSYAIRALGCVSGVMITASHNPQAYNGYKAYWKEGSQILDDIADQIANHMDAITDYQQIKQI
PFEEALASGSASYIDESIEEAYKKEVLGLTINDTNIDKSVRVVYTPLNGVGNLPVREVLRRRGFENVYVVPEQEMPDPDFTTVGYPNPEVPKAFAY
SESLGKSVDADILLATDPDCDRVALEVKDSKGEYIFLNGNKIGALLSYYIFSQRCALGNLPHHPVLVKSIVTGDLSKVIADKYNIETVETLTGFKN
ICGKANEYDISKDKTYLFGYEESIGFCYGTFVRDKDAVSASMMVVEMTAYYKERGQTLLDVLQTIYDKFGYYNERQFSLELEGAEGQERISRIMED
FRQDPILQVGEMTLENSIDFKDGYKDFPKQNCLKYYFNEGSWYALRPSGTEPKIKCYLYTIGCTEADSLSKLNAIESACRAKMNSTK

SEQ ID 265

ATGAGTAATATGACTTACAACGAGGTATATCAAGAATGGTTGCACAATAATGATCTTAGTGATGATATTAAAGCAGATTTAGCAGCCATAAAAGAC
AATGAGGCTGAGATTCAAGATCGTTTTTACAAAACACTTGAATTTGGAACAGCAGGGCTAAGAGGAAAACTTGGAGCAGGCACCAATCGCATGAAT
ACCTATATGGTTGGTAAGGCAGCACAAGCTTTAGCTAATACTATTATTGATCATGGACCTGAAGCGGTTAAAAAGGGCATTGCGGTTAGTTATGAT
GTTCGCTATCAATCTAGAACATTTGCAGAATTAACATGCTCTATTATGGCAGCTAACGGTATTAAGGCGTACCTTTATAAAGGGATTCGGCCAACA
CCAATGTGTTCGTACGCTATTCGTGCTTTGGGATGTATTTCTGGTGTTATGATTACGGCTAGTCACAATCCCCAAGCTTACAATGGTTACAAAGCT
TATTGGCAAGAAGGTTCTCAAATTTTGGATGACATTGCGGATCAAATTGCACAACACATGGCTGCACTAACTCAGTATCAGGAAATCAAACAAATG
CCTTTTGAAAAGGCTCTGGACAGTGGACTTGTTACTTATATTGATGAGAGTATTGAAGAAGCATATAAAAAAGAAGTGCTTGGTTTAACGATTAAT
GATACTGACATTGATAAGTCAGTCCGAGTAGTCTATACCCCTTTAAATGGTGTTGGGAATCTACCAGTGCGTGAGGTTTTAAGACGCCGCGGTTTT
GAAAATGTTTATGTGGTACCTGAGCAGGAAATGCCCGATCCTGATTTTACAACAGTTGGCTATCCTAATCCCGAAGTCCCTAAAACTTTTGCATAT
TCAGAAAAATTAGGTAAGGCAGTTGATGCTGATATTTTGATTGCAACTGATCCAGATTGTGACCGTGTGGCTTTAGAAGTTAAAAATGCAGTCGGT
GACTATGTTTTTCTCAATGGCAATAAAATCGGAGCGCTTTTATCTTACTATATCTTTTCACAACGATTTGACTTAGGCAATTTACCGGCTAATCCT
GTTTTAGTGAAATCCATTGTAACAGGAGACTTGTCACGGGCTATTGCTAGCCATTATGGTATTGAAACCGTTGAAACATTGACTGGTTTTAAGAAT
ATTTGTGGCAAGGCAAACGAATATGATGTGACGAAACAAAAAAACTACCTGTTTGGTTATGAAGAAAGTATTGGTTTTTGCTATGGCACTTTTGTT
CGTGACAAAGACGCTGTTAGCGCCTCTATGATGATTGTAGAAATGGCAGCTTACTACAAGAAAAAAGGGCAGAATTTACTAGATGTTTTGCAGACT
ATTTATGCGACATTTGGGTATTATAATGAACGTCAAATTGCCTTGGAGCTTGAGGGGATAGAAGGACAAAAACGCATTGCGAGGATAATGGAAGAT
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CTCAAATTTTATTTGGATGATGGTTCTTGGTATGCACTTAGACCATCAGGAACAGAGCCTAAAATAAAATTTTATTTATATACTATTGGCCAAACA
CAAGAAAATAGTGCAACAAAATTAGATGCTATTGAAGCAGCGTGTCGCACAAAAATAAATCAGGTTAAT

SEQ ID 266

MSNMTYNEVYQEWLHNNDLSDDIKADLAAIKDNEAEIQDRFYKTLEFGTAGLRGKLGAGTNRMNTYMVGKAAQALANTIIDHGPEAVKKGIAVSYD
VRYQSRTFAELTCSIMAANGIKAYLYKGIRPTPMCSYAIRALGCISGVMITASHNPQAYNGYKAYWQEGSQILDDIADQIAQHMAALTQYQEIKQM
PFEKALDSGLVTYIDESIEEAYKKEVLGLTINDTDIDKSVRVVYTPLNGVGNLPVREVLRRRGFENVYVVPEQEMPDPDFTTVGYPNPEVPKTFAY
SEKLGKAVDADILIATDPDCDRVALEVKNAVGDYVFLNGNKIGALLSYYIFSQRFDLGNLPANPVLVKSIVTGDLSRAIASHYGIETVETLTGFKN
ICGKANEYDVTKQKNYLFGYEESIGFCYGTFVRDKDAVSASMMIVEMAAYYKKKGQNLLDVLQTIYATFGYYNERQIALELEGIEGQKRIARIMED
FRQTPIASVAEMALDKTIDFIDGYQDFPKQNCLKFYLDDGSWYALRPSGTEPKIKFYLYTIGQTQENSATKLDAIEAACRTKINQVN

SEQ ID 267

ATGACTGAATTAATAGATGGTAAAGCCTTATCACAAAAAATGCAGGCTGAGTTAGGGCGAAAAGTTGAAAGGTTAAAGGAACAGCATGGTATCATA
CCTGGTTTAGCTGTAATCCTTGTTGGGGATAATCCAGCTAGCCAAGTGTACGTTCGAAATAAAGAACGCTCTGCATTAGAAGCTGGTTTTAAAAGT
GAGACTCTACGATTATCTGAATCCATTTCTCAAGAAGAACTGATTGATATTATCCATCAATACAATGAAGATAAAAGTATCCATGGTATTTTAGTT
CAACTTCCGTTACCACAACATATTAACGATAAAAAAATTATTTTAGCAATAGATCCTAAGAAAGATGTTGATGGTTTCCACCCAATGAATACGGGT
CATCTTTGGTCAGGACGACCGATGATGGTACCTTGTACGCCAGCTGGTATTATGGAGATGTTTAGAGAGTACCATGTGGATTTAGAGGGAAAACAT
GCTGTTATCATCGGAAGGTCCAATATTGTTGGTAAGCCAATGGCACAACTTCTCCTTGATAAAAACGCAACAGTTACTTTGACACATTCAAGAACT
CGAAACCTTTCTGAGGTAACAAAGGAGGCTGATATCCTTATTGTTGCGATTGGTCAGGGGCACTTTGTTACAAAAGACTTCGTTAAAGAAGGTGCT
GTGGTGATTGATGTTGGTATGAATCGCGATGAAAATGGTAAATTGATTGGAGACGTTGTATTTGAACAAGTGGCAGAAGTTGCTAGTATGATAACA
CCTGTTCCTGGGGGCGTAGGACCTATGACGATTACAATGCTTTTGGAACAAACTTATCAAGCAGCTCTTAGAAGTGTGAGTCTA

SEQ ID 268

MTELIDGKALSQKMQAELGRKVERLKEQHGIIPGLAVILVGDNPASQVYVRNKERSALEAGFKSETLRLSESISQEELIDIIHQYNEDKSIHGILV
QLPLPQHINDKKIILAIDPKKDVDGFHPMNTGHLWSGRPMMVPCTPAGIMEMFREYHVDLEGKHAVIIGRSNIVGKPMAQLLLDKNATVTLTHSRT
RNLSEVTKEADILIVAIGQGHFVTKDFVKEGAVVIDVGMNRDENGKLIGDVVFEQVAEVASMITPVPGGVGPMTITMLLEQTYQAALRSVSL

SEQ ID 269

ATGTCAATGACAGAACTAATTGATGGTAAAGCCTTAGCTCAAAAGATGCAACAAGAGTTAGCAGCTAAAGTCAACAATCTAAAACAAAAAAAAGGA
ATTGTACCAGGCTTAGCCGTTATTCTTGTAGGTGATGATCCTGCTAGTCAGGTGTATGTCCGTAATAAAGAGCGTGCAGCTCTTACTGTAGGTTTT
AAAAGTGAGACCGTTAGATTATCAGAATTCATTTGTCAAGAAGAGCTTATTGCAGTAATCGAACGTTACAATGCAGATAACACTATTCATGGTATT

TTAGTGCAGCTACCCCTGCCAAATCATATTAATGATAAAAAAATTATTCTCGCCATTGATCCCAAAAAAGATGTGGATGGTTTTCACCCGATGAAT
ACAGGTCACCTTTGGTCAGGACGTCCCTTGATGGTTCCTTGTACTCCATCAGGGATTATGGAATTGCTTCGAGAATATAATGTTAACCTTGAAGGT
AAACATGCCGTCATTATTGGCAGATCGAATATCGTTGGAAAACCAATGGCACAGCTCTTACTGGACAAAAATGCAACAGTCACGTTGACACATTCA
AGAACACGTCAATTAGAAGAAGTATGTCGCTGTGCAGATGTGTTGATTGTGGCAATCGGACAAGGTCATTTCATAACAAAACAATATATAAAAGAT
GGTGCGATAGTGATTGATGTAGGAATGAACCGTGATGATAATGGCAAGCTAATTGGAGATGTGGCCTTTGATGAGGTGGCAGAAGTTGCAGCGAAA
ATCACCCCTGTACCAGGAGGTGTCGGTCCTATGACGATTGCTATGTTGCTAGAGCAAACTTATCAATCTGCTCTCCGTAGTACTCATAAA

SEQ ID 270

MSMTELIDGKALAQKMQQELAAKVNNLKQKKGIVPGLAVILVGDDPASQVYVRNKERAALTVGFKSETVRLSEFICQEELIAVIERYNADNTIHGI
LVQLPLPNHINDKKIILAIDPKKDVDGFHPMNTGHLWSGRPLMVPCTPSGIMELLREYNVNLEGKHAVIIGRSNIVGKPMAQLLLDKNATVTLTHS
RTRQLEEVCRCADVLIVAIGQGHFITKQYIKDGAIVIDVGMNRDDNGKLIGDVAFDEVAEVAAKITPVPGGVGPMTIAMLLEQTYQSALRSTHK

SEQ ID 271

ATGATTGTTGGTGAACAAGAAGCGAGGGCGTTAATTAAGCCACGCCCTAAATCAAGCCATAAAGGTGATTATGGTAGTGTTCTTCTGATAGGAGGT
TTTTATCCCTATGGAGGTGCTATTATAATGGCAGCTTTGGCCTGTGTCAAAACTGGTGCAGGATTAGTTACTGTAGCAACCCAAAGTTGCAATATC
CCCTCTTTGCATAGTCAACTACCAGAGGTAATGGCGTTTGATAGTGATGATTACAAATGGTTGGAAAAATCAATTGTTCAAAGTGATGTTATTGTA
ATTGGTCCTGGATTAGGAGTATCAGAATCATCTCGAAAAATTTTGAACCAGACCATGGAGAAGATTCAATCACATCAAAGTGTCATCCTTGACGGA
TCAGCCTTGACTCTGTTATCAGAAGGTGCGTTTCCGCAAACAAAGGCTAAAAATTTAGTGTTGACACCTCATCAAAAAGAATGGGAGCGATTGTCA
GGTATCGCTGTATCGCAACAGACAAAAGAAAATACCCAAACCGCTCTTAAATCTTTTCCCAAAGGGACGATTTTAGTCGCTAAGAGTTCGCATACG
CGTATTTTTCAAGATTTAGACGAAAAAGAAATTATAGTAGGAGGTCCTTACCAGGCGACTGGAGGGATGGGGGATACTTTGTGTGGTATGATTGCA
GGTATGTTAGCGCAATTTAAAGAAGCCTCTCCTCTAGATAAGGTATCAGTGGGAGTTTATCTACATTCGGCAATTGCTCAAGGATTATCTAAAGAA
GCCTATGTTGTTCTACCGACAACGATTAGTGATGAGATTCCAAAAGAAATGGCTAGACTATCTAAA

SEQ ID 272

MIVGEQEARALIKPRPKSSHKGDYGSVLLIGGFYPYGGAIIMAALACVKTGAGLVTVATQSCNIPSLHSQLPEVMAFDSDDYKWLEKSIVQSDVIV
IGPGLGVSESSRKILNQTMEKIQSHQSVILDGSALTLLSEGAFPQTKAKNLVLTPHQKEWERLSGIAVSQQTKENTQTALKSFPKGTILVAKSSHT
RIFQDLDEKEIIVGGPYQATGGMGDTLCGMIAGMLAQFKEASPLDKVSVGVYLHSAIAQGLSKEAYVVLPTTISDEIPKEMARLSK

SEQ ID 273

ATGTCAGACTATTTATCCGTGTCGACACTGACTAAGTATTTAAAATTAAAATTTGACAAAGACCCTTATTTAGAGAGGGTTTATTTAACTGGGCAA
GTGTCTAATTTTCGTCGTCGCCCAAACCATCAATATTTCTCTTTAAAAGATGATAAATCAGTCATTCAGGCGACAATGTGGTCAGGTCACTTCAAA
AAATTGGGTTTTGAATTAGAGGAAGGGATGAAGGTTAATGTAGTTGGCCGTGTTCAACTTTATGAACCAAGCGGCTCCTACTCTATTATTGTTGAA
AAAGCAGAACCGGATGGTATAGGAGCTCTTGCTATCCAATTTGAACAACTAAAGAAGAAACTCTCTCAAGCAGGTTATTTTGATGATCGTCATAAG
CAATTAATTCCTCAATTTGTTAGAAAAATAGGAGTTGTGACTAGTCCAAGTGGAGCCGTTATTCGGGATATTATTACAACAGTATCTCGTCGATTT
CCAGGAGTGGAAATATTACTTTTCCCCACAAAAGTTCAAGGAGAGGGCGCAGCTCAGGAAATAGCACAAACTATTGCTTTAGCTAACGAGAAAAAG
GATTTGGATCTATTAATTGTTGGCCGTGGGGGAGGTTCTATTGAGGACTTATGGGCATTTAATGAAGAATGTGTTGTAGAAGCTATTTTTGAATCT
CGTCTTCCCGTTATTTCTAGTGTCGGACATGAAACTGATACAACTTTAGCAGATTTTGTAGCCGATCGCAGAGCAGCAACTCCAACTGCAGCAGCT
GAGCTTGCTACACCGGTTACTAAAATTGATATCTTGTCTTGGATTACTGAACGTGAAAATAGAATGTATCAGTCTAGCCTTCGTCTTATCAGGACA
AAAGAGGAGAGGTTGCAAAAATCAAAGCAATCAGTTATTTTTAGGCAACCAGAGCGTCTATATGATGGTTTCCTTCAAAAATTAGATAACCTAAAT
CAGCAGTTAACATATTCTATGCGTGATAAACTACAAACAGTAAGACAAAAGCAAGGTTTGCTTCATCAAAAACTGCAAGGCATAGATTTAAAACAG
CGTATTCATATTTACCAAGAGCGTGTTGTGCAAAGTAGACGACTATTATCAAGTACAATGACTAGTCAGTATGACAGCAAGCTAGCACGTTTTGAA
AAGGCTCAAGATGCGCTTATATCATTGGATAGTTCTAGAATTGTAGCGCGTGGTTACGCTATTATCGAAAAAAACCATACTTTAGTATCTACTACT
AATGGAATAAATGAAGGAGATCATTTGCAAGTTAAGATGCAAGATGGTCTTTTAGAAGTTGAGGTGAAGGATGTCAGACAAGAAAACATT

SEQ ID 274

MSDYLSVSTLTKYLKLKFDKDPYLERVYLTGQVSNFRRRPNHQYFSLKDDKSVIQATMWSGHFKKLGFELEEGMKVNVVGRVQLYEPSGSYSIIVE
KAEPDGIGALAIQFEQLKKKLSQAGYFDDRHKQLIPQFVRKIGVVTSPSGAVIRDIITTVSRRFPGVEILLFPTKVQGEGAAQEIAQTIALANEKK
DLDLLIVGRGGGSIEDLWAFNEECVVEAIFESRLPVISSVGHETDTTLADFVADRRAATPTAAAELATPVTKIDILSWITERENRMYQSSLRLIRT
KEERLQKSKQSVIFRQPERLYDGFLQKLDNLNQQLTYSMRDKLQTVRQKQGLLHQKLQGIDLKQRIHIYQERVVQSRRLLSSTMTSQYDSKLARFE
KAQDALISLDSSRIVARGYAIIEKNHTLVSTTNGINEGDHLQVKMQDGLLEVEVKDVRQENI

SEQ ID 275

GTGAAAGGTGGCTTGATGGCAGATTATTTAACCGTCACTCATTTGACGAAATATTTAAAATTAAAATTTGACCGTGACCCTTATTTGGAACGGGTT
TATCTGACTGGTCAAGTGTCCAATTTTCGAAAACGACCAACTCATCAATATTTTTCCTTAAAAGATGAAAGTGCTGTGATTCAAGCCACCATGTGG
GCAGGAGTCTATAAAAAACTAGGATTCGACCTAGAAGAAGGCATGAAAATTAATGTAATTGGGCGAGTCCAACTTTATGAACCTAGTGGCTCTTAC
TCTATCGTGATTGAAAAGGCAGAGCCAGATGGTATAGGTGCCTTGGCTTTGCAGTTTGAACAATTAAAGAAAAAATTAACGGCAGAAGGTTATTTT
GAGCAAAAACACAAGCAGCCCTTGCCACAGTTTGTATCAAAAATTGGGGTCATTACAAGTCCTAGTGGTGCTGTGATTCGAGATATTATCACAACC
GTTTCACGGCGTTTTCCAGGGGTTGAGATTTTATTATTCCCAACTAAAGTACAAGGTGATGGAGCCGCCCAAGAAGTAGTGGCTAATATTCGAAGA
GCCAATCAAAGAGAGGATTTGGACTTGCTCATTGTCGGCCGTGGAGGTGGCTCGATAGAAGACCTTTGGGCCTTCAACGAGGAAATAGTGGTTCAG
GCTATCTTTGAATCGCAACTTCCAGTGATTTCGAGTGTGGGTCATGAAACAGACACGACTTTAGCGGATTTTGTGGCAGATCGCAGAGCAGCCACA
CCAACAGCAGCAGCAGAGTTAGCAACGCCTATTACAAAAACAGATCTTATGTCTTGGATAGTAGAGCGGCAAAATCGTTCCTATCAGGCCTGCTTG
AGGCGGATTAAGCAACGGCAAGAGTGGGTGGATAAACTCTCGCAATCTGTTATTTTTAGGCAACCAGAACGATTATATGATGCCTACCTGCAAAAA
ATTGATCGCCTTAGCATGACCCTGATGAATACGATGAAAGATCGTCTGAGTTCCGCCAAAGAAAACAAGGTTCAGTTGGACCATGCCTTGGCCAAT
AGTCAATTACAGACAAAAATCGAGCGATACCAAGACCGTGTTGCTACCGCTAAGCGTTTACTGATGGCTAATATGGCTAGTCAATATGATAGTCAG
CTGGCTCGCTTTGAAAAAGCACAGGATGCTTTGCTATCACTGGATGCCAGCCGAATTATCGCCCGTGGTTATGCAATGATTGAAAAAAATCAAGCA
CTGGTAGCCTCTGTAAGTCAGATAACAAAGGGTGATCAGTTAACCATTAAGATGCGTGATGGACAATTAGATGTAGAGGTAAAAGATGTCAAAAAC
GAAAACATT

SEQ ID 276

VKGGLMADYLTVTHLTKYLKLKFDRDPYLERVYLTGQVSNFRKRPTHQYFSLKDESAVIQATMWAGVYKKLGFDLEEGMKINVIGRVQLYEPSGSY
SIVIEKAEPDGIGALALQFEQLKKKLTAEGYFEQKHKQPLPQFVSKIGVITSPSGAVIRDIITTVSRRFPGVEILLFPTKVQGDGAAQEVVANIRR
ANQREDLDLLIVGRGGGSIEDLWAFNEEIVVQAIFESQLPVISSVGHETDTTLADFVADRRAATPTAAAELATPITKTDLMSWIVERQNRSYQACL
RRIKQRQEWVDKLSQSVIFRQPERLYDAYLQKIDRLSMTLMNTMKDRLSSAKENKVQLDHALANSQLQTKIERYQDRVATAKRLLMANMASQYDSQ
LARFEKAQDALLSLDASRIIARGYAMIEKNQALVASVSQITKGDQLTIKMRDGQLDVEVKDVKNENI

SEQ ID 277

ATGTCAGACAAGAAAACATTTGAAGAAAATTTACAGGAATTAGAGACAATTGTCTCACGTTTAGAAACAGGTGATGTTGCCTTAGAAGATGCCATT
GCTGAATTTCAAAAAGGAATGCTTATTTCAAAAGAGTTACAAAGAACTTTAAAAGAAGCTGAAGAGACGCTTGTAAAAGTGATGCAAGCTGACGGA
ACGGAAGTAGAAATGGATACT

SEQ ID 278

MSDKKTFEENLQELETIVSRLETGDVALEDAIAEFQKGMLISKELQRTLKEAEETLVKVMQADGTEVEMDT

SEQ ID 279

ATGTCAAAAACGAAAACATTTGAAGAAAATTTACAAGATTTAGAGACTATTGTGAACAAACTTGAAAATGGGGATGTCCCTTTGGAAGAAGCTATT
TCAGAATTTCAAAAAGGAATGCTTCTCTCAAAAGAACTTCAAAAGACCTTACAAGCGGCAGAAAAAACACTCGTCAAAGTGATGCAAGCTGATGGC
ACAGAAGTAGATATGGATGAT

SEQ ID 280

MSKTKTFEENLQDLETIVNKLENGDVPLEEAISEFQKGMLLSKELQKTLQAAEKTLVKVMQADGTEVDMDD

SEQ ID 281

TTGATGGTTACTATTGAAAAAATTGATGAAGCTATTCATCGTTATTACAAACAGACACATAGTGTCGTTTCTCCTGATTTGATTAAGGCTATCCTC
TACTCAGTTGATGGAGGTGGGAAACGTATTCGTCCACGCATCCTTTTAGAAATTTTAGAGGGATTTGGAGTTGAACTAATAGATGGTCATTATGAT
GTGGCTGCTGCTTTGGAGATGATTCACACCGGCTCATTAATCCATGATGATTTACCGGCGATGGATAATGATGATTTTCGTCGTGGCCGCTTAACA
AACCATAAAAAGTTTGATGAAGCTACAGCGGTTTTAGCTGGAGATTCCCTTTTTTTAGACCCATTTGATTTAGTTGTAAAAGCTGGTTTTAAAGCT
GATGTTACTGTTAGGTTAATAGAGTTATTGTCTATGTCTGCGGGTAGTTTTGGCATGGTTGGTGGACAAATGTTAGATATGAAGGGAGAAAACAAA
GTTTTATCTATTGACGATTTAAGCTTGATTCATATTAATAAAACGGGACGCCTGTTAGCTTATCCCTTTGTTGCAGCAGGTATTTTAGCTGAGAAG
TCGGAAGAAGTAAAAGGAAAACTGCATCAAGCTGGCCTTTTAATCGGTCATGCTTTTCAAGTACGTGATGATATTTTAGATGTGACTGCTAGTTTT
GAAGAATTGGGGAAGACACCAAATAAAGACATTGTAGCAGAAAAGACAACTTATCCAAATTTATTGGGTTTGGATAAGTCACAGGAAATACTTGAT
GATACTTTGAAAAAAGCTCAGGCAATTTTTCAAAATCTAGAGAAAAAAGCTAACTTTAATGCTAGAAAAATAATAGATATAATAGAGGGATTACGG
TTGAATGGC

SEQ ID 282

MMVTIEKIDEAIHRYYKQTHSVVSPDLIKAILYSVDGGGKRIRPRILLEILEGFGVELIDGHYDVAAALEMIHTGSLIHDDLPAMDNDDFRRGRLT
NHKKFDEATAVLAGDSLFLDPFDLVVKAGFKADVTVRLIELLSMSAGSFGMVGGQMLDMKGENKVLSIDDLSLIHINKTGRLLAYPFVAAGILAEK
SEEVKGKLHQAGLLIGHAFQVRDDILDVTASFEELGKTPNKDIVAEKTTYPNLLGLDKSQEILDDTLKKAQAIFQNLEKKANFNARKIIDIIEGLR
LNG

SEQ ID 283

ATGGACAAATTAGCTAGAATTGACGAAGCCATTCGTCGCTACTATAAGACGACTAGTAACGGTGTATCTGAAGAGTTGATTGATGCTATCTTGTAT
TCTGTTGACAGTGGTGGCAAGCGCATTCGCCCACTTATCTTATTAGAGATGATTGAGGGATTTGGGGTATCGTTACAGAATGCTCATTTTGATTTG
GCTGCAGCTCTTGAAATGATTCATACAGGAAGTCTGATTCACGATGATTTGCCAGCCATGGATAATGATGATTACCGACGTGGCAGACTGACCAAT
CACAAACAATTTGGAGAAGCCACGGCCATTTTGGCGGGAGACAGCTTATTTTTAGACCCCTTTGGGTTAATAGCTCAAGCTGAATTAAATAGTGAG
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GATCTTGGAAAAACGCCTAAAAAGGACTTATTCGCAGAAAAAGCTACTTATCCAAGTTTACTGGGGTTAGAAGCCTCTTACCAACTGCTGACAGAG
AGTTTAGATCAGGCTTTGACGATTTTTCAGACACTAGAAAGCGATGTAGGCTTTAAGCCTCAAATAATTACAAAACTGATAGAAGGGTTACGACTT
AATGCC

SEQ ID 284

MDKLARIDEAIRRYYKTTSNGVSEELIDAILYSVDSGGKRIRPLILLEMIEGFGVSLQNAHFDLAAALEMIHTGSLIHDDLPAMDNDDYRRGRLTN
HKQFGEATAILAGDSLFLDPFGLIAQAELNSEVKVALIQELSLASGTFGMVGGQMLDMKGENQALSLPQLSLIHLNKTGKLLAFPFKAAALITEQA
MTVRQQLEQAGMLIGHAFQIRDDILDVTASFEDLGKTPKKDLFAEKATYPSLLGLEASYQLLTESLDQALTIFQTLESDVGFKPQIITKLIEGLRL
NA

SEQ ID 285

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGGCAGGAATGGTGATT
AACGTTATCAATGGAGAACGTTATGATAAACCAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAAATATGTTAGT
AGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTT
ACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTGTT
CGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTCAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAA
ATTGGTAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAA
CATCTTGATTTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGAC
CAAATACAAGATGTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID 286

MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLKYVSRGGLKLEKALQVFEISVADKLTIDIGASTGGF
TDVMLQSGARLVYAVDVGTNQLVWKLRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVALIKPQFEAGREQ
IGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFLMHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID 287

ATGCCTAAAGAAAGAGTAGATGTGTTAGCCTATAAGCAAGGATTATTTGAGACCAGAGAGCAAGCTAAGCGTGGTGTCATGGCAGGCTTAGTGGTC
TCTGTGATTAATGGCCAACGCTATGACAAGCCAGGTGACAAAATTGACGATGGGACTGAGTTAAAACTTAAAGGTGAAAAACTCAAATACGTCAGT
CGTGGTGGATTAAAACTGGAAAAGGGGCTGCACGTTTTTGGTGTATCAGTTGCTAATCAAATTGGGATTGATATTGGCGCTTCAACAGGTGGTTTT
ACCGATGTTATGTTACAAGATGGGGCCAAACTAGTCTATGCCGTCGACGTTGGGACTAACCAGTTGGTATGGAAACTCAGACAAGATCCACGAGTA
AGAAGTATGGAACAGTATAACTTTCGTTATGCTCAGCCAGAAGACTTTAATGAGGGACAGCCTGTATTTGCCAGTATTGATGTGTCCTTTATTTCT
CTCAGCTTGATTTTGCCAGCCCTGCATAACGTTTTGTCAGATCAGGGACAGGTTATTGCTCTCATTAAACCGCAATTTGAAGCTGGGCGCGAGCAG
ATTGGTAAAAAAGGCATCGTCAAGGACAAACAGATTCATGAAAAAGTGATTCAAAAGGTCATGGATTTTGCCTCAGGTTACGGATTTACAGTTAAG
GGACTTGATTTTTCTCCTATTCAGGGTGGTCATGGCAATATCGAATTTTTAGCTCATCTTGCTAAGTCACAGACACCTGAAACGTTAGCCCCGCAT
TTGATTCAGAAAGTTGTTGCCAAGGCACATAAGGAGTTTGAGAAACATGAAAAAGAG

SEQ ID 288

MPKERVDVLAYKQGLFETREQAKRGVMAGLVVSVINGQRYDKPGDKIDDGTELKLKGEKLKYVSRGGLKLEKGLHVFGVSVANQIGIDIGASTGGF
TDVMLQDGAKLVYAVDVGTNQLVWKLRQDPRVRSMEQYNFRYAQPEDFNEGQPVFASIDVSFISLSLILPALHNVLSDQGQVIALIKPQFEAGREQ
IGKKGIVKDKQIHEKVIQKVMDFASGYGFTVKGLDFSPIQGGHGNIEFLAHLAKSQTPETLAPHLIQKVVAKAHKEFEKHEKE

SEQ ID 289

ATGAAGAAGAGTGAACGTTTAAATTTAATTAAGCAAATTGTTCTTAACCATGCTGTTGAAACACAACATGAGTTGTTACGCAGATTGGAAGCTTAT
GGGGTAACTCTAACTCAAGCAACTATTTCACGTGATATGAATGAAATTGGCATTATAAAAGTGCCATCAGCAAAAGGTCGCTATATTTACGGTTTG
TCAAATGAAAACGACCCTATCTTTACAACTGCTGTGGCAAAGCCTATTAAAACAAGTATTTTATCAATATCAGATAAGCTACTAGGTTTAGAGCAA
TTTATCAATATTAATGTCATACCAGGTAACAGTCAATTAATTAAAACCTTCATAATGTCACATTGTCAAGAACATATTTTTAGTTTGACAGCTGAC
GATAATAGTCTCCTTTTGATTGCAAAATCAGAAGCAGATGCTGATCACATTCGTCAATCAATGATTGCAATGTTGGAGAAAAAAGAT

SEQ ID 290

MKKSERLNLIKQIVLNHAVETQHELLRRLEAYGVTLTQATISRDMNEIGIIKVPSAKGRYIYGLSNENDPIFTTAVAKPIKTSILSISDKLLGLEQ
FININVIPGNSQLIKTFIMSHCQEHIFSLTADDNSLLLIAKSEADADHIRQSMIAMLEKKD

SEQ ID 291

TTGTTGCCAAGGCACATAAGGAGTTTGAGAAACATGAAAAAGAGTGAACGACTTGAATTAATCAAAAAAATGGTTTTGACGCATCCAATTGAGACG
CAACATGACCTCTTAAGATTATTGGCAGAGCATGGGTTAGAATTAACCCAGGCTACTATTTCAAGAGACATGAATGAAATTGGTATAGTAAAGATT
CCTTCTGGCAGTGGACGTTACATCTATGGTCTTTCTCAAGATAGTGGAAAAAAGATCGTTCAAGGACCTAGATCGATAAAGAGCACTATTTTAGCT
GTATCTGACAAAACAAAAGGTTTAGAACAACACCTCTATTTAAAAGTCGTACCTGGCAATAGTAAATTAATCAAACGTTATTTATTAGCAGATTTT
TCAAAAGCTATTTTTAGTCTTATTGCTGATGATGATAGTTTATTGTTAATTGCAAAGTCTCCTTCAGAAGCAGATATGATACGCCAAGAAATTTTG
CTTTGGATGCAGGGTATAACC

SEQ ID 292

LLPRHIRSLRNMKKSERLELIKKMVLTHPIETQHDLLRLLAEHGLELTQATISRDMNEIGIVKIPSGSGRYIYGLSQDSGKKIVQGPRSIKSTILA
VSDKTKGLEQHLYLKVVPGNSKLIKRYLLADFSKAIFSLIADDDSLLLIAKSPSEADMIRQEILLWMQGIT

SEQ ID 293

ATGGAAGTTTTATCTTCCTTACGTGAAAAAGCAGATTTAATAGCTAACATCAATCGAGATAACTCTCCTCCTGAAGCCACTTTTACCAATGGCTTA
AAGCCCTCTCCGGGATTCGTTGAAATA

SEQ ID 294

MEVLSSLREKADLIANINRDNSPPEATFTNGLKPSPGFVEI

SEQ ID 295

ATGCTTTTAGAAATTTCTATTAAGAATTTCGCTATTATCGAAGAAATTTCACTTAATTTTGAAACAGGAATGACTGTTTTAACTGGTGAGACTGGT
GCAGGGAAATCTATCATTATTGATGCTATGAATATGATGTTAGGATCCCGTGCTAGCGTTGAAGTGATTCGCCATGGTGCTAACAAAGCAGAAATT
GAAGGATTTTTCTCTGTTGAAAAAAATCAATCATTAGTCCAATTATTGGAAGAAAATGGCATTGAATTAGCAGATGAATTAATTATTCGCCGAGAA
ATCTTTCAAAATGGGCGCAGCGTTAGTCGAATTAATGGGCAAATGGTGAATTTGTCAACACTAAAAGCTGTGGGGCATTATTTGGTAGACATTTAT
GGTCAGCATGACCAAGAGGAACTAATGAAACCTAACATGCACATTCTGATGTTAGATGAATTTGGTAATACAGAATTTAATGTCATAAAAGAACGT
TATCAAAGTCTTTTTGATGCTTATCGTCAGCTTCGTAAACGCGTATTGGATAAGCAAAAAAATGAACAAGAGAATAAATCACGTATTGAAATGCTA
GAATTTCAAATAGCAGAAATTGAGTCTGTAGCCCTTAAATCAGATGAAGACCAAACGCTACTCAAGCAACGTGATAAATTAATGAATCATAAGAAT
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AATGATGTTTTAGACTATTTTGATAACATTACTAAAGAATATAGTCTATTGACAGGTAGTGAAGAGTCCTCAGATGCTTTAGAAAAAGAATTAAAG
ATTTTAGAACACGATTTGATTGAATCAGCAAATCAATTAAGTTTAGAGCGCCATAAGCTAGCTAAACAATTGGAAAATGAAATCAAACAAGAATTA
ACAGAGCTTTATATGGAGAAAGCTGATTTCCAAGTTCAATTTACAAAAGGAAAATTTAATAAAGAAGGGAACGAAATCGTTGAATTTTATATTTCA
ACGAATCCCGGAGAGGGCTTTAAGCCATTGGTAAAAGTGGCTTCAGGAGGAGAGTTATCTCGATTGATGTTAGCTATTAAATCTGCTTTTTCACGT
AAGGAAGATAAAACTTCCATTGTATTTGATGAGGTGGATACAGGAGTTTCTGGTCGCGTGGCCCAGGCTATCGCTCAAAAAATTCACAAGATTGGT
AGTCATGGACAAGTTTTAGCAATTTCTCATTTAGCTCAGGTTATTGCAATAGCGGATTACCAATATTTTATTGAAAAAATTTCCAGTGACTCTTCA
ACAGTTTCAACGGTAAGGCTTTTAAGCTATGAAGAACGTGTAGAAGAAATCGCTAAAATGTTGGCAGGAAACAATGTAACAGACACTGCACGTACT
CAAGCTAAAGAATTACTTGGTAGT

SEQ ID 296

MLLEISIKNFAIIEEISLNFETGMTVLTGETGAGKSIIIDAMNMMLGSRASVEVIRHGANKAEIEGFFSVEKNQSLVQLLEENGIELADELIIRRE
IFQNGRSVSRINGQMVNLSTLKAVGHYLVDIYGQHDQEELMKPNMHILMLDEFGNTEFNVIKERYQSLFDAYRQLRKRVLDKQKNEQENKSRIEML
EFQIAEIESVALKSDEDQTLLKQRDKLMNHKNIADTLTNAYLMLDNEEFSSLSNVRSAMNDLMALEEFDREYKDLSTNLSEAYYVIEEVTKRLGDV
IDDLDFDAGLLQEIENRLDVINTITRKYGGDVNDVLDYFDNITKEYSLLTGSEESSDALEKELKILEHDLIESANQLSLERHKLAKQLENEIKQEL
TELYMEKADFQVQFTKGKFNKEGNEIVEFYISTNPGEGFKPLVKVASGGELSRLMLAIKSAFSRKEDKTSIVFDEVDTGVSGRVAQAIAQKIHKIG
SHGQVLAISHLAQVIAIADYQYFIEKISSDSSTVSTVRLLSYEERVEEIAKMLAGNNVTDTARTQAKELLGS

SEQ ID 297

GTGATGTTATTAGAAATTTCTATTAAAAATTTTGCTATTATTGATGAAATTTCCCTAAATTTTGAAAATGGTATGACGGTTTTGACGGGTGAAACT
GGAGCAGGAAAGTCTATTATCATTGATGCTATGAATATGATGCTTGGTGCGCGTGCTAGTACAGAAGTGATTCGTCGTGGAGCTAATAAAGCAGAA
ATTGAGGGGTTCTTTTCGGTAGATGCTACCCCAGAACTGGTTGCGTGTCTGGAATCATCAGGTATTGCTATGGAAGAAGAACTGATTATTCGCCGA
GATATCTTTGCCAATGGCAGAAGCGTGAGCCGCATTAATGGTCAGATGGTTAACCTAGCCACCTTAAAACAGGTCGGACAGTTTTTGGTAGATATT
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AATTATCAGCTTATTTTTGATCGTTATAAAAGCTTGCGTCGCCAGGTTATTGACAAACAAAAAAATGAAAAGGAACACAAAGATCGTATTGATATG
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CAAATTGCTGATACCCTGACCAATGCCTACGTCATGCTAGATAATGACGATTTTTCAAGTCTATCCAATATTCGCTCTAGCATGAATGACTTACTA
TCAATTGAGCAGTTTGATTCAGAGTACAAAGGGATGTCGACTTCGATTTCTGAAGCCTATTATATTCTTGAAGAAGTGAGCAAGCAATTATCAGAT
ACCATTGACCAACTGGATTTTGATGGTGGGCGATTACAGGAAATTGAATTTCGCTTGGATATACTCAATAGCTTAACTCGTAAATACGGTGGTAAT
GTGAATGATGTGCTTGACTACTACGATAATATCGTCAAAGAATACCAGCTATTAACAGGAGATGACTTGTCTTCAGGGGATCTAGAGGCAGAATTG
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TCTACTAATCCAGGCGAAGGATTCAAGCCCCTTGTCAAGGTGGCTTCTGGAGGAGAGTTATCACGCCTTATGTTAGCCATCAAGGCTGCTATTTCT
AGAAAAGAAGATAAGACGAGTATTGTTTTTGATGAAGTAGATACAGGTGTTTCTGGTCGCGTTGCGCAAGCCATTGCCCAAAAAATTTATAAAATT
GGGCGACATGGGCAAGTTCTCGCTATTTCACACTTACCTCAAGTTATTGCTATTGCTGATTATCAGTATTTTATTTCTAAAGAAAGTAAAGAAGAG
TCCACCGTTTCTAAGGTAAGGTTATTAACTCCTGAAGAACGTGTGGAAGAAATTGCTAGCATGATTGCAGGAACAGATATGACACAAGCTGCTCTT
ACGCAGGCTCGTGAACTACTTGCCAAACAT

SEQ ID 298

VMLLEISIKNFAIIDEISLNFENGMTVLTGETGAGKSIIIDAMNMMLGARASTEVIRRGANKAEIEGFFSVDATPELVACLESSGIAMEEELIIRR
DIFANGRSVSRINGQMVNLATLKQVGQFLVDIHGQHDQEELMRPQLHQQILDAFGDKAFEQLKENYQLIFDRYKSLRRQVIDKQKNEKEHKDRIDM
LAFQIAEIEAAALSRGEDDRLNQERDRLMNHKQIADTLTNAYVMLDNDDFSSLSNIRSSMNDLLSIEQFDSEYKGMSTSISEAYYILEEVSKQLSD
TIDQLDFDGGRLQEIEFRLDILNSLTRKYGGNVNDVLDYYDNIVKEYQLLTGDDLSSGDLEAELKSLEKQLVAAASELSVSRHQLAEQLEAEIKAE
LKELYMEKADFKVHFTTSKFNRDGNESLEFYISTNPGEGFKPLVKVASGGELSRLMLAIKAAISRKEDKTSIVFDEVDTGVSGRVAQAIAQKIYKI
GRHGQVLAISHLPQVIAIADYQYFISKESKEESTVSKVRLLTPEERVEEIASMIAGTDMTQAALTQARELLAKH

SEQ ID 299

ATGAGTAAAATCAAAATTGTAACGGATTCTTCCATTACCATTGAACCAGAACTTATTAAAGAGCTTGACATTACAGTTGTTCCCTTGTCAGTTATG
ATAGATGGTACCTTGTATTCAGACAATGACTTAAAAGCACAAGGGGAATTCTTGAACCTAATGCGTGGAAGTAAGGAATTGCCAAAAACAAGTCAA
CCACCTGTAGGTGTTTTTGCAGAAATTTATGAAAAATTAATGAATGAAGGTGTGGAACATATCATTGCAATTCATTTAACGCATACACTATCAGGA
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GTAGAAGCTGCGAAATTAGCTAAAGAGGGAGCTGATTTAGATACCATCTTGGCTCGTGTGGAAGAAGTACGCCAGAAGTCAGAATTATTTATTGGC
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ACAAACCATGAATTAGTACCGATTGTTAAAGGTCGCGGTCTAAAGACCTTCAGCAAATGGTTAGATAATTTTGTTGAAAGTGCCCAAACACGAAAA
ATTGCTGAAATTGGCATCTCCTACTGTGGTAAAGCTGATATGGCTAATAACTTTAGAGAAAAACTAGCTGTTCTAGGTGCTCCTATATCCGTTTTA
GAAACTGGCTCAATCATCCAAACTCATACTGGTGAGGATGCATTTGCTGTTATGGTTCGTTATGAA

SEQ ID 300
MSKIKIVTDSSITIEPELIKELDITVVPLSVMIDGTLYSDNDLKAQGEFLNLMRGSKELPKTSQPPVGVFAEIYEKLMNEGVEHIIAIHLTHTLSG
TIEASRQGANIAGADVTVIDSTFTDQCQKFQVVEAAKLAKEGADLDTILARVEEVRQKSELFIGVSTLENLVKGGRIGRVTGLLSSLLNIKVIMEL
TNHELVPIVKGRGLKTFSKWLDNFVESAQTRKIAEIGISYCGKADMANNFREKLAVLGAPISVLETGSIIQTHTGEDAFAVMVRYE
SEQ ID 301
ATGGAAAAATACATGGGAACTATAAAAATTGTTACAGATTCATCAATAACTATTGAACCAGAATTAATTAAAGCTTTAGATATTACTGTAGTACCT
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GTTATGGCACTTAAAAATGATGAGTTAAAAACGCTTGTCAAAGGTCGAGGTAATAAAACATTTACGAAATGGTTAGATAGTTACCTCGCTAAAAAT
AGTCATCGCCCGATTGCAGAGATAGCTATTTCTTATGCTGGTGAAGCTAGCCTGGCATTAACCTTAAAAGAAAGAATCGCAGCTTATTACAACCAC
TCTATTTCGGTTTTAGAAACAGGCTCTATCATCCAAACACATACAGGAGAAGGAGCTTTTGCGGTTATGGTTCGTTATGAA
SEQ ID 302
MEKYMGTIKIVTDSSITIEPELIKALDITVVPLSVMIDSKLYSDNDLKEEGHFLSLMKASKSLPKTSQPPVGLFAETYENLVKKGVTDIVAIHLSP
ALSGTIEASRQGAEIAEAPVTVLDSGFTDQAMKFQVVEAAKMAKAGASLNEILAAVQAIKSKTELYIGVSTLENLVKGGRIGRVTGVLSSLLNVKV
VMALKNDELKTLVKGRGNKTFTKWLDSYLAKNSHRPIAEIAISYAGEASLALTLKERIAAYYNHSISVLETGSIIQTHTGEGAFAVMVRYE
SEQ ID 303
GTGAGGATGCATTTGCTGTTATGGTTCGTTATGAATAAGAAAAAAATACTTACCGGACTTTCTTTTTTTCTGGTAAGTCTTCTTTTATCTTTTGGG
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TACCTAAACTTTCCACAATTAACTAAAATGCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTTAT
TTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCT
CTCTTTACTGGAGACCATTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAATGAAACAAGAAAAAACTGG
CCG
SEQ ID 304
MRMHLLLWFVMNKKKILTGLSFFLVSLLLSFGIFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSESLHNRYSYQV
TSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPF
YLNFPQLTKMQTVIDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFHPNNIGYQIMSNAVMEKINETRKNW
P
SEQ ID 305
TTGCGGTTATGGTTCGTTATGAATAATCGTCATTTATTTAGTGGGATATTTTTCTTTGTTATTAGTTTATGTCTGGCCTTTTTATTGCTAAATATT
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SEQ ID 306
LRLWFVMNNRHLFSGIFFFVISLCLAFLLLNIIIPKSNSRLKKSDFLKKEQVAIQYVAIGDSLTEGVGDLTHQGGFVPLLTNDLSEYFKANVNHQN
YGVSGDTSQQILDRMIKQKQIQLSLKKADIMTLTVGGNDVMAVIRKNLADLQVSSFRKPARQYQKRLRQIIELARKDNKDLPIFILGIYNPFYLNF
PELTDMQKVIDDWNTKTKEVVGEYDRVYFVPINDLLYKGINGQEGIVHSSGDQTTIVNDALFTGDHFHPNNTGYQIMSNAVMEKIKKHEKKIKP
SEQ ID 307
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TTCGATATTTTTAAGAAAAAGCCC
SEQ ID 308
MKQEKTGRNLNFWKWAFLLLLAINLSFTAVIASRLIQVREPNTGKISTGVQDKVKVGTFTTNKSQLNKTIALYLKQYQTKKMNYKIYAASSSILFE
GSYQLLGYEVPLYIYFEPYRLTNGAVQLKVTSFSVGTLPLPEKDVLQYIKSSYKLPNFVDIKPKKSVININLQDLKNKEGIYLKATAIDLVNDNFS
FDIFKKKP
SEQ ID 309
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TATAAGAAA
SEQ ID 310
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YKK
SEQ ID 311
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SEQ ID 312
MANKQDLIAKVAEATELTKKDSAAAVDAVFAAVADYLAEGEKVQLIGXXLIN
SEQ ID 313
ATGGCTAACAAACAAGATTTAATCGCAAAGGTTGCAGAAGCAACTGAATTGACTAAAAAAGATTCAGCAGCAGCAGTTGATGCCGTGTTTTCTACA
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CAAACTGGTGCAGAAATTGAAATTGCAGCTTCAAAAGTTCCAGCCTTCAAAGCTGGTAAAGCTCTTAAAGACGCTGTTAAA
SEQ ID 314
MANKQDLIAKVAEATELTKKDSAAAVDAVFSTIEAFLAEGEKVQLIGFGNFEVRERAARKGRNPQTGAEIEIAASKVPAFKAGKALKDAVK
SEQ ID 315
TTGGCTACTAAAGTAGATGTTTCAAAAGATGGCTTAACTTATACAGCTACATTACGTAAAGGCTTGAAGTGGTCAGATGGCAGTAAACTTACTGCA
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GGTGTTATTCGTAATACTACAGGTTTGTCAATAGACTTTACACATGCTTATAAAAATAAT
SEQ ID 316
MATKVDVSKDGLTYTATLRKGLKWSDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQEKDLNKLGVKAEGDDKVVITLSSPSP
QFIYYLAFTNFMPQKQEVVEKYGKDYATTSKNTVYSGPYTVEGWNGSNGTFTLKKNKNYWDAKNVKTKEVRIQTVKKPDTAVQMYKRGELDAANIS
NTSAIYQANKNNKDVTDVLEATTAYMEYNTTGSVKGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAKYVAPGYEYNK
TEAAKLFKEGLAESGLTKLKLTITADADAPAAKNSVDYIKSTWEAALPGLTVEEKFVTFKQRLEDSRKQNFDIVVSLWGGDYPEGSTFYGLFKSDS
QNNDGKFANKDYDAAYNKAISEDAMKPAESAKDYKEAEKILFEQGAYNPLYFRSGKGLQNPKLKGVIRNTTGLSIDFTHAYKNN
SEQ ID 317
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GCAAAGGCTAAGTCAAATGCAAAATATGCTGAGAAGTTAGCTGATCACGTTGAAAAA
SEQ ID 318
VTFMKKSKWLAAVSVAILSVSALAACGNKNASGGSEATKTYKYVFVNDPKSLDYILTNGGGTTDVITQMVDGLLENDEYGNLVPSLAKDWKVSKDG
LTYTYTLRDGVSWYTADGEEYAPVTAEDFVTGLKHAVDDKSDALYVVEDSIKNLKAYQNGEVDFKEVGVKALDDKTVQYTLNKPESYWNSKTTYSV
LFPVNAKFLKSKGKDFGTTDPSSILVNGAYFLSAFTSKSSMEFHKNENYWDAKNVGIESVKLTYSDGSDPGSFYKNFDKGEFSVARLYPNDPTYKS
AKKNYADNITYGMLTGDIRHLTWNLNRTSFKNTKKDPAQQDAGKKALNNKDFRQAIQFAFDRASFQAQTAGQDAKTKALRNMLVPPTFVTIGESDF
GSEVEKEMAKLGDEWKDVNLADAQDGFYNPEKAKAEFAKAKEALTAEGVTFPVQLDYPVDQANAATVQEAQSFKQSVEASLGKENVIVNVLETETS
THEAQGFYAETPEQQDYDIISSWWGPDYQDPRTYLDIMSPVGGGSVIQKLGIKAGQNKDVVAAAGLDTYQTLLDEAAAITDDNDARYKAYAKAQAY
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SEQ ID 319
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CCTACATTAGCATCTGTTTCACGCTTCTTCCGTAGTGAAATGATTGAAACTTTAAATTCTGATTATGTGCAACTAGCTCGTTCAAAAGGTATGACA
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GCACTAATTGAGCAGATTTTCTCGATTCCAGGAATTGGGCAGCAGTTTGTTACTTCGATTCCAACAAAAGACTATCCTGTTATTATGGGGACAACC
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SEQ ID 320
MLFLAILRKGNDMIKYILKRVAILLVTLWVVITLSFFLMQILPGTPYNNPKLTEEMIALLNKQYGLDKPVWQQYLTYLWNVLHGDFGTSYQSVNQP
VSRMISLRLGVSVHLGVQALVFGVLGGILVGAISARHKNDKVDGILSVIATLGISMPSFIIGILLLDYFGFKWNLLPLSGWGTFSQTILPSLALGL

PTLASVSRFFRSEMIETLNSDYVQLARSKGMTIRQVTRKHAYRNSMIPILTLIGPLAAGLLTGSALIEQIFSIPGIGQQFVTSIPTKDYPVIMGTT
IVYAVMLMVAILITDVVISIVDPRVRLQ

SEQ ID 321

ATGGCAGATAAAAACAGAACATTTAAACTTGTAGGTGCAGGATCTTCTAGCACACAAGAAAAAATTGAAAAGCCTGCTCTTTCGTTTATGCAAGAT
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AGCATTAAGTACGCTGGAAATACAGAATCTACAGACGCTTATAAGTCTCAAAATGTCCCTGAAAAAGTTAAGTATGCTTTAGGTACAGATTCTCTA
GGGAGAAGTGTTGCTAAGCGCATCATCGTAGGTATTCGGATTTCCTTACTTGTAGCTATTGCAGCTACATTCATTGATTTAATTATCGGTGTTACA
TACGGTCTTGTTTCAGGTTTTGCTGGAGGACGCCTTGATACATTAATGCAACGTATCGTAGAGGTAATTTCATCAATTCCAAACTTAGTTATCGTT
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TTAACCCTATCATATCGAGAAAGAGAGTTTGTGCTTGCTGCACGTTCACTTGGGGAAAGTCCAATTAAAATAGCCTTCAAACATATTTTACCTAAC
ATTTCTGGTATTATCATTGTACAAATTATGATGACAATCCCAAGTGCTATTATGTATGAAGCGGTACTTTCAGCAATCAATTTAGGTGTTAAACCA
CCGACAGCTTCATTAGGATCATTGATTTCAGATGCACAAGAAAATTTACAATATTATCCATATCAAGTTATCTTGCCAGCTTTAGCATTGGTAATG
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SEQ ID 322

MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRLKKNKLAVVSLYLLALLLTFSLASNLFVTQKDANGFDSKKVTTYRNLPPKLSSNLPFWNG
SIKYAGNTESTDAYKSQNVPEKVKYALGTDSLGRSVAKRIIVGIRISLLVAIAATFIDLIIGVTYGLVSGFAGGRLDTLMQRIVEVISSIPNLVIV
TMLGLVLGNGITAIIISIAFTGWTSMSRQVRNLTLSYREREFVLAARSLGESPIKIAFKHILPNISGIIIVQIMMTIPSAIMYEAVLSAINLGVKP
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SEQ ID 323

ATGGAATCGATTGATAAATCTAAATTTCGATTTGTTGAGCGCGATAGTGAAGCCTCCGAAGTGATTGATACCCCTGCTTATTCTTACTGGAAATCA
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CAATCTCTGTTTGATGGTGTTTGGTATGGGGCACGTAATTCTATTTTAATCTCAGTTATAGCGACACTAATTAATATCACCATTGGGGTAGTGTTA
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SEQ ID 324

MESIDKSKFRFVERDSEASEVIDTPAYSYWKSVFRQFFSKKSTVFMLVILVTVLMMSFIYPMFANYDFNDVSNINDFSKRYIWPNAEYWFGTDKNG
QSLFDGVWYGARNSILISVIATLINITIGVVLGAIWGVSKAFDKVMIEIYNIISNIPSMLIIIVLTYSLGAGFWNLILAFCITGWIGVAYSIRVQI
LRYRDLEYNLASQTLGTPMYKIAVKNLLPQLVSVIMTMLSQMLPVYVSSEAFLSFFGIGLPTTTPSLGRFIANYSSNLTTNAYLFWIPLVTLILVS
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SEQ ID 325

ATGGAAAAAGAAACTATTTTAAGTGTTAATAATCTTCATGTTGACTTCCACACATATGCTGGAGAAGTAAAAGCAATTCGTGATGTCAACTTTGAA
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SEQ ID 326

MEKETILSVNNLHVDFHTYAGEVKAIRDVNFELKKGETLAIVGESGSGKSVTTRTLIGLNAKNSEISGNVQFKGRNLVELSEEEWTKVRGNEISMI
FQDPMTSLDPTMKIGMQIAEPMMIHQKISKKDALKLALELMKDVGIPNAEEHINDYPHQWSGGMRQRAVIAIALAADPEILIADEPTTALDVTIQA
QILNLMKKIQAERDSSIVFITHDLGVVAGMADRVAVMYAGKIVEFGTVDEVFYNPQHPYTWGLLNSMPTTDTESGSLESIPGTPPDLLNPPKGDAF
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SEQ ID 327

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SEQ ID 328

MTENRKKLVEVKNVSLTFNKGKANEVRAIDNVSFDIYEGEVFGLVGESGSGKTTVGRSILKLYDISDGEITFNGEVISHLKGKALHSFRKDAQMIF
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VNLMQKLQREQGLTYLFIAHDLSMVKYISDRIGVMHWGKLLEVGTSDDVYNNPIHPYTKSLLSAIPEPDPESERQRVHQPYNPAIEQDGQERQMHE
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SEQ ID 329

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SEQ ID 330

MSEKLVEVKDLEISFGEGKKKFVAVKNANFFIKKGETFSLVGESGSGKTTIGRAIIGLNDTSSGQILYDGKVINGRKSKSEANELIRKIQMIFQDP
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LKRMQAEKGLTYLFIAHDLSVVRFISDRIAVIHKGVIVEVAETEELFNNPIHPYTQSLLSAVPIPDPILERQKELVVYHPDQHDYTLDKPSMVEIK
PNHFVWANQAEIEKYQKEL

SEQ ID 331

ATGACAAAAAACAATAAATCTGTCAGCGAGACAGAAAAGAGCAAAGCTCAAACTTTTAATGAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGG
CGTGCC

SEQ ID 332

MTKNNKSVSETEKSKAQTFNESLILAQDERWRRA

SEQ ID 333

GTGACGGTAACTAACCAGAAAGGGACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAA
GCGAGCGCAGGCGGTTCTTTAAGTCTGAAGTTAAAGGCAGTGGCT

SEQ ID 334

MTVTNQKGTANYVPAAAVIRRSRALSGFIGRKASAGGSLSLKLKAVA

SEQ ID 335

TTGTACGCTTTGGAAACTGGAGGACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGG
TGGCGAAAGCGGCTCTCTGGTCTG

SEQ ID 336

MYALETGGLECRRGEWNSMCSGEMRRYMEEHRWRKRLSGL

SEQ ID 337

GTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
GATGAGTGC

SEQ ID 338

MAKAALWSVTDAEARKRGEQTGLDTLVVHAVNDEC

SEQ ID 339

GTGCTAGGTGTTAGGCCCTTTCCGGGGCTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGG
AAT

SEQ ID 340

MLGVRPFPGLSAAANALSTPPGEYDRKVETQRN

SEQ ID 341

TTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCC
TTC

SEQ ID 342

MKLKGIDGGPHKRWSMWFNSKQREEPYQVLTSF

SEQ ID 343

TTGTTAGTTGCCATCATTAAGTTGGGCACTCTAGCGAGACTGCCGGTAATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTAT
GACCTGGGCTACACACGTGCTACAATGGTTGGTACAACGAGTCGCAAGCCGGTGACGGCAAGC

SEQ ID 344

MLVAIIKLGTLARLPVINRRKVGMTSNHHAPYDLGYTRATMVGTTSRKPVTAS

SEQ ID 345

TTGTTTAGTTTTGAGAGGTCTTGTGGGGCCTTAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCAGCGGTTCGATCCCGCTAGGCTCC
ATTGAATCGAAAGGTTCAAATTGTTCATTGAAAATTGAATATCTATATCAAATTCCACGATCTAGAAATAGATTG

SEQ ID 346

MFSFERSCGALAQLGERLLCTQEVSGSIPLGSIESKGSNCSLKIEYLYQIPRSRNRL

SEQ ID 347

ATGAAAATTTTTGAGAAAGCTCCTGCCAAACTTAATTTAGGATTAGATATTAAAGGACGATGTGACGATGGTTATCATGAATTAGCTATGATTATG
GTTAGTATTGATCTTAATGACTACGTTACCATTTCTGAGCTAAAGGAAGATTGTATTGTTATCGATTCTGATAGTAGCAAAATGCCTTTAAATAAT
GATAATGATGTGTTTAAAGCTGCAGATATAATCAAAAATCAATATGGTATTAATAAAGGTGTTCATATTAGATTAGAAAAATCCATTCCTGTCTGT
GCAGGACTGGGGGGGTGGTTCTACTGATGCTGCTGCTACAATAAGAGCTCTTAATCGATTATGGAATCTTCAAATGGACTATGACGAAATGGTTGCT
ATTGGTTTTAAAATTGGTAGTGATGTTCCTTATTGTCTTGGTGGGGGATGTTCGTTAGTATTAGGTAAAGGTGAAATTGTTAAACCCTTACCGACA
TTGAGACCATGTTGGATAGTTCTGGTTAAGCCGGATTTTGGTATTTCAACTAAATCCATTTTTAGAGATATTGATTGTAAGTCTATAAGTAGAGTT
GATATTGATTTATTAAAGTCTGCTATTTTGTCATCAGATTATCAGTTAATGGTCAAATCTATGGGAAATTCACTCGAGGATATTACAATTACTAAA
AATCCAGTTATAAGTACAATAAAAGAACGTATGTTAAATTCTGGAGCCGATGTTGCATTAATGACAGGAAGTGGACCAACTGTTTTTTCAATGTGT
TCTACAGAGAAAAAAGCTGATCGTGTTTTTAATAGTATGAAAGGTTTTTGCAAAGAAGTTTATAAAGTTAGGTTGTTGAGA

SEQ ID 348

MKIFEKAPAKLNLGLDIKGRCDDGYHELAMIMVSIDLNDYVTISELKEDCIVIDSDSSKMPLNNDNDVFKAADIIKNQYGINKGVHIRLEKSIPVC
AGLGGGSTDAAATIRALNRLWNLQMDYDEMVAIGFKIGSDVPYCLGGGCSLVLGKGEIVKPLPTLRPCWIVLVKPDFGISTKSIFRDIDCKSISRV
DIDLLKSAILSSDYQLMVKSMGNSLEDITITKNPVISTIKERMLNSGADVALMTGSGPTVFSMCSTEKKADRVFNSMKGFCKEVYKVRLLR

SEQ ID 349

ATGATGGATATTGGTATACCGATTGGTAGTGATGTGCCTTATTGCTTGCTTTCAGGTTGTGCCCAAGTCACTGGTAAAGGTGAAGTGGTTTGTCGC
ATTTTGGGGCTGTTATCGTCTTGGGTGGTTTTGGTTAAACCAGATTTTGGTATCTCGACT

SEQ ID 350

MMDIGIPIGSDVPYCLLSGCAQVTGKGEVVCRILGLLSSWVVLVKPDFGIST

SEQ ID 351

ATGACAGTTTTAGAACAAAAATTAGACCATTTAGTGAGTCAAATCTTGCTTAAAGCAGAAAATCAACATGAATTATTGTTTGGTACTTGTCAAAGT
GATGTTAAATTGACTAATACGCAAGAACACATTCTGATGCTTTTATCACAAGAGCAGTTGACAAATTCTGATTTAGCTAAGAAGTTAAATATTAGT
CAGGCAGCTGTAACTAAAGCAGTAAAAAGTTTAATTTCTCAGGATATGTTGAAAGCGAATAAAGATTCTAAAGATGCTCGTATTACTTATTTTGAG
TTATCTGAACTTGCTAAACCCATTGCAGATGAACACACACATCATCATGACAATACGTTAGGGGTTTACGGAAGATTAGTAAATCATTTTTCAAAG
GACGAAAAGGTCGTTTTAGAACGTTTTCTTGATCTTTTCTCTAGAGAATTAGAAGGG

SEQ ID 352
MTVLEQKLDHLVSQILLKAENQHELLFGTCQSDVKLTNTQEHILMLLSQEQLTNSDLAKKLNISQAAVTKAVKSLISQDMLKANKDSKDARITYFE
LSELAKPIADEHTHHHDNTLGVYGRLVNHFSKDEKVVLERFLDLFSRELEG
SEQ ID 353
ATGGGGATTTTAGAAAAAAAACTTGATAACTTAGTAAATACTATTTTATTAAAAGCAGAAAATCAGCATGAGTTATTATTTGGAGCTTGTCAAAGT
GACGTTAAGCTTACTAATACGCAAGAACATATTTTAATGTTACTATCTCAGCAACGTCTCACTAATACAGATTTGGCTAAGGCATTAAATATTAGT
CAGGCGGCAGTAACTAAGGCTATCAAGAGTTTGGTCAAACAAGACATGTTAGCAGGAACTAAGGATACGGTTGATGCTAGGGTGACTTATTTTGAA
TTAACCGAGTTAGCTAAGCCTATTGCGTCAGAACATACCCATCATCATGATGAAACCTTAAATGTTTACAACCGTTTATTACAAAAATTCTCCGCG
AAAGAATTAGAGATTGTAGATAAGTTTGTAACAGTTTTTGCTGAGGAATTAGAAGGG
SEQ ID 354
MGILEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALNISQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFE
LTELAKPIASEHTHHHDETLNVYNRLLQKFSAKELEIVDKFVTVFAEELEG
SEQ ID 355
ATGCGATATATTACAGTTAGTGGTCTTACTTTTCAGTACGATAGCGATCCTGTGCTGGAAGGGGTTAATTACCATTTAGACAGTGGGGAGTTTGTT
ACCTTAACAGGTGAAAATGGGGCTGCTAAATCAACTTTAATAAAGGCTACTTTAGGTATTTTAACGCCCAAAGTGGGTACAGTTAATATCTCTAAA
GAAAACAAAGAAGGAAAAAAATTACGTATTGCCTATTTACCTCAACAGATTGCAAGTTTTAACGCTGGCTTTCCATCGTCAGTTTATGAATTTGTG
AAATCTGGACGATACCCTAGAAATGGTTGGTTTAGAAGACTGACTAAACATGATGAAGAACATATTAGGGTTAGTTTAGAAGCTGTTGGTATGTGG
GATAATCGCCATAAAAAGATAGGAAGTTTATCTGGCGGTCAAAAGCAGAGGGCTGTCATTGCTAGGATGTTTGCTTCTGATCCAGATATTTTTGTA
TTGGATGAGCCAACAACTGGTATGGACGCAGGGACTACTGAGAAATTTTATGAGTTAATGCATCATAATGCTCATAAGCATGGTAAGTCTGTTTTG
ATGATTACTCACGATCCTGATGAAGTAAAGGGGTATGCTGACCGAAATATTCATCTTGTTAGGAACCAATCTTTACCATGGCGTTGTTTCAATGTC
CATACAAACGAAATGGAGGTTGAATCAGATGCTACT
SEQ ID 356
MRYITVSGLTFQYDSDPVLEGVNYHLDSGEFVTLTGENGAAKSTLIKATLGILTPKVGTVNISKENKEGKKLRIAYLPQQIASFNAGFPSSVYEFV
KSGRYPRNGWFRRLTKHDEEHIRVSLEAVGMWDNRHKKIGSLSGGQKQRAVIARMFASDPDIFVLDEPTTGMDAGTTEKFYELMHHNAHKHGKSVL
MITHDPDEVKGYADRNIHLVRNQSLPWRCFNVHTNEMEVESDAT
SEQ ID 357
ATGAGATACATATCAGTGAAAAATCTCTCCTTTCAATATGAAAGTGAGCCAGTTTTAGAAGGGATCACTTATCATTTAGATAGTGGAGAATTTGTC
ACCATGACCGGTGAAAATGGTGCTGCAAAGTCAACCTTAATAAAAGCAACCTTAGGAATTTTACAACCAAAGGCTGGACGAGTTACTATTGCTAAA
AAAAATAAAGACGGTAAACAATTAAGAATTGCTTACTTGCCGCAGCAAGTAGCTAGCTTTAACGCTGGTTTTCCATCCACCGTTTACGAGTTTGTC
AAATCAGGTCGCTACCCACGTAGTGGTTGGTTTAGACATTTGAACAAACACGATGAAGAGCATGTGCAAGCAAGCTTAGAAGCAGTCGGCATGTGG
GAAAACCGTCATAAGAGAATTGGTAGTTTATCAGGTGGTCAAAAACAACGTGTGGTTATTGCCCGTATGTTTGCTTCTGACCCTGATATTTTTGTG
CTAGACGAGCCAACAACGGGAATGGATAGCGGTACTACTGATACCTTTTATGAACTGATGCACCACAGTGCACATCAACATGGGAAATCCGTTCTG
ATGATTACCCATGACCCAGAAGAAGTGAAGGCTTATGCTGATCGGAACATTCATTTAGTCAGAAACCAAAAACTTCCTTGGCGTTGTTTCAACATT
CATGAAGCTGAAACAGATGACGAAAAAGGAGGTCATGGTCATGCT
SEQ ID 358
MRYISVKNLSFQYESEPVLEGITYHLDSGEFVTMTGENGAAKSTLIKATLGILQPKAGRVTIAKKNKDGKQLRIAYLPQQVASFNAGFPSTVYEFV
KSGRYPRSGWFRHLNKHDEEHVQASLEAVGMWENRHKRIGSLSGGQKQRVVIARMFASDPDIFVLDEPTTGMDSGTTDTFYELMHHSAHQHGKSVL
MITHDPEEVKAYADRNIHLVRNQKLPWRCFNIHEAETDDEKGGHGHA
SEQ ID 359
TTGTATACAGTACGCAAATACTCTAATACAACTGCCGCCAAAGTAACAACGAAAATAGTTGACCATGTAGGCGAGATACCTAAAACAACGCCTAAT
GCAACACCGGCTAAGGAAACG
SEQ ID 360
MYTVRKYSNTTAAKVTTKIVDHVGEIPKTTPNATPAKET
SEQ ID 361
ATGTCCATACAAACGAAATGGAGGTTGAATCAGATGCTACTTGATATGCTTTCCTATGATTTTATGCAACGAGCGCTCTTAGCAGTTGTGGCTATT
AGTATTTTTGCTCCAATTTTAGGCATCTTCCTAATTTTACGTCGTCAGAGTTTGATGAGTGATACTTTGAGTCACGTTTCCTTAGCCGGTGTTGCA
TTAGGCGTTGTTTTAGGTATCTCGCCTACATGGTCAACTATTTTCGTTGTTACTTTGGCGGCAGTTGTATTAGAGTATTTGCGTACTGTATACAAA
CATTATATGGAAATATCAACTGCTATCCTGATGTCGATGGGGTTGGCTATATCTTTAATCGTTATGAGTAAAGCTCATAATGTTGGTAATGTCAGT
CTTGAACAGTATTTATTTGGTTCTATTATTACTATTGGGAAGGAACAAGTGATTGCTTTGTTTGTTATTGCATTAATCACTTTTATTTTAACCATC
CTATTTATTAGACCAATGTATATATTAACGTTTGATGAGGATACAGCTTTTGTAGATGGATTGCCTGTGCGTACAATGTCTATTTTGTTCAATGTT
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GCTAGTGCAACAATAACGATGATTTTTATTGGCATTTTCCTATTAGTTAGCTTAGTAGGCTTGCTTCGCAAACGT
SEQ ID 362
MSIQTKWRLNQMLLDMLSYDFMQRALLAVVAISIFAPILGIFLILRRQSLMSDTLSHVSLAGVALGVVLGISPTWSTIFVVTLAAVVLEYLRTVYK
HYMEISTAILMSMGLAISLIVMSKAHNVGNVSLEQYLFGSIITIGKEQVIALFVIALITFILTILFIRPMYILTFDEDTAFVDGLPVRTMSILFNV
VTGIAIALTIPAAGALLVSTIMVLPASIAMRLGRNFKTVIFLGMLIGFVGMVAGIFLSYYWETPASATITMIFIGIFLLVSLVGLLRKR
SEQ ID 363
ATGGTCATGCTTGATATTTTATTCTATGATTTCATGCAACGGGCGGTAATGGCGGTAGTTGCCATTAGTATTTTTGCTCCGATTTTAGGTATTTTC
CTTATTTTACGTCGTCAAAGTTTGATGAGCGATACCCTTAGTCATGTTTCTTTGGCTGGGGTAGCGCTTGGGGTAGTCCTTGGTATTTCACCAACC
ATCACTACTATTATTGTTGTGGTTTTAGCTGCTATTTTGTTAGAATACCTGCGTGTAGTTTACAAACACTACATGGAGATTTCAACGGCGATTTTG
ATGTCACTTGGCTTGGCCCTATCTCTGATTATTATGAGTAAGTCGCATAGTTCATCAAGCATGAGTTTAGAACAATACCTTTTTGGATCGATCATC
ACGATTAGTATGGAACAAGTTGTCGCCTTGTTTGCTATTGCTGCGATTATTTTAATCTTGACCGTTCTCTTCATTAGACCGATGTACATTCTGACC
TTTGATGAAGATACTGCTTTTTGTAGATGGTTTGCCCGTTCGCTTGATGTCTGTTCTATTCAATATCGTCACTGGGGTTGCTATTGCTTTGACCATT
CCAGCAGCAGGAGCACTTTTGGTTTCTACCATTATGGTCTTGCCAGCAAGTATCGCAATGAGATTGGGTAAAAACTTTAAAACAGTTATCTTACTG
GGAATTGTCATCGGTTTTAGCGGTATGTTATCTGGTATTTTCTTATCTTATTTCTTTGAAACGCCAGCTAGTGCCACTATTACCATGATTTTCATT
AGTATTTTCCTCTTAGTTAGTCTAGGTGGAATGCTTAAAAAACGGTTATTT
SEQ ID 364
MVMLDILFYDFMQRAVMAVVAISIFAPILGIFLILRRQSLMSDTLSHVSLAGVALGVVLGISPTITTIIVVVLAAILLEYLRVVYKHYMEISTAIL
MSLGLALSLIIMSKSHSSSSMSLEQYLFGSIITISMEQVVALFAIAAIILILTVLFIRPMYILTFDEDTAFVDGLPVRLMSVLFNIVTGVAIALTI
PAAGALLVSTIMVLPASIAMRLGKNFKTVILLGIVIGFSGMLSGIFLSYFFETPASATITMIFISIFLLVSLGGMLKKRLF
SEQ ID 365
GTGACTCCAATATACGAAGGAAATAATTTAGTACCTAGCCGAGTTGAACTTCAGTATGTTGGAATTGATAAACAAGGAAAACTTCTAGAAATCAAA
TTAGGCGGCGGCAAAGAACAAGTTGATGAATACGGCGTCACAACTGTTACATTAGAAAATACGTCTCCACTCGCAAAAATTGATTACAAAACTGGT
ATGCTAATCAAAGAAGATGGGAAACAGGCAGAAGAAGGTGAAGATCCAAATAGCGATGCTGATGAAAACGAAGCAGCTATTGAAAGTGCATCTGAT

ATAGAAGAAAATACTAACACTAATACTTCTGAATCAGATACAAATAATGTAGCTCCCCAAAATAGAATCGTCTACGTTGCAAATAAGGGTCGTTCA
AATACTTATTGGTATAGTTTAGAAAACATAAAAAATGCAAATACCGCTAATATCGTTCAAATGACTGAACAAGAAGCGTTAAATCAACACAAACAT
CACAGCACTACTGAAGCACAA

SEQ ID 366

MTPIYEGNNLVPSRVELQYVGIDKQGKLLEIKLGGGKEQVDEYGVTTVTLENTSPLAKIDYKTGMLIKEDGKQAEEGEDPNSDADENEAAIESASD
IEENTNTNTSESDTNNVAPQNRIVYVANKGRSNTYWYSLENIKNANTANIVQMTEQEALNQHKHHSTTEAQ

SEQ ID 367

ATGGATATGTCTAAATCAAATCGTCGTACTTGGCAAGGTTTAGTTGTTATTTTAATAGCTATTCTCACCACTTTTACCACAAGTACTGTTACGGCA
GCCAGAAAAATTAGAAATTTCCCTGATACCACGGAAATTTTGTTAGGAACGAAGGCGACTGAGACACCAGGAATCTTACCATTCACTGGTAGCTAC
CAATTAGTTTTGGGCGATCTTGACAATCTGCAAAGGCCAACCTTCGCACACATCCAGCTAAAAGATCAAGATGAGCCTAATATTAAACGAAAAGGA
CTTAAATTCAATCCTCCTGGCTGGCATAATTACAAATTGACTGACGCTAATGGAAAAACAACTTGGTTAATGGACCGTGGCCATTTAGTTGGTTAC
CAATTTAGCGGCTTAAATGACGAGCCTAAAAACCTAGTTACAATGACAAAATATCTTAATACTGGCTTTAGTGACAAAAATCCTTTAGGAATGCTC
TATTATGAAAATAGATTAGATAGCTGGTTAGCTCTACACCCTAACTTCTGGCTAGACTATAAAGTTACTCCTGTTTATCATAAAAATGAGTTAGTT
CCTCGCCAAGTAGTTCTACAGTATGTTGGAATTGATGAAAATGGAGATCTACTTCAAATTAAGTTAGGTAGTGAAAAAGAAAGTGTAGACAACTTT
GGAGTAACATCAGTTACATTAGATAACGTATCTCCTTTAGCTGAATTGGATTACCAAACAGGAATGATGCTAGATTCAACTCAAAACGAAGAAGAT
AGTAATTTAGAAACCGAAGAGTTTGAAGAAGCGGCT

SEQ ID 368

MDMSKSNRRTWQGLVVILIAILTTFTTSTVTAARKIRNFPDTTEILLGTKATETPGILPFTGSYQLVLGDLDNLQRPTFAHIQLKDQDEPNIKRKG
LKFNPPGWHNYKLTDANGKTTWLMDRGHLVGYQFSGLNDEPKNLVTMTKYLNTGFSDKNPLGMLYYENRLDSWLALHPNFWLDYKVTPVYHKNELV
PRQVVLQYVGIDENGDLLQIKLGSEKESVDNFGVTSVTLDNVSPLAELDYQTGMMLDSTQNEEDSNLETEEFEEAA

SEQ ID 369

ATGAATATTTTTGATGAACTCAAAGAACGTGGACTCGTTTTTCAGACAACTGACGAAGATGCTTTACGCAAAGCTCTTGAAGAAGGTTCTGTCTCT
TACTATACTGGCTACGATCCTACGGCTGACAGCCTTCATCTTGGACATTTAGTTGCTATTTTAACCTCTCGTCGCTTACAACTTGCTGGTCACAAG
CCTTATGCACTTGTGGGAGGCGCAACTGGACTTATTGGGGACCCTTCATTTAAAGATGTTGAGCGCAGTTTACAAACAAAGAAAACTGTAGTTAGT
TGGGGTAATAAAATCCGCGGTCAATTATCTAATTTTCTAGAGTTTGAAACAGGTGATAACAAAGCTGTATTGGTAAATAATTATGATTGGTTCAGC
AATATTAGTTTCATTGATTTCTTACGAGATGTTGGTAAATATTTTACTGTCAATTATATGATGAGTAAAGAATCTGTTAAAAAACGTATCGAAACA
GGGATTTCCTATACTGAATTTGCTTATCAAATTATGCAAGGATATGACTTTTACGAATTAAATAAGAACTATAATGTCACTTTGCAAATTGGTGGT
TCTGACCAATGGGGCAACATGACTGCTGGAACCGAACTTATTAGACGAAAATCAAATGGTGTATCTCATGTTATGACTGTTCCATTGATAACAGAT
TCTACAGGAAAAAAATTCGGAAAATCTGAAGGAAATGCTGTTTGGCTTGATGCTGACAAAACCTCTCCTTATGAAATGTACCAATTTTGGCTCAAT
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CACCAACGCTTAGCACAAAAAACACTAGCACGTGAAGTTGTAACTCTTGTTCATGGTGAAAAAGCTTATAAGGAGGCCGTTAATATCACGGAACAG
CTATTTGCTGGCAATATAAAAGGATTGTCTGTTAAAGAGCTCAAACAAGGTTTACGTGGAGTACCAAATTATCACGTTCAGACGGAAGATAACCTC
AATATCATAGACCTTCTAGTCACTTCAGGAGTTGTCAATTCTAAACGTCAAGCTCGAGAAGATGTCTCCAATGGAGCTATTTATATTAATGGAGAT
CGTATTCAAGATTTAGAATATACTATCTCAGAAAATGATAAGCTTGAAAATGAAATTACAGTCATTCGTCGTGGAAAGAAAAAATACTTTGTATTA
AACTTTAAA

SEQ ID 370

MNIFDELKERGLVFQTTDEDALRKALEEGSVSYYTGYDPTADSLHLGHLVAILTSRRLQLAGHKPYALVGGATGLIGDPSFKDVERSLQTKKTVVS
WGNKIRGQLSNFLEFETGDNKAVLVNNYDWFSNISFIDFLRDVGKYFTVNYMMSKESVKKRIETGISYTEFAYQIMQGYDFYELNKNYNVTLQIGG
SDQWGNMTAGTELIRRKSNGVSHVMTVPLITDSTGKKFGKSEGNAVWLDADKTSPYEMYQFWLNVMDADAVRFLKIFTFLSLKEIEDIRIQFEEAP
HQRLAQKTLAREVVTLVHGEKAYKEAVNITEQLFAGNIKGLSVKELKQGLRGVPNYHVQTEDNLNIIDLLVTSGVVNSKRQAREDVSNGAIYINGD
RIQDLEYTISENDKLENEITVIRRGKKKYFVLNFK

SEQ ID 371

ATGAATATTTTTGAAGAACTCAAAGCTCGTGGCTTGGTCTTTCAAACGACTGATGAACAAGCCCTTGTCAAAGCATTAACAGAAGGGCAAGTATCC
TATTATACCGGTTATGATCCAACCGCTGACAGCCTTCATCTGGGCCATCTAGTGGCTATCTTAACATCTCGTCGCTTGCAACTAGCAGGGCACAAA
CCTTACGCTCTTGTGGGGGGTGCCACAGGTTTAATTGGTGATCCTTCCTTTAAAGATGCAGAGCGCAGCCTTCAAACCAAAGAAACAGTTTTGGAG
TGGAGTGACAAGATTAAAGGGCAGTTGTCTACTTTCCTTGATTTTGAAAATGGTGATAATAAAGCAGAGCTTGTCAACAACTACGACTGGTTCTCG
CAAATCAGCTTTATTGACTTCCTCCGTGATGTCGGTAAATACTTCACCGTTAACTACATGATGAGTAAAGACTCTGTTAAAAAACGCATTGAAACA
GGCATTTCTTACACTGAGTTTGCTTACCAAATCATGCAGGGCTACGACTTCTACGAACTCAATGACAAGCATAATGTAACCTTACAAATTGGCGGC
TCTGACCAGTGGGGTAATATGACAGCTGGTACTGAATTGCTCCGCAAAAAGGCTGATAAAACTGGGCACGTCATGACTGTACCACTCATCACTGAC
TCAACCGGGAAAAAATTCGGTAAATCAGAAGGTAATGCTGTCTGGCTTGATGCCGATAAGACGTCTCCTTACGAGATGTACCAATTCTGGTTAAAT
GTCATGGATGATGATGCAGTGCGTTTCTTGAAAATCTTCACCTTCTTATCTCTAGATGAGATTGCAGAAATTGAAACTCAATTTAATGCCGCTCGT
CACGAGCGTCTCGCTCAAAAAACCTTGGCACGCGAAGTGGTTACCTTGGTTCATGGCGAAGAAGCTTATAAACAAGCTCTTAACATTACCGAGCAG
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AATATTGTCGAGATTTTAGTAGCTGCTAAGATTTCCCCATCAAAACGCCAGGCGCGTGAAGACGTGCAAAATGGAGCAATCTACATTAACGGAGAC
CGCGTTCAAGATTTAGATTACCAATTAAGTAATGATGATAAAATTGATGATCAATTAACCGTTATTCGCCGCGGTAAGAAAAAATACGCTGTTCTC
ACTTAC

SEQ ID 372

MNIFEELKARGLVFQTTDEQALVKALTEGQVSYYTGYDPTADSLHLGHLVAILTSRRLQLAGHKPYALVGGATGLIGDPSFKDAERSLQTKETVLE
*WSDKIKGQLSTFLDFENGDNKAELVNNYDWFSQISFIDFLRDVGKYFTVNYMMSKDSVKKRIETGISYTEFAYQIMQGYDFYELNDKHNVTLQIGG*
SDQWGNMTAGTELLRKKADKTGHVMTVPLITDSTGKKFGKSEGNAVWLDADKTSPYEMYQFWLNVMDDDAVRFLKIFTFLSLDEIAEIETQFNAAR
HERLAQKTLAREVVTLVHGEEAYKQALNITEQLFAGNIKNLSANELKQGLSNVPNYHVQSIDNHNIVEILVAAKISPSKRQAREDVQNGAIYINGD
RVQDLDYQLSNDDKIDDQLTVIRRGKKKYAVLTY

SEQ ID 373

ATGTTTAAAGGTAATAAGAAGTTGAATAGTTCTAAATTAGGTGATTACACACCACTTGAATTTGGTTCTATTTTTTTAAGAATTGTAAAGCTTTTA
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CCAAGTAAAAATAGTTTAGTGACACAAGTTAATACACTTACTAGGGTGTCTAGGTTAACTTATTCTGATAAATCACAAATTTCAGAGATTGCCACT
GATTTACAACGTACACCAGTGGCAAAGGATGCTATATCTGATAATATTAAAAAGGCTATCATTGCAACAGAGGACGAAAATTTCAATGACCATAAA
GGTGTAGTTCCCAAAGCCGTACTACGTGCTGCAGCGGGATCTGTTCTGGGGTTTGGAGAGAGTAGCGGTGGTTCAACGCTGACACAACAATTATTA
AAGCAGCAAATTTTGGGAGATGATCCGTCATTTAAACGCAAATCAAAAGAAATTATTTATGCTCTAGCATTAGAGCGTTACATGGATAAGGATTCG
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GTTTCCGCAAAAGATTTAACAATTCCTCAGGCAGCTTTCCTTGCAGGTTTACCGCAAAGTCCTATTGTATATTCTCCTTATACTGCAGATGCCCAG
TTGAAATCAGATAAAGATCTTAGTTTTGGTATAAAGCGCCAAAAAAATGTGTTATACAATATGTATAGAACGAGAGCTTTAACCAAAGATGAGTAC
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GAAGCTCAAAAAGTGATGTACAATTACCTCATTAAAAAGGATAATGTTTCAGAGCATGATTTAAAAAATGATGAGACTAGAGCGACGTACAGACAC
CGCGCTATTGAAGAGATTCAACAGGGAGGGTATACTATTAAAACTACTATCAATAAATCTGTTTATCAAGCCATGCAGGATGCTGCAGCTCAATAC
GGAGGGTTGTTAGATGATGGTACTGGCAAGGTTCAAATGGGAAATGTACTAACGGACAATTCTAGTGGTGCTATTATAGGATTTATTGGTGGTCGT

AACTATAGTGAGAATCAAAATAACCATGCTTTTGATACGGCACGCTCTCCAGGGTCAAGTATTAAACCGATATTACCTTACGGAATTGCTATTGAT
CAAGGGATGTTAGGAAGTGGTAGTGTTCTTTCAAATTATCCAACGACATATTCAAGTGGCGAAAAGATTATGCATGCGGATGAAGAAGGTACTGCT
ATGGTTAACCTTCAAGAGTCATTGGACATTTCTTGGAACATTCCAGCTTTCTGGACTTACAAGATGCTACGAGATCGAGGCGTTGATGTAAAAAAC
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CTTTATCAAATGATTGCAAATGGTGGTGTTTATCATAAGCAGTATATGATAGAAAGTATAGAGGATAGTAATGGGAAAGTGATTTATAATCACGAA
AGTAAACCTGTCCGTGTCTTTTCGAAAGCAACAGCTACTATCTTACAGCAGCTATTACATGGACCAATTAACTCCGGAAAGACTACAACCTTTAAA
AATCGCTTACAAGGTTTAAATAGTGGTTTAGCTGGGGTAGATTGGATTGGAAAAACGGGTACTACTAACTCAACTTCTGATGTTTGGTTGATGCTT
TCTACACCTAAAGTGACTTTAGGTGGATGGGCAGGACATGATAATAATGCCTCTTTAGCGAAATTGACAGGTTACAATAATAATGCTAATTATATG
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CTTAAGTCTACAGGTTTACAGCCAGGTGTAGTAACAGTAAACGGTCGTCGAATCACTGTTGGAGGTGAAAGCACAACAAGTTATTGGGCAAAAAAT
GGACCTGGAACGATGACCTATCGTTTTGCTATTGGGGGAACTGATAGTGATTATCAAAAAGCTTGGTCTACTTTGGGTGGAAAACGA

SEQ ID 374

MFKGNKKLNSSKLGDYTPLEFGSIFLRIVKLLSDFIYVIILLFVMLGVGLAVGYLASQVDSVKVPSKNSLVTQVNTLTRVSRLTYSDKSQISEIAT
DLQRTPVAKDAISDNIKKAIIATEDENFNDHKGVVPKAVLRAAAGSVLGFGESSGGSTLTQQLLKQQILGDDPSFKRKSKEIIYALALERYMDKDS
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SKPVRVFSKATATILQQLLHGPINSGKTTTFKNRLQGLNSGLAGVDWIGKTGTTNSTSDVWLMLSTPKVTLGGWAGHDNNASLAKLTGYNNNANYM
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SEQ ID 375

ATGAGGTATTTTATGGTGAAATGGAACACGAAACAAAAGCGTATAAGTCATCAAAGATTAGGTCTCTTGGATTTGGGGCCGGTGCTATTACGTACG
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AAAAAT

SEQ ID 376

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YKHENKPIRIFSAATATILQELLRGPITSGATTTFKNRLAAINPWLANADWIGKTGTTENYTDVWLVLSTPKVTLGGWAGHDDNTSLAPLTGYNNN
SNYLAYLANAINQADPNVIGVGQRFNLDPGVIKANVLKSTGLQPGTVNVNGHTFSVGGEMTTSLWSQKGPGAMTYRFAIGGTDADYQKAWGNFGFR
KN

SEQ ID 377

TTGGCAGGACATGAAGTTCAGTACGGAAAACACCGTACACGTCGTAGCTTTTCAAGAATTAAGGAAGTTCTTGATTTACCAAACTTAATTGAAATT
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TCTGAAGTCGTTCAAGAAGAT

SEQ ID 378

MAGHEVQYGKHRTRRSFSRIKEVLDLPNLIEIQTDSFQDFLDAGLKEVFEDVLPISNFTDTMDLEFVGYELKEPKYTLEEARIHDASYSAPIFVTF
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SEQ ID 379

TTGGCAGGACATGAAGTTCGATACGGAAAACACCGTACACGTCGTAGCTTTTCAAGAATCAAAGAAGTTCTTGATTTACCAAATTTGATTGAAATT
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ACTGACGAAAAA

SEQ ID 380

LAGHEVRYGKHRTRRSFSRIKEVLDLPNLIEIQTDSFQDFLDSGLKEVFEDVLPISNFTDTMELEFVGYEFKEPKYTLEEARIHDASYSAPIFVTF
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DSGAAVIAQQNGKVVFSDAEKVEIRRQDGSLDVYHITKFRRSNSGTAYNQRTLVKVGDIVEKGDFIADGPSMENGEMALGQNPVVAYMTWEGYNFE
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SEQ ID 381

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GCAGTTGGTACTATTGCAGCTCAATCTATCGGTGAACCAGGGACACAGCTTACAATGCGTACCTTCCATACCGGTGGTGTTGCTTCAAATACTGAT
ATTACACAAGGTCTCCCACGTATCCAAGAAATCTTTGAAGCACGTAACCCTAAAGGTGAGGCAGTTATTACTGAAGTTAAGGGTGAAGTCGTTGCA
ATTGAAGAAGACTCTTCAACACGTACTAAGAAAGTATTCGTTAAAGGTCAGACAGGTGAGGGAGAATACGTTGTTCCATTTACAGCACGTATGAAA
GTTGAAGTTGGTGATGAAGTAGCTCGTGGTGCGGCCTTAACTGAAGGATCTATCCAACCAAAACGTCTCCTTGAAGTTCGTGATACTTTATCTGTT
GAAACGTACCTACTTGCTGAAGTACAAAAAGTTTACCGTAGCCAAGGGGTAGAAATCGGAGATAAACACGTTGAGGTAATGGTTCGTCAAATGCTC
CGTAAAGTTCGTGTCATGGATCCAGGAGATACAGATCTTCTTCCAGGTACACTTATGGATATTTCAGACTTTACAGATGCTAACAAAGATATTGTT
ATTTCTGGTGGAATCCCTGCGACAAGCCGTCCTGTCCTTATGGGTATTACTAAGGCTTCCCTTGAAACTAATTCATTCTTATCAGCTGCATCCTTC
CAAGAAACAACACGTGTCCTTACAGATGCTGCTATCCGTGGTAAGAAAGATCACTTACTTGGTCTTAAAGAAAATGTTATTATCGGTAAAATCATT
CCAGCGGGTACTGGTATGGCTCGTTACCGTAATATTGAACCACTTGCTGTTAATGAAGTTGAGATTATTGAAGGAACTCCTGTTGATGCAGAAGTT
ACGGAAGTATCAACACCTACAACAGAAGAT

SEQ ID 382

MMINRRKVKLVVDVNRFKSMQITLASPSKVRSWSYGEVKKPETINYRTLKPEREGLFDEVIFGPTKDWECACGKYKRIRYKGIICDRCGVEVTRAK
VRRERMGHIELKAPVSHIWYFKGIPSRMGLTLDMSPRALEEVIYFAAYVVIDPMDTPLEPKSLLTEREYREKLQEYGYGSFVAKMGAEAIQDLLKR
VDLDAEIAVLKEELKSATGQKRVKAVRRLDVLDAFKKSGNKPEWMVLNILPVIPPDLRPMVQLDGGRFAASDLNDLYRRVINRNNRLARLLELNAP
GIIVQNEKRMLQEAVDALIDNGRRGRPITGPGSRPLKSLSHMLKGKQGRFRQNLLGKRVDFSGRSVIAVGPTLKMYQCGVPREMAIELFKPFVMRE
IVARDLAGNVKAAKRMVERGDERIWDILEEVIKEHPVLLNRAPTLHRLGIQAFEPVLIDGKALRLHPLVCEAYNADFDGDQMAIHVPLSEEAQAEA
RLLMLAAEHILNPKDGKPVVTPSQDMVLGNYYLTMEDAGREGEGMIFKDHDEAVMAYQNGYVHLHTRVGIAVDSMPNKPWTEEQKHKIMVTTVGKI
LFNDIMPEDLPYLIEPNNANLTEKTPDKYFLEPGQDIQAVIDNLEINIPFKKKNLGNIIAETFKRFRTTETSAFLDRLKDLGYYHSTLAGLTVGIA
DIPVIDNKAEIIDAAHHRVEDINKAFRRGLMTEEDRYVAVTTTWREAKEALEKRLIETQDPKNPIVMMMDSGARGNISNFSQLAGMRGLMAAPNGR
IMELPILSNFREGLSVLEMFFSTHGARKGMTDTALKTADSGYLTRRLVDVAQDVIIREDDCGTDRGLTITAITDGKEVTETLEERLIGRYTKKSIK
HPETGEILVGADTLITEDMAAKVVKAGVEEVTIRSVFTCNTRHGVCRHCYGINLATGDAVEVGEAVGTIAAQSIGEPGTQLTMRTFHTGGVASNTD
ITQGLPRIQEIFEARNPKGEAVITEVKGEVVAIEEDSSTRTKKVFVKGQTGEGEYVVPFTARMKVEVGDEVARGAALTEGSIQPKRLLEVRDTLSV
ETYLLAEVQKVYRSQGVEIGDKHVEVMVRQMLRKVRVMDPGDTDLLPGTLMDISDFTDANKDIVISGGIPATSRPVLMGITKASLETNSFLSAASF
QETTRVLTDAAIRGKKDHLLGLKENVIIGKIIPAGTGMARYRNIEPLAVNEVEIIEGTPVDAEVTEVSTPTTED

SEQ ID 383

GTGGTTGACGTAAATCGTTTTAAAAGTATGCAAATCACATTAGCCTCACCAAGTAAGGTCCGTTCATGGTCTTATGGTGAAGTTAAAAAACCTGAA
ACAATCAACTACCGTACATTAAAACCAGAACGTGAAGGACTCTTTGACGAAGTCATCTTTGGTCCAACAAAAGACTGGGAATGTGCGTGTGGTAAG
TACAAACGTATCCGTTATAAAGGGATCGTTTGTGATCGCTGTGGGGTTGAGGTAACTCGTGCTAAAGTACGTCGTGAACGTATGGGTCACATTGAG
TTAAAAGCTCCTGTATCACATATCTGGTATTTCAAAGGGATTCCATCTCGTATGGGATTGACTCTTGATATGAGTCCTCGTGCCCTTGAAGAAGTG
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GAGTATGGTCATGGGTCATTTGTCGCTAAGATGGGTGCTGAAGCCATTCAAGATCTCTTGAAACGTGTGGACTTGGCAGCTGAAATCGCTGAATTA
AAAGAAGAGTTGAAATCTGCTTCTGGTCAAAAACGGATTAAAGCAGTTCGTCGTTTAGACGTCCTTGATGCCTTTAACAAATCTGGAAATAAACCA
GAATGGATGGTTCTTAACATCCTGCCGGTTATTCCACCAGATCTTCGTCCGATGGTTCAATTGGATGGTGGTCGTTTTGCGGCATCAGACTTGAAT
GACTTGTACCGTCGTGTGATTAACCGTAATAACCGTTTGGCACGTTTGTTAGAACTTAATGCCCCTGGCATCATTGTTCAAAATGAAAAACGAATG
CTTCAAGAAGCCGTTGATGCTTTGATTGATAATGGTCGTCGTGGTCGTCCAATCACTGGACCAGGAAGTCGTCCATTGAAATCATTGAGCCACATG
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ATGTATCAATGTGGTGTCCCACGTGAAATGGCTATCGAGCTTTTTAAACCATTTGTAATGCGCGAAATTGTTGCCAAAGAATATGCTGGTAACGTT
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CCGACTCTTCACAGACTTGGTATTCAGGCTTTTGAACCCGTTCTTATTGACGGTAAGGCACTTCGTCTTCACCCACTTGTGTGTGAGGCCTACAAT
GCCGACTTCGATGGAGACCAAATGGCCATTCACGTGCCACTTTCAGAAGAAGCACAAGCTGAAGCTCGTCTTTTGATGCTTGCTGCAGAGCACATC
TTGAACCCTAAAGATGGTAAACCAGTTGTTACTCCATCTCAGGATATGGTTCTTGGTAACTACTATCTTACGATGGAAGATGCTGGTCGCGAAGGC
GAAGGTATGATTTTCAAGGATAAAGACGAAGCTGTGATGGCATATCGTAATGGTTATGCTCATCTTCATAGTCGTGTGGGTATCGCTGTTGACAGC
ATGCCAAACAAACCTTGGAAAGACAATCAAAGACATAAAATCATGGTGACAACTGTTGGTAAGATTCTCTTTAACGATATCATGCCAGAGGACCTT
CCTTACCTCCAAGAGCCAAACAATGCCAACTTGACAGAAGGAACACCTGATAAATACTTCCTTGAACCTGGTCAAGACATCCAAGAAGTGATTGAT
CGCTTAGACATCAATGTGCCATTTAAGAAGAAAAACCTCGGTAACATCATTGCGGAAACCTTCAAACGTTTCCGTACAACAGAAACATCAGCCTTC
CTTGACCGCTTGAAAGACCTTGGTTACTACCACTCAACCCTTGCTGGTTTGACAGTGGGTATCGCTGACATTCCTGTTATTGATAATAAAGCTGAA
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ACATGGCGTGAAGCTAAAGAAGCCCTTGAAAAACGTCTGATTGAAACACAAGATCCTAAGAACCCAATCGTTATGATGATGGACTCAGGAGCTCGT
GGTAACATCTCAAACTTCTCACAGCTTGCTGGTATGCGTGGTTTGATGGCTGCTCCTAACGGACGCATCATGGAACTTCCTATCTTGTCAAACTTC
CGTGAAGGTTTGAGCGTTTTGGAAATGTTCTTCTCAACCCACGGTGCACGTAAAGGGATGACCGATACGGCCCTTAAAACAGCCGACTCAGGTTAC
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GGTAAAGAAGTTACCGAAACGCTTGAAGAGCGTCTTCAAGGTCGTTACACACGTAAATCAGTCAAACACCCTGAAACTGGTGAAGTCTTGATTGGT
GCTGACCAATTAATCACTGAAGACATGGCTCGTAAGATTGTTGATGCAGGTGTTGAAGAAGTGACCATTCGTTCTGTCTTTACCTGTGCGACTCGT
CATGGTGTCTGCCGTCACTGTTATGGTATCAACTTGGCAACTGGTGATGCTGTTGAAGTGGGTGAAGCAGTTGGTACTATTGCTGCCCAATCTATC
GGTGAGCCTGGTACTCAGCTTACCATGCGTACCTTCCACACGGGTGGTGTAGCCTCAAATACCGATATCACCCAGGGTCTTCCTCGTATTCAAGAG
ATCTTTGAAGCACGTAATCCTAAAGGGGAAGCGGTCATTACTGAAGTGAAAGGGAATGTCGTCGAGATTGAAGAAGATGCGTCAACTCGTACCAAG
AAAGTCTACGTTCAAGGAAAAACTGGCATGGGCGAATATGTCATACCATTTACAGCACGTATGAAAGTTGAAGTTGGCGACGAAGTTAATCGCGGA
GCTGCCCTTACAGAAGGGTCAATTCAACCGAAACGTCTCCTTGAAGTGCGTGATACCTTGTCAGTTGAAACGTACCTTCTTGCAGAAGTACAAAAA
GTTTACCGTAGCCAAGGGGTAGAAATCGGAGACAAACACGTTGAGGTAATGGTTCGCCAAATGCTTCGTAAAGTTCGTGTCATGGATCCAGGTGAT
ACAGACCTCCTTCCAGGTACACTTATGGATATTTCTGATTTCACAGATGCTAACAAAGATATTGTTATCTCTGGTGGTATTCCTGCGACATCTCGT
CCTGTTCTTATGGGTATTACTAAGGCTTCCCTTGAAACCAATTCCTTCTTATCAGCTGCATCCTTCCAAGAAACAACTCGTGTTCTTACAGATGCT
GCTATCCGTGGTAAAAAAGATCATCTTCTTGGTCTTAAAGAAAATGTTATCATTGGTAAAATCATCCCAGCTGGTACTGGTATGGCTCGTTACCGT
AACATTGAACCACAAGCGATGAATGAGATTGAAGTGATTGATCATACAGAAGTCTCAGCAGAAGCCGTTTTTACAGCAGAAGCAGAA

SEQ ID 384

VVDVNRFKSMQITLASPSKVRSWSYGEVKKPETINYRTLKPEREGLFDEVIFGPTKDWECACGKYKRIRYKGIVCDRCGVEVTRAKVRRERMGHIE
LKAPVSHIWYFKGIPSRMGLTLDMSPRALEEVIYFAAYVVIDPKDTPLEPKSLLTEREYREKLQEYGHGSFVAKMGAEAIQDLLKRVDLAAEIAEL
KEELKSASGQKRIKAVRRLDVLDAFNKSGNKPEWMVLNILPVIPPDLRPMVQLDGGRFAASDLNDLYRRVINRNNRLARLLELNAPGIIVQNEKRM
LQEAVDALIDNGRRGRPITGPGSRPLKSLSHMLKGKQGRFRQNLLGKRVDFSGRSVIAVGPTLKMYQCGVPREMAIELFKPFVMREIVAKEYAGNV
KAAKRMVERGDERIWDILEEVIKEHPVLLNRAPTLHRLGIQAFEPVLIDGKALRLHPLVCEAYNADFDGDQMAIHVPLSEEAQAEARLLMLAAEHI
LNPKDGKPVVTPSQDMVLGNYYLTMEDAGREGEGMIFKDKDEAVMAYRNGYAHLHSRVGIAVDSMPNKPWKDNQRHKIMVTTVGKILFNDIMPEDL
PYLQEPNNANLTEGTPDKYFLEPGQDIQEVIDRLDINVPFKKKNLGNIIAETFKRFRTTETSAFLDRLKDLGYYHSTLAGLTVGKILFNDIMPEDL
IIDAAHHRVEEINKAFRRGLMTDDDRYVAVTTTWREAKEALEKRLIETQDPKNPIVMMMDSGARGNISNFSQLAGMRGLMAAPNGRIMELPILSNF
REGLSVLEMFFSTHGARKGMTDTALKTADSGYLTRRLVDVAQDVIIREDDCGTDRGLLIRAITDGKEVTETLEERLQGRYTRKSVKHPETGEVLIG
ADQLITEDMARKIVDAGVEEEVTIRSVFTCATRHGVCRHCYGINLATGDAVEVGEAVGTIAAQSIGEPGTQLTMRTFHTGGVASNTDITQGLPRIQE
IFEARNPKGEAVITEVKGNVVEIEEDASTRTKKVYVQGKTGMGEYVIPFTARMKVEVGDEVNRGAALTEGSIQPKRLLEVRDTLSVETYLLAEVQK
VYRSQGVEIGDKHVEVMVRQMLRKVRVMDPGDTDLLPGTLMDISDFTDANKDIVISGGIPATSRPVLMGITKASLETNSFLSAASFQETTRVLTDA
AIRGKKDHLLGLKENVIIGKIIPAGTGMARYRNIEPQAMNEIEVIDHTEVSAEAVFTAEAE

SEQ ID 385

ATGTATCAAGTTGTAAAAATGTTTGGTGATTGGGAACCATGGTGGTTTATTGAAGGTTGGGAGGAAGATATTACTGAAATTGCTGAGTATGATACC
TTATCAGAAGCTTTGCTCTATTTTCAAGAGGAGTGGGATAGGGGACAGGAAAAGTGGCCTTATTTTCAAAGTAAGTCTAGTTTGTTGGCAACGTTT
TGGAGTATAAAAGAAAAACGTTGGTGTGAAGAATGTGATGAGTACCTCCAACAGTATCATTCCTTAATGTTATTGAAAGAATGGCAAGAAATTCCT
AAGGAAGAATCTATTGAGCGATTTGAAGTATTTAATAAGATAGCTGAGTTGCCATCGGCATGTTCTTTAAATTTG

SEQ ID 386

MYQVVKMFGDWEPWWFIEGWEEDITEIAEYDTLSEALLYFQEEWDRGQEKWPYFQSKSSLLATFWSIKEKRWCEECDEYLQQYHSLMLLKEWQEIP
KEESIERFEVFNKIAELPSACSLNL

SEQ ID 387

ATGTATCAAGTAATTAAAATGTATGGTGATTGGGAGCCTTGGTGGTTCATCGATGGATGGCAAGACGATATTATAGATGAGCAACAATTTAGTGAC
TGGCAAGAAGCGCTTGATTATTTTAATCAAGAATGGCAGCGCATGAAAGCTATTTTTCCTAGTTATCATAGTCAAAAGAATTTGTTAGCTACTTTT
TGGGAAAAAGAAGATAAAAGATGGTGCGAGGACTGTGACGAAGATTTGCAGCAGTTTCATTCTCTTTTACTCCTTAAAAATAAAGATATTGTACCA
AGCAATAATTATATCCCTGAATTTGAACAACGAAATGATTCACCACAGGTAGCTTATCTTTGCAAGTTAAACCTT

SEQ ID 388

MYQVIKMYGDWEPWWFIDGWQDDIIDEQQFSDWQEALDYFNQEWQRMKAIFPSYHSQKNLLATFWEKEDKRWCEDCDEDLQQFHSLLLLKNKDIVP
SNNYIPEFEQRNDSPQVAYLCKLNL

SEQ ID 389

ATGGTTCAATCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTCCCAAAGGTGATTGTTATGAACTC
TATATGCGTATTGATGATGAAAGGCGGTTTATTGATGTTTTTGAGTTTAATAGGATGGCTAGTCTTATTAGTCACTTTAAATTTGTGGCAGGCATG
AACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTCAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGAT
TATCGTGGTCAAGAATCTTTAGTTATTCGTATTTTGTATTCAGGTCATCAGGACTTAAAATATTGGTTTGATAATATAAAGCAAATGAAGGAAGTA
CTGGGTATAAGAGGGCTATATCTTTTTTCCGGCCCTGTGGGGAGTGGTAAAACAACTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAAATAAG
CAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTACAACTCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTA
ATCAAACTGTCTTTACGGCATCGTCCAGATATTTTAATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTGCTGTTATTCGTGCAAGTTTAACG
GGAGTGATGGTTTTTTCTACTATTCATGCTAAAAGTATTCCCGGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAAT
AGTCTAAAATTAATAGCATATCAACGTTTAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTTTAAAAAACACTCATCAGACAAGTGG
AATAGACAAGTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAAGTAGT
CCAACTTTT

SEQ ID 390

MVQSLAKQVIHQAVEVNAQDIYIIPKGDCYELYMRIDDERRFIDVFEFNRMASLISHFKFVAGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGD
YRGQESLVIRILYSGHQDLKYWFDNIKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDAL
IKLSLRHRPDILIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVYDRLIELGVNYQELENSLKLIAYQRLIGGGSLIDFETGNFKKHSSDKW
NRQVDILAEEGHISKKQAQVEKIIPQETTESSPTF

SEQ ID 391

ATGGTACAAGCATTAGCAAAAGCTATTCTAGCAAAAGCTGAACAGGTTCATGCACAAGATATTTATATTTTGCCAAGAGCAGATCAATATGATCTT
TTTTTACGAATAGGAGATGAAAGGAGATTAGTTGATGTTTATCAGAGCGATCGGATGGCTCCTCTTATTAGTCACTTTAAATTCGTTGCAGGAATG
ATAGTTGGTGAAAAGAGACGTTGTCAGGTGGGTTCATGTGATTATAAGCTTAGTAAAGATAAGCAGTTATCTTTGCGCTTATCTAGCGTGGGTGAT
TATCGCGGGCAAGAAAGCTTAGTGATTCGTCTGCTTCATCATCAAAATAAAAGTGTACATTATTGGTTTGATGGATTGACAAAAGTAGCCAATCAG
GTTGGCGGTAGAGGGTTGTATTTATTTGCAGGACCAGTTGGGTCTGGGAAGACAACCTTGATGTACCAGCTGATTTCGAATTATCATCAAGAAGCA
CAGGTTATTAGTATAGAAGATCCTGTAGAAATTAAAAATCACCAAATTTTACAATTACAAGTGAATGATGATATTGGTATGACTTATGACAATTTG
ATCAAACTGTCTTTACGCCATCGACCAGATATTTTAGTTATTGGTGAGATTCGAGATAGTCAAACAGCAAGAGCCGTTATTAGGGCTAGTCTAACA
GGTGCCATGGTTTTTTCAACGGTTCACGCTAAAAGTATCTCGGGTGTTTATGCAAGATTGTTAGAACTTGGTGTAACGAAAGCAGAACTGTCTAAT
TGCTTAGCATTAATTGCTTACCAAAGGTTACTTAATGGAGGAGCATTGATTGACTCTACTCAAAACGAATTTGAATATTATTCCTCATCGAACTGG
AATCAACAAATTGATCAGCTTCTTGAGGCAGGACATCTCAATCCCAAGCAAGCTAAGCTTGAAAAAATTATC

SEQ ID 392

MVQALAKAILAKAEQVHAQDIYILPRADQYDLFLRIGDERRLVDVYQSDRMAPLISHFKFVAGMIVGEKRRCQVGSCDYKLSKDKQLSLRLSSVGD
YRGQESLVIRLLHHQNKSVHYWFDGLTKVANQVGGRGLYLFAGPVGSGKTTLMYQLISNYHQEAQVISIEDPVEIKNHQILQLQVNDDIGMTYDNL
IKLSLRHRPDILVIGEIRDSQTARAVIRASLTGAMVFSTVHAKSISGVYARLLELGVTKAELSNCLALIAYQRLLNGGALIDSTQNEFEYYSSSNW
NQQIDQLLEAGHLNPKQAKLEKII

SEQ ID 393

ATGGTCACCTTCTTAAAGAGGAGTAAGTTATTGTCTGATTGTTATACAGATAGTATGAATAAGGCATTATTAGAGGGAAAAGATTTATCAAAAATG
TTAGGAGAGTTAGGTTTTTCTGACACTGTTATCACACAGGTTGCATTAGCTGATTTGCATGGTAACATTTCAAGGAGCCTACTAAAGATTGAGTCT
TATTTAGCTAATCTTTTGTTAGTTAGAAAAAAAGTAATAGAAGTAGCTACTTACCCATTGATATTATTGTCTTTTCTGGTGCTAATTATGATTGGC
CTTAGGAATTATTTAATGCCCCAATTAGGAGAAAATAATTTTGCAACTAGACTGATTACAAATGTGCCGAATATTTTCTTATTACTTTTAGCAGTT
GTACTTATTTTTAGTTTAATATTTTATATTATTCAAAAGCGATTGTCGCGCATTAAAGTAGCTTGTTTTTTTAACAACAATTCCCTTAGTTGGATCA
TATGTTAAGCTTTATTTAACTGCTTACTATGCCCGTGAGTGGGGAAATTTATTAAGTCAAGGTATTGAATTGGACCAAATTGTTAAAGTAATGCAA
AATCAGAAATCCAAACTTTTTAGGGAAATAGGATATGACATGGAAGAAGGTTTTCTATCAGGTAAAGCATTTCACCAAAAAGTATTAGACTATCCG
TTTTTCTTAACTGAGCTTAGTTTAATGATTGAATATGGCCAAGTTAAGGCGAAATTAGGAACAGAGTTAGATATATATGCTGATGAGAAGTGGGAG
GATTTTTTTACAAAATTAGCTAGAGCGACCCAGTTAATCCAACCCGTTATTTTTATTTTTGTAGCTCTTATCATTGTTATGATTTATGCAGCAATG
CTGTTACCAATGTATCAAAATATGGAGATATTATCA

SEQ ID 394

MVTFLKRSKLLSDCYTDSMNKALLEGKDLSKMLGELGFSDTVITQVALADLHGNISRSLLKIESYLANLLLVRKKVIEVATYPLILLSFLVLIMIG
LRNYLMPQLGENNFATRLITNVPNIFLLLLAVVLIFSLIFYIIQKRLSRIKVACFLTTIPLVGSYVKLYLTAYYAREWGNLLSQGIELDQIVKVMQ
NQKSKLFREIGYDMEEGFLSGKAFHQKVLDYPFFLTELSLMIEYGQVKAKLGTELDIYADEKWEDFFTKLARATQLIQPVIFIFVALIIVMIYAAM
LLPMYQNMEILS

SEQ ID 395

TTGATCAGCTTCTTGAGGCAGGACATCTCAATCCCAAGCAAGCTAAGCTTGAAAAAATTATCTAGTAAACATCAGCATAAATTCATTCAATTACTA
GCTAATCTTTTATCTACAGGATTTAGCTTCGCAGAGGTTATTGCTTTTTTAAAAAGAAGCCAGTTGCTTCAGCTAGATTATGTTCTTAAAATGGAA
GAGTCTTTATTAAAAGGACAAGGCTTAGCAGATATGTTGTCGGGTTTAGGTTTTTCAGATGCTATTCTTACTCAAATTAGTTTAGCTGATAGACAC
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TATAGTCGGCTAAGCCGTTATCCTTTTTTAGGTAAACTGTTAAAACAATACTTAACTAGTTATTATGCTAGAGAATGGGGTACGTTAATAGGTCAA
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GGGCAAGCCTTTCACATTAAAGTAGCTACCTACCCTTTTTTTAAAAAAGAATTAAGTTTAATGATTGAATACGGTGAAATCAAATCGAAACTGGGG
GCTGAGTTGGAAATCTATGCCCAGGAAAGCTGGGAACAATTTTTTAGTCAGCTTTATCAAGTGACACAACTTATTCAACCAGCTATTTTTTTAGTA
GTTGCTGTGACAATCGTCATGATTTATGCGGCAATCCTATTACCAATTTACCAAAATATGGGAGGTATTTTT

SEQ ID 396

LISFLRQDISIPSKLSLKKLSSKHQHKFIQLLANLLSTGFSFAEVIAFLKRSQLLQLDYVLKMEESLLKGQGLADMLSGLGFSDAILTQISLADRH
GNIETTLVAIQHYLNQMARIRRKTVEVITYPLILLLFLFVMMLGLRRYLVPQLETQNQITYFLNHFPAFFIGFCSGLILLFGMVWLRWRSQSRLKL
YSRLSRYPFLGKLLKQYLTSYYAREWGTLIGQGLDLMTILDIMAIEKSSLMKELAEDIRMSLLEGQAFHIKVATYPFFKKELSLMIEYGEIKSKLG
AELEIYAQESWEQFFSQLYQVTQLIQPAIFLVVAVTIVMIYAAILLPIYQNMGGIF

SEQ ID 397

ATGAAAAATTTATTGTTAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAATGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTA
CTAGTTTATCAAGGACTGACAAAATTGTTGGCTCAACAGATAGTAGTGATGTCTTCTTCCAGTCAGTCTGAATGGGTGTTATTAACTCAGCAACTA
AATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAAT
AAAGATGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATG
GTAAAACTTGTTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAACT

SEQ ID 398

MKNLLLKCKDKKVKAFTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLLTQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSN
KDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID 399

TTGAGTAAACAATTAAGTAACATAAAAGCTTTTACCCTTCTAGAGGCGTTAATAGCCTTACTCGTGATATCAGGGTCTTTATTGGTTTATCAAGGT
TTGACCCGAACCCTCCTTAAACATAGCCATTATCTAGCCCGTCATGATCAAGATAATTGGCTCTTATTTTCTCATCAATTGCGAGAGGAGTTAAGT
GGAGCAAGGTTTTACAAAGTAGCTGATAATAAACTATACGTTGAAAAAGGAAAGAAAGTACTAGCTTTTGGCCAATTTAAAAGTCATGATTTTCGA
AAATCAGCTAGTAATGGAAAAGGGTATCAACCCATGTTATTTGGAATATCACGTAGTCATATTCACATAGAGCAGTCACAGATTTGCATTACTTTA
AAGTGGAAAAGTGGGTTAGAAAGGACTTTTTATTATGCCTTTCAAGAC

SEQ ID 400

LSKQLSNIKAFTLLEALIALLVISGSLLVYQGLTRTLLKHSHYLARHDQDNWLLFSHQLREELSGARFYKVADNKLYVEKGKKVLAFGQFKSHDFR
KSASNGKGYQPMLFGISRSHIHIEQSQICITLKWKSGLERTFYYAFQD

SEQ ID 401

ATGAATTTTGAAAAAATTGAGACAGCCTATGAGCTGATTTTAGAAAATATCCAAACGATTGAGAACCAATTAAAAACTCATATTTATGATGCCTTA
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GAATGGCGTCGCACTTTCCAGTTCATTTTTATCAAATCTGCGCAAACAGAGCAATTACAAGCTAATCATCAGTTTACGCCAGATAGTATTGGTTTT
ATCTTGTTATTTCTTTTGGAAGAATTAACGAGTCAAGAGACAGTGGATGTCTTGGAAATTGGAAGTGGAACTGGGAATTTAGCTCAGACTCTCCTC
AATAACAGCTCGAAAGAGTTAAATTATATGGGCATTGAAGTTGATGATCTTTTGATTGATCTATCAGCAAGCATTGCTGAAATTATAGGTTCTAGT
GCCCAATTTATCCAAGAGGATGCTGTTAGACCACAAATTTTGAAAGAAAGCGATGTAATCATTAGTGATTTACCAGTTGGCTATTATCCTAATGAT
GGTATTGCTAAACGATATGCTGTATCAAGTTCTAAAGAGCACACCTATGCTCACCATCTATTGATGGAGCAATCTCTTAAATATTTGAAAAAAGAT
GGAATCGCTATATTTTTAGCACCCGAAAACCTTTTAACAAGTCCACAAAGTGATTTGCTGAAGGAGTGGTTAAAAGGATATGCAGATGTCATTGCC

GTTTTAACTCTACCAGAAACTATTTTTGGAAGTCGTCAAAATGCGAAATCTATATTTGTTCTCAAGAAGCAAGCAGAACAAAAACCAGAAACCTTT
GTATATCCGCTGACAGATTTGCAAAATCGTGAGAATATGGCAAACTTCATTGAAAATTTTCAAAAATGGAGCAGAGAAAATAGTCATTACTCAAAA
AATATGATAAAA

SEQ ID 402

MNFEKIETAYELILENIQTIENQLKTHIYDALIEQNSYYLGSSCDLDMVVVNNQKLRQLDLSQEEWRRTFQFIFIKSAQTEQLQANHQFTPDSIGF
ILLFLLEELTSQETVDVLEIGSGTGNLAQTLLNNSSKELNYMGIEVDDLLIDLSASIAEIIGSSAQFIQEDAVRPQILKESDVIISDLPVGYYPND
GIAKRYAVSSSKEHTYAHHLLMEQSLKYLKKDGIAIFLAPENLLTSPQSDLLKEWLKGYADVIAVLTLPETIFGSRQNAKSIFVLKKQAEQKPETF
VYPLTDLQNRENMANFIENFQKWSRENSHYSKNMIK

SEQ ID 403

GTGACACTTCTTTTCATTTCAAGTGTAATTTGGTATGATAAGGTTATGACTTTTGAAAAAATTGAAGAAGCTTATCAGCTGCTCTTAGAGAACTGT
CAACTAATTGAAAATGATCTAAAAACACATATATACGATGCCATTGTTGAACAAAACTCCTTTTATTTAGGGGCTGAGGGAGCTAGTCCTCAAGTT
GCTCAAAATAGTGATAAACTGAAAGCCTTGTGCCTGACAAAAGAAGAATGGCGTAAGGCCTACCAGTTTCTTTTTATTAAGGCAGCTCAGACTGAG
CAACTCCAAGCCAACCATCAGTTCACACCAGATGCTATTGGCTTCATTCTGCTGTATCTTTTGGAACAATTGAGTGATAAAGATAGCTTAGAGGTA
CTTGAGATTGGAAGTGGAACAGGGAACCTAGCCCAAACCCTTCTCAACAACACGAGCAAGAGCCTTGATTATGTAGGGATTGAACTTGATGATCTC
TTGATTGATCTGTCAGCCAGTATTGCTGAGATAATGGATTCTTCAGCTCATTTTATTCAAGAAGATGCGGTAAGGCCTCAATTACTAAAAGAAAGT
GACATTGTCATCAGTGACTTACCAGTTGGTTATTATCCTAACGATGATATTGCCAAACGGTACAAGGTGGCTAGTTCAGATAAGCATACCTATGCC
CATCATTTATTAATGGAACAGTCTTTAAAATACTTGAAAAAAGACGGTTTTGCGATTTTTCTGGCACCAGTCAATTTATTGACGAGCCCTCAGAGC
CAGTTGTTGAAACAGTGGTTAAAAGATTATGCTCAGGTGGTGACCTTGATTACGCTACCAGATTCTATTTTTGGTCATCCCTCAAATGCCAAGTCC
ATTATTGTCTTACAAAAACAAACAGACCACCCAATGGAAACCTTTGTCTATCCAATTCGGGATTTGAAGCTTGCAGAGAATATTCATGATTTTATG
GAAAATTTCAAAAAATGGAAACTGAGTAATGTCAAT

SEQ ID 404

VTLLFISSVIWYDKVMTFEKIEEAYQLLLENCQLIENDLKTHIYDAIVEQNSFYLGAEGASPQVAQNSDKLKALCLTKEEWRKAYQFLFIKAAQTE
QLQANHQFTPDAIGFILLYLLEQLSDKDSLEVLEIGSGTGNLAQTLLNNTSKSLDYVGIELDDLLIDLSASIAEIMDSSAHFIQEDAVRPQLLKES
DIVISDLPVGYYPNDDIAKRYKVASSDKHTYAHHLLMEQSLKYLKKDGFAIFLAPVNLLTSPQSQLLKQWLKDYAQVVTLITLPDSIFGHPSNAKS
IIVLQKQTDHPMETFVYPIRDLKLAENIHDFMENFKKWKLSNVN

SEQ ID 405

ATGTCAAAAACAATAGCAATTAATGCTGGAAGTTCAAGTTTGAAATGGCAATTATATGAAATGCCAGAGGAGAAAGTAGTTGCCAAAGGGATTATC
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AAAATTCTTTTAGAAGATCTAACAAAACATGGTATTATCAAAGACTTTAATGAAATTACAGGTGTTGGTCATCGTGTCGTTGCTGGTGGTGAATAT
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CCAATCCCACAAAAGTACTATACTGATTATAAAGTACGTAAATACGGTGCACACGGGACAAGCCACCAATACGTTGCACAAGAAGCAGCTAAGCAA
TTAGGACGTCCTTTAGAAGAATTAAAATTAATCACAGCACATGTGGGTAATGGTGTTTCTATTACAGCAAATTATCATGGACAGTCTATTGATACA
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GAATTGGAAGATGCAGCAGCTGTTGTTAATATGCTTAACAAACAATCAGGATTGCTTGGAGTATCAGGAACTTCAAGTGATATGCGAGATATTGAA
GCAGGTCTTCAAAGTAAAGATCCAAATGCAGTGTTAGCCTATAATGTCTTTATTGACCGTATTAAGAAATTTATTGGACAATACTTGGCAGTATTA
AATGGCGCGGATGCTATTATTTTTACTGCAGGTATGGGAGAAAATGCGCCATTAATGCGTCAAGATGTTATCGCAGGATTATCATGGTTTGGCATT
GAACTTGATCCAGAAAAAAATGTTTTTGGTTATTTTGGAGATATCACAAAACCAGATTCAAAAGTGAAGGTTTTAGTTATTCCTACTGATGAAGAA
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SEQ ID 406

MSKTIAINAGSSSLKWQLYEMPEEKVVAKGIIERIGLKDSISTVKFDDKKDEQILDIVDHTQAVKILLEDLTKHGIIKDFNEITGVGHRVVAGGEY
FKESALVDDKVVEQVEELSALAPLHNPAAAAGIRAFREILPDITSVCVFDTAFHTTMQPHTYLYPIPQKYYTDYKVRKYGAHGTSHQYVAQEAAKQ
LGRPLEELKLITAHVGNGVSITANYHGQSIDTSMGFTPLAGPMMGTRSGDIDPAIIPYLVANDPELEDAAAVVNMLNKQSGLLGVSGTSSDMRDIE
AGLQSKDPNAVLAYNVFIDRIKKFIGQYLAVLNGADAIIFTAGMGENAPLMRQDVIAGLSWFGIELDPEKNVFGYFGDITKPDSKVKVLVIPTDEE
LMIARDVERLKAK

SEQ ID 407

ATGTCAAAGACAATTGCAATTAATGCAGGTAGTTCTAGTTTAAAATGGCAACTTTATCAGATGCCAGAAGAAGCAGTGTTAGCACAAGGAATTATT
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ATTCGTGCCTTCCGTGATATTTTGCCAGATATTACCAGTGTTTGTGTGTTTGACACGTCATTTCACACTAGCATGGCAAAGCATACTTACCTTTAC
CCAATTCCTCAAAAATATTATACGGACTACAAGGTTCGTAAATATGGGGCGCATGGGACAAGTCATAAATATGTAGCGCAAGAAGCTGCTAAAATG
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GCTGGTTTACAAGAAGATAATCCAGATGCTGTTTTAGCTTACAATATCTTTATTGATCGCATTAAAAAATGCATTGGTCAATATTTTGCTGTTTTG
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GACATTGATCCTGAGAAAAATGTTTTTGGATACCGTGGTGACATTTCAACTCCTGAGTCAAAAGTGAAGGTGCTTGTTATCTCAACAGACGAAGAA
TTGTGCATCGCGCGTGACGTTGAACGTTTAAAAAATACAAAA

SEQ ID 408

MSKTIAINAGSSSLKWQLYQMPEEAVLAQGIIERIGLKDSISTVKYDGKKEEQILDIHDHTEAVKILLNDLIHFGIIAAYDEITGVGHRVVAGGEL
FKESVVVNDKVLEQIEELSVLAPLHNPGAAAGIRAFRDILPDITSVCVFDTSFHTSMAKHTYLYPIPQKYYTDYKVRKYGAHGTSHKYVAQEAAKM
LGRPLEELKLITAHIGNGVSITANYHGKSVDTSMGFTPLAGPMMGTRSGDIDPAIIPYLIEQDPELKDAADVVNMLNKKSGLSGVSGISSDMRDIE
AGLQEDNPDAVLAYNIFIDRIKKCIGQYFAVLNGADALVFTAGMGENAPLMRQDVIGGLTWFGMDIDPEKNVFGYRGDISTPESKVKVLVISTDEE
LCIARDVERLKNTK

SEQ ID 409

ATGAAAAATTCTCTACAAAAGTTACGAAAATCTAGGAAATTAAGTCAAGCAGAACTTGCAGTTGCACTTGGAGTTACTAGGCAAACTATTATTTCT
CTAGAAAAAAGAGAAATACACGGCATCTTTGGAGCTAGCATTTAAGATAGCGCGTTATTTTGATAAACAAATTGAGGAAGTTTTTATTTATACAGAA
AGTGAAGGAGGA

SEQ ID 410

MKNSLQKLRKSRKLSQAELAVALGVTRQTIISLEKEKYTASLELAFKIARYFDKQIEEVFIYTESEGG

SEQ ID 411

ATGAAGGAGATGGCAATGGAGGTTATTCTTAAAAATCGGCTCAAAGAATTACGAGCTAGAGATGGAATTAATCAAACGGAAATGGCTAAACTGGCA
GGAGTATCGAGGCAGACCATCAGTCTCATTGAGCGTAACGAGTACACCCCATCAGTTATAATTGCCATGAAAATTGCAAAGGTATTTCAGGAACCA
GTTGAAGAGGTGTTTCGTCTAGTGGAGGTCGAGGAA

SEQ ID 412
MKEMAMEVILKNRLKELRARDGINQTEMAKLAGVSRQTISLIERNEYTPSVIIAMKIAKVFQEPVEEVFRLVEVEE
SEQ ID 413
TTGGAGGTTTTTGTGTCATTTATTATTAGAAAAGGCAAAATTTTAGCTTTGCTAATAGCATTTTTAGTTATTAATCAACTTGTTCCTATATTGGCT
GTGTGGCTCCTAAAGAATCACTATCAAACGCCTTTTACTAGTATATTGTTGATTGGCTTAGAATTACTTATTATTGCTCTTTTCCTTTATTATGCC
AAGGTTAAACAAATAATCAGATGGAAAGCATTATTGACAAGGAAAGCATTAGTTACTATTCTCTTAGGTTGGTTATCATTGAGGGTTCCACAAATT
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GTTTATTATAAAACTGAGCACTTAGAATATAGTATAATGATTCATTTTATTAACAATGCTCTTGCTTATAGCGTGTTAATCAGTACAATGATGAAT
AAC
SEQ ID 414
MEVFVSFIIRKGKILALLIAFLVINQLVPILAVWLLKNHYQTPFTSILLIGLELLIIALFLYYAKVKQIIRWKALLTRKALVTILLGWLSLRVPQI
IGYLIMTMQGVKDTANQTVIMELTKQLPLALMLIFAIIGAPIMEEIIFRYIIPKELFAKHQKWGFVIGTLAFALIHSPSDIGSFIIYAGMGAILSF
VYYKTEHLEYSIMIHFINNALAYSVLISTMMNN
SEQ ID 415
ATGAAAGGATTCATTAATTATTTAAAAATAGCAGTGCTCATTATTCTGGCTATGGTTTTCAATGTCCTTCCGATGATTTTATTGCAAAAGCAACAC
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CAAGACACTTTTATTAAACAGCAAAAAATGAGATTGGTTGACTGGGGTTATTTAGCATTATTTTGGTTAATCATCCGTGTGATAGCTATTGTAGGT
ACCCTTGTTAACCAGCTATGGTCTGGTCAACAAGTGAGTGCTAATGATGCTGCAATACATACCTTAGCTAGACTTATCAAAGGTGGTTTCCCGCTT
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AAATCACTTAAGGTGGCAGGTTTAGTGACCTCTCTTGTTTTTGCTTTACCACATGCCACCAATAGTGTTGAATTTATCATGTACAGCTGTATGGGC
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TCAATAGGCTTAGGAGTCATA
SEQ ID 416
MKGFINYLKIAVLIILAMVFNVLPMILLQKQHDIPMVLNWGIGIFYLVIVGSVLIVLWGLYQAKQDTFIKQQKMRLVDWGYLALFWLIIRVIAIVG
TLVNQLWSGQQVSANDAAIHTLARLIKGGFPLYTALFVLVIAFIAPIMEELVFRGFPMIDLFKGKSLKVAGLVTSLVFALPHATNSVEFIMYSCMG
IFLFVAYQRRGNLKDAILLHIFNNLIEVILLMSIGLGVI
SEQ ID 417
ATGAAAATTGGAATTATCGGCGTCGGAAAAATGGCCAGTGCAATTATTCAAGGCCTCAAACAAACCCAACATGACATTATCATATCCGGATCTTGC
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ACTACTATTGCTGGCCTTTTAGACTTAGAAAAAAATGGTCTGACGCATAGTGTTATTTCTGCCATTGATGCTACTATTGAGAAAGCAAAAAACTT
SEQ ID 418
MKIGIIGVGKMASAIIQGLKQTQHDIIISGSCLERSKEIAERLDVTYAESHQSLINQADIIMLGIKPQLFEKVLLPLDITKPIISMAAGISLARLS
QLTRSDLPLIRIMPNINAQILQSCTAICYNNHVSDELRQLAKEITDSFGSSFDIAETNFDTFTALAGSSPAYIYLFIEALAKAGVKYGFPKEQALS
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SEQ ID 419
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ATCAAGCCTCAACTATTTGAAACGGTACTCAAACCGCTTCACTTCAAACAGCCTATTATATCTATGGCAGCAGGCATTTCCCTTCAACGACTAGCA
ACATTCGTAGGACAAGACCTTCCGCTGCTACGTATCATGCCAAACATGAATGCACAAATTCTCCAAAGCAGTACCGCTTTAACGGGAAATGCTTTG
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TTAGCAGGGTCAAGTCCTGCCTATATTTATCTCTTTATTGAGGCTTTGGCTAAGGCTGGCGTCAAGAATGGCATACCTAAAGCAAAGGCGCTGGAG
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ACAACTATTGCTGGTCTGATGGAGTTAGAACGCCTTGGCCTCACAGCTACTGTCAGCTCTGCCATTGACAAAACCATCGATAAAGCTAAAAGCTTG
SEQ ID 420
MKIGIIGVGKMASAIIKGLKQTPHELIISGSSLERSKEIAEQLALPYAMSHQDLIDQVDLVILGIKPQLFETVLKPLHFKQPIISMAAGISLQRLA
TFVGQDLPLLRIMPNMNAQILQSSTALTGNALVSQELQARVRDLTDSFGSTFDISEKDFDTFTALAGSSPAYIYLFIEALAKAGVKNGIPKAKALE
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SEQ ID 421
ATGTCAGATTTATTTAACAAAATTAAAACCGTAACTGAGCTTGATGGGATTGCTGGCTATGAACACAATATCCGCAACTTCCTTCGTCAAGAAATA
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GCCCATATGGATGAAGTCGGCTTTATGGTTAGTCATATTCAGCCAGATGGAACATTTCGTGTACTTGAGGTTGGAGGATGGAATCCCCTAGTAGTC
AGCTCACAACGCTTTACCCTCTACACACGTTCTGGTGATGCTATTCCTGTTATATCAGGCTCAGTTCCTCCTCACTTTCTTCGTGGACAAAGCGGT
GGAACAACATTACCCAAAATTAGTGACATTGTTTTTGATGGAGGATTCACAGATAAAAATGAAGCTGAAAGCTTTGGCATTGCTCCTGGCGATATC
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ACAACTAAATTCAACCCAGATATCTTCTTAGCTGTCGATTGTTCCCCAGCTGGAGATATTTATGGGGAACAAGGCAAAATAGGAGAGGGAACCTTA
ATCCGTTTTTATGATCCCGGACATATCATGCTTAAAGATATGAGAGATTTCTTACTTACAACAGCTGAAGAAGCAGGTATAAAATACCAATATTAT
GCTGCAAATGGTGGTACCGATGCTGGGGCTGCTCACCTAAAAAATAGTGGTATTCCTTCTACAACTATCGGTGTCTGTGCACGCTACATTCATTCT
CATCAAACACTCTACGCTATGGATGATTTTCTACAAGCACAAGCTTACCTTCAGGCCATCGTTAACAAATTAGACCGCTCGACGGTGGATATTATT
AAAGGTTAT
SEQ ID 422
MSDLFNKIKTVTELDGIAGYEHNIRNFLRQEITPLVDQVETDGLGGIFGVKNTHETNAPKVMVAAHMDEVGFMVSHIQPDGTFRVLEVGGWNPLVV
SSQRFTLYTRSGDAIPVISGSVPPHFLRGQSGGTTLPKISDIVFDGGFTDKNEAESFGIAPGDIIVPKSETILTANQKHIMSKAWDNRYGVLMVTE
LLKSLKDQSLSNTLIAGANVQEEVGLRGAHVSTTKFNPDIFLAVDCSPAGDIYGEQGKIGEGTLIRFYDPGHIMLKDMRDFLLTTAEEAGIKYQYY
AANGGTDAGAAHLKNSGIPSTTIGVCARYIHSHQTLYAMDDFLQAQAYLQAIVNKLDRSTVDIIKGY
SEQ ID 423
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ACCCCGCTGGTTGACCGTGTTGAAACAGACGGGCTTGGTGGCATTTTTGGTATCAGAGATAGTAAAGCTGAAAAAGCCCCCCGTATTTTAGTAGCT

GCGCACATGGACGAAGTCGGTTTTATGGTCAGTGATATCAAAGTTGACGGAACGCTACGCGTGGTTGGTATCGGTGGTTGGAACCCACTTGTTGTC
AGTTCACAACGGTTTACCCTTTACACACGCACTGGCCAAGTTATTCCCCTTATTTCAGGATCGGTACCTCCCCATTTTTTACGTGGGGCAAATGGC
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ACCACCAAGTTCGACCCTGAACTCTTTTTCGCAGTAGATTGTTCGCCTGCTGGTGATATTTATGGCAATCCTGGAACAATCGGAGATGGTACCTTG
TTGCGTTTCTACGACCCAGGCCATGTCATGCTCAAAGATATGCGCGACTTCTTACTGACTACTGCTGAGGAAGCTGGTGTCAATTTCCAATACTAT
TGTGGCAAGGGAGGCACAGATGCAGGTGCTGCACACCTTCAAAATGGTGGTGTCCCATCAACAACCATCGGAGTCTGTGCACGCTACATTCACTCT
CATCAAACCCTCTACGCTATGGATGATTTCGTAGAAGCCCAAGCCTTCTTACAAGCCATTATCAAAAAACTGGATCGCTCAACCGTTGACTTGATT
AAATGTTAC

SEQ ID 424

MTDLFSKIKEVTELDGIAGYEHSVRDYLRTKITPLVDRVETDGLGGIFGIRDSKAEKAPRILVAAHMDEVGFMVSDIKVDGTLRVVGIGGWNPLVV
SSQRFTLYTRTGQVIPLISGSVPPHFLRGANGSASLPHIEDIVFDGGFTDKAEAERFGITPGDIIIPQSETILTANQKNIISKAWDNRYGVLMITE
MLEALKGQDLNNTLIAGANVQEEVGLRGAHVSTTKFDPELFFAVDCSPAGDIYGNPGTIGDGTLLRFYDPGHVMLKDMRDFLLTTAEEAGVNFQYY
CGKGGTDAGAAHLQNGGVPSTTIGVCARYIHSHQTLYAMDDFVEAQAFLQAIIKKLDRSTVDLIKCY

SEQ ID 425

ATGGTTAATCATTCAAACAGAAAGAAAAAACATGAAAGAAAAATTATTAGTACCTGCTTTAAATTGTTTGCTAGGTCTACTCTTCCTAGG

SEQ ID 426

MVNHSNRKKKHERKIISTCFKLFARSTLPR

SEQ ID 427

GTGTCTAATTCCGGGGGGTATGGTATAATAACAGTTATGAAAAATAAAAAAATCTTATTTGGGACTGGCCTTGCTGGTGTGGGTTTACTGGCAGCT
GCTGGTTATACCCTAACTAAAAAAGTAACAGATTATAAACGTCAGCAAATCACTCAGACCTTAAGAGAATTTTTTAGTCAGATGGGTGATATTCAG
GTATTTTATTTTAATGAATTTGAATCTGATATTAAAATGACCAGTGGTGGTCTTGTCTTGGAAGATGGCAGAATTTTCGAATTCATTTATCGTCAA
GGTGTTCTTGATTATGTGGAGGTGAGCAAA

SEQ ID 428

MSNSGGYGIITVMKNKKILFGTGLAGVGLLAAAGYTLTKKVTDYKRQQITQTLREFFSQMGDIQVFYFNEFESDIKMTSGGLVLEDGRIFEFIYRQ
GVLDYVEVSK

SEQ ID 429

ATGAGGGATATGAGTAAAAAGAAAATAGGTATGATTTCAGGTATCTTTGGATTTAGTTTAGCTATTGGCCTAGGAATAGTTATCAAAGATTATTGC
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AAACAAGATTATATTTCAGGTGGGGTTGTTATGTCAAACGGCAAACAGTACCAATTCACCTATCACAGTCGACAAATTAGTTTTGAGGAGGACAAG
GGA

SEQ ID 430

MRDMSKKKIGMISGIFGFSLAIGLGIVIKDYCQDRQRRQMTRDLRTFFSPLGQIEVLYINPCQVKQDYISGGVVMSNGKQYQFTYHSRQISFEEDK
G

SEQ ID 431

ATGATTTTACCAGAATCTTATGAAGAAATAGCAGCCTATATTGATAGCACTAAGAAAGTTGTTTTCTTTTTTACAGCAGATTGGTGTCCAGATTGT
CAATTTATATATCCAGTAATGCCATCAATTGAAAAAGATTTCTCAGATTTTGTCTTTGTACGTGTTAATCGTGATGACTATATAGAATTAGCTCAG
CAGTGGAATATTTTTGGGATTCCGAGTTTCGTTGTTGTGGAAAATGGTCAGGAACTGGGTCGTTTGGTTAATAAGAATCGCAAAACAAAGGCTGAA
ATTACTAAATTTCTCGCTGAAATTAACTATAAA

SEQ ID 432

MILPESYEEIAAYIDSTKKVVFFFTADWCPDCQFIYPVMPSIEKDFSDFVFVRVNRDDYIELAQQWNIFGIPSFVVVENGQELGRLVNKNRKTKAE
ITKFLAEINYK

SEQ ID 433

ATGATCAGACCGACTTCTTATGAGTCATTAGCGACTCTTATTGAAAAAGAAGATAAGCTGGTGTTATTTTTTACGGCAGACTGGTGTCCAGACTGT
CAATTTATTTATCCTATTATGCCAGAAATTGAAGCAGAACTTACAGATATGACTTTTGTTTGTGTTAATCGTGATCAGTTTATAGAGGTAGCACAA
AAGTGGAATATTTTTGGTATTCCTAGTTTTGTCGTGATTGAAAAAGGTCAGGAAGTAGGGCGTCTGGTTAACAAAATGAGAAAGACAAAAACTGAG
ATTATGCATTTTTTAGCTGCTTATCAA

SEQ ID 434

MIRPTSYESLATLIEKEDKLVLFFTADWCPDCQFIYPIMPEIEAELTDMTFVCVNRDQFIEVAQKWNIFGIPSFVVIEKGQEVGRLVNKMRKTKTE
IMHFLAAYQ

SEQ ID 435

ATGATTTTTACTTATAATAGAGAGCATGTTGGTGATACCTTAATGGTTATTGTTAAGGATAGTCAAGGAGCTAAGCTAGATGTTGATCGTCGCGGA
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ATAACTTTATCTGATCAAGATATTAAAATCCTTAATGCAGAACTACTGAAAGAAGGATTCGAAGACTCTCTTGTTAATAATATTGAACCTACATTT
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CTTCGTGGAGAAGATAGCTTTGGAATGTTATGTAGTGCTCGCGAGTTAGCTCTTCCAAATGCTCCTCAAGTCAGAGGTATCATTGAATTATCTGAT
CAGGTAATTGTTGGAGAGTCTTTCGACGCCAATAAACATTGGAAAAAT

SEQ ID 436

MIFTYNREHVGDTLMVIVKDSQGAKLDVDRRGQVARVYLQDSKETVAWNIFEVSSLIVIEGAGQITLSDQDIKILNAELLKEGFEDSLVNNIEPTF
VVAQIKEIIDHPDSDHLHICQAEINDGKTVQIVCGAPNASVGLKTVAALPGAMMPNGSLIFPGKLRGEDSFGMLCSARELALPNAPQVRGIIELSD
QVIVGESFDANKHWKN

SEQ ID 437

ATGATTTTTGCATACAATAAAGAACAAGTTGGCGATGTCTTGATGGTTATCTTACAAGACACCAAAGATATCAAACGTCAAGTAGAACGAAAAGGC
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TTGCGTGGTGAAGAAAGTTATGGTATGATGTGCTCTCCTCGTGAGTTAGCCTTGCCAAATGCACCGCAAAAACGTGGCATTATTGAATTTGATGAG
TCAGCTGTGGTAGGAGAAGCTTTTGACCCAGCCAAACATTGGAAAGGT

SEQ ID 438

MIFAYNKEQVGDVLMVILQDTKDIKRQVERKGKVARVFAEESGKTLAWNIFEASSLITIEGNGQIFLTDENLARLNAELAKEGFSERLEPIVGPVF
VVGQIVEMVAHPDSDHLNICQVAIGEDQTVQIVAGAPNAALGLKTIVALPGAIMPNGSLIFPGKLRGEESYGMMCSPRELALPNAPQKRGIIEFDE
SAVVGEAFDPAKHWKG

SEQ ID 439
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TATTCATTACAACCAAACCATTTTAAAACTGAAACTGGTTGGCTAAACAAAATGCTTGCTATCGAGCTAAGTGTTGCTGACAAAGCTCCTTATAAA
GATATTGCTTTTTTGCAACACATCACACTTAAAAAGTCATTG
SEQ ID 440
MTNVTSYKEMLAKPWGKIQYEITFAQLSHIKNQNVLDFGAGFCLTEQHLAKENNVTAIEPNPKLLYDNQSDNIYKILGSYEALRDLPDQSFDTIIC
HNVLEYIDKHNHPAYFDEFSRLLKPNGELSLIKHNITGKILQSVIFSNDTSTAMELLTGEANFKSASFDQGNIYTLEELKQNTNLLVERYQGIRTF
YSLQPNHFKTETGWLNKMLAIELSVADKAPYKDIAFLQHITLKKSL
SEQ ID 441
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GTTAATAGACGCTTTAAAGGAAGTAATGGTGAGCGTGAAGCAGATTTTATTAATGTGGTTATGTGGGGTCGTCTAGCGGAAACCCTTGCGAGCTAT
GGGACAAAGGGCTCTTTAATTTCAATAGATGGTGAATTGCGTACGCGCAAGTACGAAAAGGATGGTCAAACGCACTATATCACTGAAGTATTAGCA
TCATCATTTCAGTTGCTAGAAAGCCGTGCCCAACGTGCTATGCGTGAAAATAACGTTTCTGGTGATTTGTCAGATTTAGTATTGGAAGAAGAGGAG
CTCCCCTTT
SEQ ID 442
MYNKVIMIGRLTAKPEMVKTPTDKSVTRATVAVNRRFKGSNGEREADFINVVMWGRLAETLASYGTKGSLISIDGELRTRKYEKDGQTHYITEVLA
SSFQLLESRAQRAMRENNVSGDLSDLVLEEEELPF
SEQ ID 443
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CAATCATTTCAACTGCTTGAAAGTCGTGCTCAGCGCGCTATGAGAGAAAATAATGTTACTAATGATCTAGTTGATTTAGTCTTAGAAGAAGATACT
CTTCCCTTT
SEQ ID 444
MYNKVIAIGRLVAKPELVKTATDKHVARLSLAVNRRFKNASGEREADFISVVVWGKLAETLVSYASKGSLMSIDGELRTRKYDKDGQVHYVTEVLC
QSFQLLESRAQRAMRENNVTNDLVDLVLEEDTLPF
SEQ ID 445
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GTCTCGTATCAATACCAGTACATGGGGACTACTTTTGAATTCATGTGGCAAGCTATGAAAGAGGAGTTTGGCTTACCGAAAACAGTAAAAGAGTAT
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CATGGCTATCGCTTAGCAGTTGCGTCCTCATCTCCAATGGTAGATATTAAGCGTAATCTAAAAGAGTTGGGTGTGACAGAATGCTTTGAATACATG
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ATGGCAGACAAGGTTATTTCAGATTATCAAGATATCTATATTTATCTTCCGGAG
SEQ ID 446
MLFTESNLFLLKIERQTITIKGIESRFKMEKVIIFDMDGVIVDSEYTFLDNKTEMLREEGIDTDVSYQYQYMGTTFEFMWQAMKEEFGLPKTVKEY
IAEMNRRRQAIVARDGVRPIKGAQRLIHWLHQHGYRLAVASSSPMVDIKRNLKELGVTECFEYMVTGEDVSSSKPAPDVFLRAAELLDVDPKVCIV
IEDTRNGSLAAKAAGMYCFGFANPDYPPQDLSMADKVISDYQDIYIYLPE
SEQ ID 447
ATGTTGATGATTAAAGGAATTATTTTTGATATGGACGGTGTTTTATTTGATACAGAACCTTTTTATCTGAGGCGACGAGAAGATTTTTTTAAGACA
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SEQ ID 448
MLMIKGIIFDMDGVLFDTEPFYLRRREDFFKTKGIPIDHLNSKDFIGGNLQELWKELLGKNRDDAIVKAITTDYDAYKQAHKPPYQKLLITEVNSC
LEQLEKQGIKLAVASNSKRQDVLLALETTQIKDYFEIILAREDVSRGKPYPDIYNKAVQKLGLQKKQLLVVEDSQKGIAAAKAANLTVFAITDYRY
GIDQSQADHKIDHLGQLCVKIGCFGS
SEQ ID 449
TTGGTGGACCTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTT
CAGTTC
SEQ ID 450
MVDLWLDQLLVLLEEFIAFFKEAFQVLSILSVQF
SEQ ID 451
GTGGAACCTAAACTATTTAAAATCATCATTGGAATGACAATCATTTTGACAAGTTCCCATCCTGTAAAAATGCCAACAAATAGCATCTGGATACTT
TCGGCAATAATACTAATTAAAATAACTTGGCTTGTTGAAGGG
SEQ ID 452
MEPKLFKIIIGMTIILTSSHPVKMPTNSIWILSAIILIKITWLVEG
SEQ ID 453
ATGTTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTAGACAGTTAATTGAAGAG
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CCTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTA
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CTTTTCCTTGCGATTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTTGAATTGACTCGACAGACTCTG
CCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACTAACTTTGATGCTGTGGGATTAACAGAT

CGGTCAAACGTATTAGCTCATATTGGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTTATCTAAAAGTGTTATTTTTGAT
GGCGAACCAAGAATTGCGCAAGATAAAGCGGCGATTTCTTGTCCAGATCACAACTGTCAGTTAAATTCTGCTATTGTAGTTCCTCTAAAAATAAAT
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TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATC
TCAGATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTA
TTATATGGTAGTGTAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCAT
GAAAATTTTAATTCT

SEQ ID 454

MLMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVIISNITGIEIKGDRSLVERPFLTTISHSDSLANTRTLVITTASLVGG
PLVGSIVGFIGGVHRFFQGSFSGSFYIVSSVLVGIVSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVIPMMILNSLGST
LFLAILKTYLSNESQLRAVQTRDVLELTRQTLPYLRQGLTPQSARSVCEIIKRHTNFDAVGLTDRSNVLAHIGVGHDHHIAGQPVKTDLSKSVIFD
GEPRIAQDKAAISCPDHNCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFSGQLAMGITEEQNKLASMAEIKALQAQINPHF
FFNAINTISALIRIDSDKARYALMQLSTFFRTSLQGGQDREVTLEQEKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHA
FKERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLGQETVAESKGTGTALVNLNNRLNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEH
ENFNS

SEQ ID 455

TTGACAGACCTTGCCCAACAGTTTAATGCGCTCTTAGATCAAATTGATAGCTTGATGGTTGCCGTTGCGGATAAGGAAAAGGCGATTGGGCAGTAT
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GTGGTAGAAGTGACCAAGTCTCTAGCTAAGTATTTTCGTTTGGCCCTTAATCAGGGGAACGAATACATTCGTTTGGCAGATGAACTGGATCACGTT
AGCCAATACCTCTTTATTCAAAAACAGCGCTATGGAGACAAGCTAAGTTATGAAGTGCAAGGCTTAGATGTCTACGCAGACTTTGTTATTCCTAAG
CTTATCTTACAGCCCTTAGTAGAAAATGCTATCTACCATGGCATCAAAGAAGTCGATCGCAAGGGCATGATCAAGGTTACGGTATCTGATACAGCT
CAGCATCTGATGTTGACTGTTTGGGATAATGGTAAAGGCATTGAAGACTCTTCACTGACCAATAGTCAGAGCTTGTTGGCTAGGGGAGGTGTGGGC
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AGCCTTCCTAAAATGCATGAATTAATGGCAGACGACACACAGGAAAACGAG

SEQ ID 456

LTDLAQQFNALLDQIDSLMVAVADKEKAIGQYRLQALASQINPHFLYNTLDTIIWMAEFNDSKRVVEVTKSLAKYFRLALNQGNEYIRLADELDHV
SQYLFIQKQRYGDKLSYEVQGLDVYADFVIPKLILQPLVENAIYHGIKEVDRKGMIKVTVSDTAQHLMLTVWDNGKGIEDSSLTNSQSLLARGGVG
LKNVDQRLKLHYGEGYHMTIHSQSDQFTEIQLSLPKMHELMADDTQENE

SEQ ID 457

ATGAGCATGAAAATTTTAATTCTTGATGATGAAATGTTTGCCAGACAAGAATTATCGTTTTTAGTTGAACATAGCCAGGAGGTTGACAACCCTGAG
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AGTAACGCTGTTGATTATATCATGAAACCGTTTGAACAACAGCGCGTTGATATGGCTCTATCAAAAGTGAAGAAATTGAGCCAACTCACCACTGCT
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GTTGCAGCTAGTGTTGAAGATGGCGAATTAACTGTTAGTACAGTTCAGAAAACTTACACTATTCGGAAGACACTCAATTGGTTTAAGTCACGCGCT
GTAGCACCATATTTTCTCCAGATTCATCGAAACACAGTGATTAATCTAGAGATGATTGAGGAAATTCAACCTTGGTTTAATCATACTTTGTTACTA
ATTATGTCTAATGGAGAGAAATTTCCAGTAGGTCGATCGTATTTAAAAGACCTAAATGAGCATTTAACCATG

SEQ ID 458

MSMKILILDDEMFARQELSFLVEHSQEVDNPEIFQAEDISEAEKILFRQQIDLIFLDISLSEENGFTLANQLSQLAHPPLVVFATAYDNYAVKAFE
SNAVDYIMKPFEQQRVDMALSKVKKLSQLTTASDVEQAIPKKASVELLTLTLSDRSVVVKMQDIVAASVEDGELTVSTVQKTYTIRKTLNWFKSRA
VAPYFLQIHRNTVINLEMIEEIQPWFNHTLLLIMSNGEKFPVGRSYLKDLNEHLTM

SEQ ID 459

GTGTACTCATTGTTAATTGTAGAAGACGAATACCTTGTGCGCCAGGGTATTCGTTCTTTGGTTGATTTTAGCCAGTTCAAGATTGATCGGGTCAAC
GAAGCAGAAAATGGCCAGTTGGCTTGGGACTTGTTTCAGAAAGAGCCTTATGATATTGTTTTGACGGATATCAATATGCCCAAATTAAATGGGATT
CAACTAGCAGAACTCATTAAACAGGAATCCCCCCAAACTCATCTGGTATTTTTGACGGGCTACGATGATTTTAACTATGCCTTATCTGCTTTGAAA
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ACAGAAACCATTCAGGAATTGGTTGAGCAGCCTCAAAAAGAAGTATCAGCAATAGCAATGGCTATTCATGAGCGGTTGGCAGATTCTGATTTGACC
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CAAGAACGGTTGAAAAAAGCCAAGCTTCTCTTGTTAACCAGTAATCTTAAAATCTATGAAATTGCAGAGCAGGTCGGTTTTGAGGACATGAATTAT
TTTTCTCAGCGCTTTAAGCAACTGGTAGGCGTTACCCCAAGTCAGTATAAAAAAGGAGGCCAGGCA

SEQ ID 460

VYSLLIVEDEYLVRQGIRSLVDFSQFKIDRVNEAENGQLAWDLFQKEPYDIVLTDINMPKLNGIQLAELIKQESPQTHLVFLTGYDDFNYALSALK
LGADDYLLKPFSKADVEDMLGKLRKKLELSKKTETIQELVEQPQKEVSAIAMAIHERLADSDLTLKSLAQQLGFSPNYLSVLIKKELGMPFQDYLV
QERLKKAKLLLLTSNLKIYEIAEQVGFEDMNYFSQRFKQLVGVTPSQYKKGGQA

SEQ ID 461

GTGACACTGAGTTCTCTGATAGCAAGTATTAATCGTGCAACATATGCTACCACTACCAACATAACAACAGTTGAGATTGTAATAACAGCAACTAGT
TGCAAGCCTTCAGCTTTTAGGATATCAAGATTCGCTGCTACTGATATTCCTGAGGGGACAAACATAAAACCAATCATGCTTATCATCAAAGCCCCA
AAAGAGTCAACCCACTCTACCTTGATAATTTTAGCAGTTAGCAATACATACATTAGCACCAAACCAATAACCGTCGTTGGGATTGGTAGTGATTTC
GGTAATAACATTGAAATCATTTGTGAAACTAATAGAATAGCTGCATATATTGACATT

SEQ ID 462

MTLSSLIASINRATYATTTNITTVEIVITATSCKPSAFRISRFAATDIPEGTNIKPIMLIIKAPKESTHSTLIILAVSNTYISTKPITVVGIGSDF
GNNIEIICETNRIAAYIDI

SEQ ID 463

GTGACTATGAAACACACCAGTAAAGAAACCAAAACAAAAGAAGCTCCAATGTTTATTCAAATGTCAATATATGCAGCTATTCTATTAGTTTCACAA
ATGATTTCAATGTTATTACCGAAATCACTACCAATCCCAACGACGGTTATTGGTTTGGTGCTAATGTATGTATTGCTAACTGCTAAAATTATCAAG
GTAGAGTGGGTTGACTCTTTTGGGGCTTTGATGATAAGCATGATTGGTTTTATGTTTGTCCCCTCAGGAATATCAGTAGCAGCGAATCTTGATATC
CTAAAAGCTGAAGGCTTGCAACTAGTTGCTGTTATTACAATCTCAACTGTTGTTATGTTGGTAGTGGTAGCATATGTTGCACGATTAATACTTGCT
ATCAGAGAACTCAGTGTCACAGATTTATTTAAAAAGATATTACCTAACCACTATAGTAAGAAAGTAGAGGAAAAA

SEQ ID 464

MTMKHTSKETKTKEAPMFIQMSIYAAILLVSQMISMLLPKSLPIPTTVIGLVLMYVLLTAKIIKVEWVDSFGALMISMIGFMFVPSGISVAANLDI
LKAEGLQLVAVITISTVVMLVVVAYVARLILAIRELSVTDLFKKILPNHYSKKVEEK

SEQ ID 465

ATGGAACTCTTAAAAACACCCATCTTTGGTATTTGCTTTTCTTTAATACTCTATACGATAGGAGAACATTTATTTAAGAAGAGTAAAGGTTTCTTC
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CAAGCTTATAAACCAGGTGGTGATTTAATATTTTGGTTTTTAAATCCAGCGACAATTGCTTTTGCAGTTCCTCTCTATAAGAAAAATGACGTTGTT
AAAAAATATTGGGTAGAAATTCTCAGCAGTTTAGTAATCGGTATGATTGTTTCCCTTATACTTATCGTCGCTATTTCTAAAATGGTTGGGCTTAGT
CAAGTCGGAATTGCTTCAATGTTGCCACAAGCAGCAACAACAGCAATTGCTCTTCCAATAACAGCAGCAATTGGAGGGAACACAGCTGTGACAGCA
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GGTCTAGGGACCTCTGGTCATACAGTCGGAGCAGCCTTTGCATTGGAATTGGGAGAACTGCAAGGTGCGATGGCAGCTATAGCTGTGGTGGTTATC
GGTTTGGTAGTTGATTTGGTTATTCCTATCTTTAGTCATTTGATTGGTTTGCTA

SEQ ID 466

MELLKTPIFGICFSLILYTIGEHLFKKSKGFFLLQPLFFAMVSGIVILWLMSKGLGTDVKTFYTQAYKPGGDLIFWFLNPATIAFAVPLYKKNDVV
KKYWVEILSSLVIGMIVSLILIVAISKMVGLSQVGIASMLPQAATTAIALPITAAIGGNTAVTAMACILNAVIIYALGKKLVSFFHLNDSKIGAGL
GLGTSGHTVGAAFALELGELQGAMAAIAVVVIGLVVDLVIPIFSHLIGLL

SEQ ID 467

GTGACTAAATATTTGAAGTACATCTCTTTTGTTGCTTTGTTTCTGGCGAGTATCTTTTTAGTAGCTTGTCAAAATCAAAATTCACAAACCAAGGAG
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AATGAAGGTAATATTACTCATAGCACCCTATTGAAACGTTCTCCTGAACTAGATATAAAAGGAGAGCTTGCTAAAAAATATAAAATCTCTAAGGAT
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AAAGCAGATGGAAAAGCTTGGGATTTGACCTTTATTAAGAATGTTGAAGTAGTTGGGAAAAACCAGGTAAATATTCATTTGACTGAGGCGCATTCG
ACATTTACAGCACAGTTGACAGAAATCCCAATCGTCCCTAAAAAACATTACAATGATAAGTATAAGAGCAATCCTATCGGTTCAGGACCTTACATG
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CAGTGGGATGGCAAAACAGGTGCTTCCACTCTTGGAGATTTACCAAATGTATGGTTGGTGAGTCTTAACCATACTTATATTGGTGATAAACGTATC
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SEQ ID 468

MTKYLKYISFVALFLASIFLVACQNQNSQTKERTRKQRPKDELVVSMGAKLPHEFDPKDRYGIHNEGNITHSTLLKRSPELDIKGELAKKYKISKD
GLTWSFDLNDDFKFSNGEPVTADDVKFTYDMLKADGKAWDLTFIKNVEVVGKNQVNIHLTEAHSTFTAQLTEIPIVPKKHYNDKYKSNPIGSGPYM
VKEYKAGEQAIFVRNPYWHGKKPYFKKWTWVLLDENTALAALESGDVDMIYATPELASKKVKGTRLLDIASNDVRGLSLPYVKKGVVKNSPDGYPV
GNDVTSDPAIRKALTIGLNRQKVLDTVLNGYGKPAYSIIDRTPFWNPKTAIKDNKVAKAKQLLTKAGWKEQADGSRKKGNLKSEFDLYYPTNDQLR
ANLAVEVAEQAKALGITIKLKASNWDEMATKSHDSALLYAGGRHHAQQFYESHYPSLAGKGWTNITFYNNPTVTKYLDKAMTSPDLDKANKYWKLA
QWDGKTGASTLGDLPNVWLVSLNHTYIGDKRINVGKQGVHSHGHDWSLLTNIAEWTWDESAK

SEQ ID 469

ATGACTGGATCAACCGGTGATTGTTTTAGTAAAATAAAGGTCAAAATTGATACTCCAAAAACGAGTGACAAACACCTAAGTATCTTCCAGATAACT
ACAGTGGTAATATGTTTCACAGATAAATCTCCT

SEQ ID 470

MTGSTGDCFSKIKVKIDTPKTSDKHLSIFQITTVVICFTDKSP

SEQ ID 471

ATGGCAAGTGTCAATTATGACACGTCACTAACCCCTGTTCAGTACAAAGCGATTGCTCACCACTATGGTTTGGATAAGCCAGCTCCGGTCCAGTAT
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TCTTTCATACTTATGGGACTCTCCTGGGTCTTATCGGGTCTTATTGGATTTATCTTAGGAACTTTATCAGCTTTCCATCAAGGGAAATTGCTTGAT
CGAATTGTAAGGTGGTTTTCTTACCTTCAGATATCAGTACCAACTTTTTGGATTGGGCTCATTTTTTTATTAATCTTTTCTGTCCAGCTGGGGTGG
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ATTGTGATGATAGGGACATTATTTGTTTTTGCGGGCAATCTTATTGCGGATATTTTAAACAGCATAATCAATCCACAGTTAAGGAGAAAAGTA

SEQ ID 472

MASVNYDTSLTPVQYKAIAHHYGLDKPAPVQYFIWLKNFIQGHLGTSLVYRQPVIDIIRSRAGASFILMGLSWVLSGLIGFILGTLSAFHQGKLLD
RIVRWFSYLQISVPTFWIGLIFLLIFSVQLGWFPIGISSPIGTLSQDITLADRIKHLILPVFTLSILGIANVTLHTRTKMMSVLSSEYVLFARARG
ETEWQIFKNHCLRNAIVPAITLHFSYFGELFGGSVLAEQVFSYPGLGSTLTEAGLKSDTPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV

SEQ ID 473

ATGATATTGAGACGTCGAACTATTGTTTTATGGCAACTGGGTATCGCCATTTCTCTCATTCTTAGTATTCTAGCCTTAAATCTTTATTTCCATAGT
ACTCCCTTGCAAACCAATGCAGCTTTACGGAACCTTGCTCCTTCATTAAACCATCTTTTTGGGACAGATGGTTTAGGTAGGGATATGTTTGTCAGA
ACGATTAAAGGACTTTATTTCTCTCTACAAGTCTGCTTATTAGGTGCCCTTATGGGGGTCATTCTGGCGACAGTTTTTGGAGTGCTTGCAGGTTTA
GGAAATAGCATTATTGATAAAATAATAGCATGGTTAGTTGATTTGTTTATTGGTATGCCTCATTTGATTTTTATGATTCTCATTTCTTTTGTTGTT
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AAAGAATTTGTCCAACTTTCTAAAAGTATGGGAAAAACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTCAAATTTTCATT
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ACTATCGGAGAATCTTTAAAGAAACTCTTTTACCCTCAAACTGATCATTTT

SEQ ID 474

MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAPSLNHLFGTDGLGRDMFVRTIKGLYFSLQVCLLGALMGVILATVFGVLAGL
GNSIIDKIIAWLVDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKEFVQLSKSMGKTPYYIVRHHILPLIASQIFI
GFILLFPHVILHEASMTFLGFGLSAEQPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF

SEQ ID 475

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTTCACTCAATACGGAAGATTTTTAAAACCATTTCAATCAACACCGATACAAGCG
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CCTAAAAATGCATCTGTAACAGGAGATATGATTTATCGTGGTCAATCACTAAATTCTAAACGCATTAAACAGTTGCGAGGAAAAGATATTACGTTG

ATTCCACAATCAGTTAATTATTTAGATCCATCTACGAAAGTCAAACATCAGGTGCGCTTAGGTATCTCAGAAAATTCAAAGGCTACTCAAGAAGGA
TTGTTTCAACAGTTTGGTTTAAAAGAAAGTGATGGTGACTTGTATCCTTTCCAACTTTCTGGCGGAATGCTCCGACGTGTTTTGTTTACAACGTGT
ATTAGTGATAAGGTTTCTTTGATTATTGCGGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTTAGACCAACTACGCTCCTTT
GCAGATAAAGGAATAAGCGTTATATTTATCACTCATGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTTTTAAAGAGGGAAAAGCT
ATTGAAACAGCTCCAGCTAGTTTCTTTAGCGGAAATGGAGAGCAGTTACAAACAGAATTTGCTAGAAGTTTATGGCGCTCTCTCCCACAGCAAGAA
TTTTTGAAAGGAGTTACTCATGACCTTAGAGGC

SEQ ID 476

MTETLLSIKDLSITFTQYGRFLKPFQSTPIQALNLEIKKGELLAIIGASGSGKSLLAHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITL
IPQSVNYLDPSTKVKHQVRLGISENSKATQEGLFQQFGLKESDGDLYPFQLSGGMLRRVLFTTCISDKVSLIIADEPTPGLHPDALQMVLDQLRSF
ADKGISVIFITHDIVAASQIADRITIFKEGKAIETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTHDLRG

SEQ ID 477

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTTCACTCAATACGGAAGATTTTTAAAACCATTTCAATCCACACCGATCCAAGCG
CTGAATTTAGAAGTTAAAAAAGGTGAGTTATTAGCTATTATAGGTGCTAGTGGTTCAGGCAAGAGTTTATTAGCACATGCTATTATGGATATTCTT
CCTAAAAATGCAGCTGTAACAGGAGATATGATTTATCGTGGTCAATCACTAACTTCTAAACGCATCAAACAGTTGCGAGGAAAAGAAATGACGTTG
ATTCCACAATCCGTTAATTATTTAGATCCATCTATGAAAGTCAAGCATCAGGTGCGCTTGGGTATCTCAGAAAATGCTAAGGCTACTCAAGAAGGA
TTGTTTCAACAGTTTGGATTAAAAGAAAGTGATGGTGACTTGTATCCTTTCCAACTTTCTGGCGGAATGCTCCGACGTGTTTTGTTTACAACGTGT
ATTAGTGATACGGTTTCTTTGATTATTGCGGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTTAGATCAACTACGCTCCTTT
GCAGATAAAGGAATAAGCGTCATATTTATCACCCATGATATTGTAGCAGCTAGTCAAATTGCGGATCGTATTACTATTTTTAAAGAGGGAAAAGCT
ATTGAAACAGCCCCAGCTAGCTTTTTTAGCGGAGGTGGGGAGCAATTACAAACAGAATTTGCGAGACGTTTATGGCGCACACTCCCTCAGCAAGAC
TTTTTGAAAGGAGTTACTCATGACCTTAGAGGC

SEQ ID 478

MTETLLSIKDLSITFTQYGRFLKPFQSTPIQALNLEVKKGELLAIIGASGSGKSLLAHAIMDILPKNAAVTGDMIYRGQSLTSKRIKQLRGKEMTL
IPQSVNYLDPSMKVKHQVRLGISENAKATQEGLFQQFGLKESDGDLYPFQLSGGMLRRVLFTTCISDTVSLIIADEPTPGLHPDALQMVLDQLRSF
ADKGISVIFITHDIVAASQIADRITIFKEGKAIETAPASFFSGGGEQLQTEFARRLWRTLPQQDFLKGVTHDLRG

SEQ ID 479

ATGACCTTAGAGGCTAAAAAGCTTGGCTTTTATCATAAAAAAGATCAATGGCTTTTTAAGGAGATTAATTTAGAGGTAGCACCTGGTCAAGTTTTA
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AGTAATTTGCCTAGCAAAGCATTTAGACCTGTACAACTTATTCAACAACATCCTGAAAAAACGATGAATCCTTTATGGCCTATGAAAAAAGTTTG
GAAGAAGCCTATTACCCAAGTCGAGATTTACTAGATGCTTTTGGAATTCAAGAAAAATGGCTAAATCGTCGACCTAGTGAACTCTCGGGAGGAGAA
TTACAACGCTTTTCGATTGTGCGTTCATTACATCCAGAGACTAAATACCTTATTGCAGATGAAATGACTACTATGTTGGATAGCATTACACAAGCT
AGTGTATGGAAAAGCCTGTTGGAGATTGTAAAGGATAGAAATTTAGGTCTCATCGTTATTAGTCATGATTTCGCTATGTTAGAGAAACTTTGTAAC
CAATGCTATATGATTGAAGAGAATCGTATCGTATCTTTCAATGGAGAT

SEQ ID 480

MTLEAKKLGFYHKKDQWLFKEINLEVAPGQVLGIFGQSGCGKTSLSRVLAGFLHPKSGEVLVDGSNLPSKAFRPVQLIQQHPEKTMNPLWPMKKSL
EEAYYPSRDLLDAFGIQEKWLNRRPSELSGGELQRFSIVRSLHPETKYLIADEMTTMLDSITQASVWKSLLEIVKDRNLGLIVISHDFAMLEKLCN
QCYMIEENRIVSFNGD

SEQ ID 481

ATGACCTTAGAGGCTAAAAAGCTTGGCTTTTATCATAAAAAAGATCAATGGCTTTTTAAGGAGATTGATTTAGAGGTAGCACCTGGTCAAATCTTA
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AGTCATTTGCCTAACAAAGCATTTAGACCTGTACAACTTATCCAACAACATCCTGAACAAACCATGAATCCTTTATGGCCTATGAAAAAAAGTTTG
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GCGTGCTATATGATTGAAGAGAATCGTACTCAACTGTTCAAGCATACC

SEQ ID 482

MTLEAKKLGFYHKKDQWLFKEIDLEVAPGQILGIFGQSGCGKTSLSRVLAGFLQPKSGEVLVDGSHLPNKAFRPVQLIQQHPEQTMNPLWPMKKSL
EEAYYPSQDLRDAFGIQEKWLKRRPSELSGGELQRFSIVRSLHPETKYLIADEMTTMLDSITQASVWKSLLEIVKDRNLGLIIISHEFDMLEKLCD
ACYMIEENRTQLFKHT

SEQ ID 483

ATGGAACAATTTAAACATGATGCCAAAGCCTTGTTAGAGGCAATTGGGGGTAAAGAAAATATTAGTGCAGTGACACATTGTGCTACACGCATGCGA
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ATTATTGGTAATGATGTCCCTATTTTTTATAATGCTTTTGTAGCCGTTTCTGGTATTGAGGGTGTGTCTAAAGAGGCGGCAAAATCGGCTGCCCAA
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TTTCGTAATATTTTAGATGCCGTTCCATTTGAATTTTTAGGTCAAAAAGTTGTTGATGGTGTCAGGCAAGTAGACTCTTCTGGGCATCCAATTTGG
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CCAGCTCTGTTAGCTGGTTTGAGCCTGTCTTACTTAGAAATCTTCTGGAGAAAACATATTCCTGAAGTTGTTTCAATGATTTTTGTGCCATTTCTA
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GAAACTCCTATTCTGATTACTAATCAACAAGAATTCCGACCAGAAGAATTGATAGATTTACCCAAACAGATAAAACGTGGACAAGCATTAATGGTT
GCCAAGAAAATT

SEQ ID 484

MEQFKHDAKALLEAIGGKENISAVTHCATRMRFVLNDSSKAKVKVIEELPSVKGTFTNAGQFQVIIGNDVPIFYNAFVAVSGIEGVSKEAAKSAAQ
KNQNPLQRVLTMLAEIFTPIIPAIIVGGLILGFRNILDAVPFEFLGQKVVDGVRQVDSSGHPIWNTLVDVSTFWSGVDSFLWLPGEAIFHFLPVGI
VWSVTRKMGTTQILGIVLGICLVSPQLLNAYSVASTSAADIAKNWSWNFGYFTVQKIGYQAQVIPALLAGLSLSYLEIFWRKHIPEVVSMIFVPFL

SLVPAIILAHTVLGPIGWTLGKWISAIVLIGLTGPVKWLFGAIFGALYAPFVITGLHHMTNAIDTQLIADTKTHTTGLWPMIALSNIAQGSAVLAY
YFMHRHDEKEAQISLPAAISAYLGVTEPALFGVNVKYIYPFVAGMIGSSVAGLLATTFNVQANSIGVGGLPGFLSINVKYMGYFFICMAVAIFIPL
FLTLFFKKSGILTKTEEEKLVPDAVIASTTETKSAKEKAVVSGTKLSVVSPLSGLAKPLDQASDPVFSQGIMGKGVVIDPSDGELVSPVDATVSVL
FPTKHAIGLLTSEGVEFLIHIGMDTVNLEGKGFTSHVAQGDTVKVGDKLITFDIPMIKEEGYIVETPILITNQQEFRPEELIDLPKQIKRGQALMV
AKKI

SEQ ID 485

ATGGGAAAATTTGAACAGGATGCTAAGAGTCTTCTAACTGCTATTGGTGGTAAAGAAAACATCAAGGTTGTCACACACTGTGCAACGCGTATGCGT
TTTGTTTTGAATGATAATAATAAGGCAAATGTCAAAGAGATTGAAAAAATCTCTGTAGTTAAAGGGACATTTACCAATGCTGGGCAGTTTCAGGTA
ATCATTGGTAATGATGTTCCAGTTTTTTATAATGACTTTACAGCTGTTTCTAGTATTGAAGGGGTGTCTAAAGAAGCTGCCAAATCAGCAGCTAAA
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GTGGCAGGAACGCCTGCTGCTGAGATTGCCAAAAACTGGGTTTGGGATTTTGGTTTCTTTACCATTAATCGTATTGGGTATCAGGCACAGGTTATT
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CCTCTTGTGGTGACTAATCAAGATGTTTTTACGGTAACTGTTGAAGGTAGTTTACCGCGTCAGATTAAGGTTAATGATAAGTTAGCAGTAGCGGTG
AAAAAG

SEQ ID 486

MGKFEQDAKSLLTAIGGKENIKVVTHCATRMRFVLNDNNKANVKEIEKISVVKGTFTNAGQFQVIIGNDVPVFYNDFTAVSSIEGVSKEAAKSAAK
SNQNALQRVMTMLAEIFTPIIPAIIVGGLILGFRNILESVPFEFLGQQVEKGKLVFDAAGDPVWNTIVRVSPFWSGVNHFLWLPGEAIFHFLPVGI
TWSVTRKMGTTQILGIVLGICLVSPQLLNAYAVAGTPAAEIAKNWVWDFGFFTINRIGYQAQVIPALLAGLSLAYLEIFWRKRIPEVVSMIFVPFL
SLIPALILAHTVLGPIGWTIGKGISFVVLAGLTGPVKWLFGAIFGALYAPLVITGLHHMTNAIDTQLIADTATRTTGLWPMIALSNIAQGSAVFAY
YLMNRHEEREAEISLPAAISAYLGVTEPALFGVNVKYVYPFVAGMIGSGIAGLLSTTFNVQANSIGVGGLPGFMAINVKYMIPFFICMAVAIVVPM
FLTFFFRKSHIMTKTEDEAKLPETPVSDAPVATAPHKTMQGTVITLTSPLTGEVKALSEAVDPVFAQGVMGQGALLQPTEGVLVAPCDAEVSVLFP
TKHAICLVTTEGLELLMHIGMDTVNLDGQGFEALVKQGDQVKAGQTLIQFDIAAISEAGYATETPLVVTNQDVFTVTVEGSLPRQIKVNDKLAVAV
KK

SEQ ID 487

ATGACGATTGATAAACGTAAAGTTGTCTATCAAATTTATCCAAAATCATACAAAGACACAACTGGTAATGGGGTTGGTGATCTTCGTGGTATTATC
GAAAAATTACCCTATTTAGCAGAACTTGGTATTGATATGGTTTGGCTCAACCCATTTTATCCAAGTCCACAACGAGATAATGGATATGATATCTCT
GATTATACAGCTATTAACCCTGATTTTGGAACGATGGACGATTTTGAAGAAATGATTGAGGTGGGACGTCAATACCGTATAGATTTTATGCTTGAT
ATGGTGCTTAATCATTGTTCAATAGAACATGAGTGGTTTAAAAAAGCACTTGCAGGAGATCGCTACTATCAAGATTTCTTTATCTTACGTGATAAT
CCAACAGATTGGGTATCTAAATTTGGTGGAAATGCTTGGGCACCATTTGGTGATACAGGGAAGTATTATCTTCATCTTTTTGATATCACTCAAGCT
GACCTTAATTGGCGCAATGCCGATGTTCGCAAGGAACTTTTTAAAGTTGTCAATTTTTGGCGTGATAAAGGGGTTAAAGGTTTTCGATTTGATGTG
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AAGATGTTGAATAATGCTAGTTTTGGACAAGATGATTCCTTCATGACAGTTGGTGAAATGTCTTCAACGACAATTGCAAATTGCATTCTTTACACT
GCACCAGAACGTGAAGAGTTATCCATGGCTTTTAATTTTCACCACCTCAAAGTAGATTATAAAGATGGGCAAAAGTGGACCATTATGGCTTTTGAT
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CTTGATGAAGGCAAGTCACAAGAAGAGGCATTTAGCATTATTCGAGCGAAATCTCGAGACAATTCTCGAGTACCAATGCAATGGGATGATAGTACG
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SEQ ID 488

MTIDKRKVVYQIYPKSYKDTTGNGVGDLRGIIEKLPYLAELGIDMVWLNPFYPSPQRDNGYDISDYTAINPDFGTMDDFEEMIEVGRQYRIDFMLD
MVLNHCSIEHEWFKKALAGDRYYQDFFILRDNPTDWVSKFGGNAWAPFGDTGKYYLHLFDITQADLNWRNADVRKELFKVVNFWRDKGVKGFRFDV
INLIGKDEILENCPINDGKPAYTDRPITHDYLKMLNNASFGQDDSFMTVGEMSSTTIANCILYTAPEREELSMAFNFHHLKVDYKDGQKWTIMAFD
FPALRDLFHSWGEGMSEGNGWNALFYNNHDQPRALNRFVDVKRFRNEGATMLAASIHLSRGTPYIYMGEEIGMLDPDYSSMDDYVDIESLNAYQIM
LDEGKSQEEAFSIIRAKSRDNSRVPMQWDDSTNAGFSEGAPWLKVGKSYKEINVAKEKTGLIFTFYQELIRLRKQLPIIADGNYKAAFKDNEKVYA
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SEQ ID 489

ATGACAATTGATAAAAAGAAAGTCGTCTATCAAATTTACCCAAAATCCTATAAGGACACGACTGGAAATGGTGTGGGAGACTTGCTAGGGATCATT
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GATTATACGGCGGTCAACCCTGATTTTGGAACAATGGCTGATTTTGAAAATTTGGTAAAAGCTGCTAAGGAGCATCAGATTGAGTTAATGTTGGAC
ATGGTTTTGAATCACTGTTCCACAGACCACGAGTGGTTCCAAAAAGCTTTAGCAGGAGACCCTTATTATCAGGATTTCTTTATCTTGAGAGATCAG
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GACTTGAATTGGCGGAACCCACATGTTCGTGAGGAATTGGCTAAAGTGGTTAATTTTTGGCGAGATAAAGGAGTGAAGGGGTTCCGTTTTGATGTG
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CATGCTGGCTTTACGACTGGTAAGCCTTGGTTAGAGGTTGGCAAATCTTATCGAGACATCAATGTCGAAACAGAAAAAGAGGGACGTATTTTTCCT
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SEQ ID 490

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MVLNHCSTDHEWFQKALAGDPYYQDFFILRDQPTDWVSKFGGNAWAPFGDTGKYYLHLFDVTQADLNWRNPHVREELAKVVNFWRDKGVKGFRFDV
INLIGKDEELVDCPVNDGKPAYTDRPITHTYLHDLNQASFGQDDSFMTVGEMSATTIDNCLLYTAPEREELSMAFNFHHLKVDYENGQKWTIMAFD
FAALRDLFHAWGEGMSQGNGWNALFYNNHDQPRALNRFVDVTHFRNEGATMLAASIHLSRGTPYIYMGEEIGMLDPDFDSMDDYVDVESLNAYSSL
LVSGKSAEEAFAIIKAKSRDNARTPMQWDASEHAGFTTGKPWLEVGKSYRDINVETEKEGRIFPFYQRLIALRKELPIIAEGDYRAAFKDSQAVYA
FERHLGDQCLLVLNHFYADEVELELPPRYQHGQVLISNYEKVSICEKVILKPYQTLAILADN

SEQ ID 491

GTGCTGCTTGTGGAAAGGAATCTTGCTCTAGATTTTGCAATTTCTTTCTTTTTTCTTTACTCTATAACAATAGCCCAAATTCATTCAATTGATAGT
AGTGCCAGATTGGGCTCAAATGACCTAGAAAAATGTAAACGGTTACTA

SEQ ID 492

MLLVERNLALDFAISFFFLYSITIAQIHSIDSSARLGSNDLEKCKRLL

SEQ ID 493

ATGGTTGATAATAAGACTGTTGTGATAATGTTGGTATTTTTAGCTCGGAAAAATCTTTCCTTGTATGAGTTAACAGTGCAAACAAAGTTTTCAATA
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SEQ ID 494

MVDNKTVVIMLVFLARKNLSLYELTVQTKFSIKVIIEQINYLNSFLAKNHLPAIAHSAGRYQLLGDEKEHDKIVSLLEAEQFYLTQEERVCLIYLY
SFCRREFVSNVHYQDFLKVSKNTTLSDIKMLRSKLAKRGISLTYTRAKGYSLVGDEMDKHQVAFQMITQLLESPIGFWSLNYILSSWKFALSYEKL
EKTVEYFYESFQLSPIQDRLEKSLYFIILILCRYQRSVDRVLQGSPIVSEQLKELTTIIVTNLSQDISLSKPLDQKEKDYITLILSGCFEGEGTKD
DDFFEALAKAIVDEMETVSLLNFSNKEELLQGLKRHIIPAYFRLKYGLTGDSGYTQNIKEHYSDLFLLVKKALRPLEEQVGLIPDSEISYFVIHFG
GYLRQSGGTQSMSYKALILCPNGVSSSLVIKEKLRGLFPQIHFHRVSKIEQLKLIDNQTYDMVFSTIFVETKKPNYLVSLMMTAEQVQQLKELVIS
DFPKACLDDFQLDQLIATIKKYAHVHCEEELKLALRTMVKQDILRKDVRPLLHQLITEETYQTSSEQMNWKEAIRLAAKPLLASGKITESYPEAMI
EKVEEFGPFINLGKGIAIPHARPEDGVNSVGMSMLVLEQPRRTHENFLFILLCPDINFEKIPF

SEQ ID 495

TTGAGTCCAATTGCAGTCAAAAATGACATGAGACAATTGGACTCAATTTATCTTGAAAATGAAAACGCTTCATTTTATACTGACATTATAGGAGGA
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AGCAAACGTCATATACTGGCAGATATTGCTAAAATCAATGACACGTTGTCACTCTATCAGTTACCCCTTATTGCTCTGGACAGGCAGCTGGTTTAT
CCGCCAGACCTTACTGAAAAGGACTTGTTGAATCGCATGCTACCTACCTTAGACGACTATCTCTTTCAAGATGAGCGTCTGGATATGATTATCATT
TACATCATGATGGCTAAAGAATTTATCTCCATTAACCACTTGGAAAGCTTGTTACGGCTCAGCAGAAATTCTGTTATTGCTGATTTAAACTTGGTG
CGTGATCGGGTACAAGCTTTTCAGGTAACTTTAGCTTACAATCGCCAGGATGGTTATTTTTTTGAAGGAGAACCCTTAGCCTTGCGGCGTCTCTTA
GAATCAGCGGTCAGTTCTCTTTTGCAAGTCACATCTGGACCTTGGGTGTTCAGTTACTTATTGCATGAACTTGGTTTGCCCGACCAGAAAAAGGTG
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CATCGACCATTTTCACGGAACGTAAGGGCTGAAGCAGTGGATACTTTTCCTTTAGCTTCGCCAGCTGTTGAAACGATGGTGGACCAGTTATTGGTC
AACTTCCCCAGTCTAACCGAAGAAAAATATTTGGTTCAATCTAGGTTACTTGGTTGTATCCAAGGTGACTTAGAGTTAGTCTTTCAGCAACCTATT
TATGACATTATGGAGGAAATCATCAATTCGGTGGCGGTTAACACGGGATTGTCTATCACCGATACCCCAGAACTTCGTCAGAACCTATACAGTCAC
CTTTTGCCAGCTTATTACCGACTTTACTACGACATTAACTTGACCAATCCTTTGAAGGAACAAATCAAACAAGATTATGAATCTCTCTTTTACTTG
GTCAAGCGCAGCCTTTCTCCTCTAGAAAAACAATTGGGGAAATCAGTTAATGAAGATGAGGTTGCTTATTTTACCATTCATTTTGGGAGATGGTTG
CAGGCCCCTAAGAAGAGGCCAAGCAATCAGCTGGTAGCCTTATCTGTTTGCCCTAATGGCATTAGTTCGTCTCTGATGTTGGAGGCAACCTTGAAG
GAACTTTTTCCACAGCTACAGTTTATTAGGATTCACCAGCTGGACAAAATAAAGTTGTTGGATCCAGCATCCTTTGATTTGATTTTTTCAACAGTA
GCTTTTGACTGTGCTAAACCTGTTTATGTGACGCAAGCTTTGATGGGACCTGTTGAAAAAATGATGTTGAAAAAGATGGTCTGTGATGACTTTCAT
CTTCCCTTGTCAGAGCAATTCGCTTTGGATGATCTGTTGAGTATTATTCATAAACATACCACGATTACTAATAAAGAAGGACTTGTTAGTGATTTA
TCCCGTTACCTGATTGGTAACCATTTAACGATTGAAAAAGGAGGTCTAGGACTATTGGACTTGTTAACAGCAGATTTTATTAGGCAGGCTGATGCT
GTTTCGGATTGGCAGGAAGCGATTCGTTTGGCTGCTCAGCCTTTACTAGAACACCAGATGATTGAAACATCTTATATCGATGGCATGATTGATTCG
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TTACAACTAAAAGAACCTGTCAGCTTTGATTTGAAGCAAGAAGGTGATCCAGACAAGCAAGTGCAATTGATTTTTGTTTTGTCTGCTGTGGATTCT
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ATGAGTCTGATTAGCCATATGATTGAAAAAGGAGACGAATCACATGAT

SEQ ID 496

LSPIAVKNDMRQLDSIYLENENASFYTDIIGGDDMLSHELIRNYQLFSKYKGHSLEAFESILKASKRHILADIAKINDTLSLYQLPLIALDRQLVY
PPDLTEKDLLNRMLPTLDDYLFQDERLDMIIIYIMMAKEFISINHLESLLRLSRNSVIADLNLVRDRVQAFQVTLAYNRQDGYFFEGEPLALRRLL
ESAVSSLLQVTSGPWVFSYLLHELGLPDQKKVMAATLEELSRENHLTFISEKLRDLIYFFCLLAHRPFSRNVRAEAVDTFPLASPAVETMVDQLLV
NFPSLTEEKYLVQSRLLGCIQGDLELVFQQPIYDIMEEIINSVAVNTGLSITDTPELRQNLYSHLLPAYYRLYYDINLTNPLKEQIKQDYESLFYL
VKRSLSPLEKQLGKSVNEDEVAYFTIHFGRWLQAPKKRPSNQLVALSVCPNGISSSLMLEATLKELFPQLQFIRIHQLDKIKLLDPASFDLIFSTV
AFDCAKPVYVTQALMGPVEKMMLKKMVCDDFHLPLSEQFALDDLLSIIHKHTTITNKEGLVSDLSRYLIGNHLTIEKGGLGLLDLLTADFIRQADA

VSDWQEAIRLAAQPLLEHQMIETSYIDGMIDSVNELGAYIVLAPKVAVPHAAPEKGTRQLGMSLLQLKEPVSFDLKQEGDPDKQVQLIFVLSAVDS
SSHLKALQELSLILDDDEHIEQLIEAKNTEEIMSLISHMIEKGDESHD

SEQ ID 497

TTGGAGAAAGAGGCTAAGCAGATCATTGATTTAAAAAGGAATCTTTTCAAAATTGATGTCCGGGCACAAAAGGATGAAGAGAAAGTTTTCATGCGT
ACGGCGTGGCTGTTCCAAAACAAGCAT

SEQ ID 498

MEKEAKQIIDLKRNLFKIDVRAQKDEEKVFMRTAWLFQNKH

SEQ ID 499

TTGGAGAAAGAGGCTAAGCAGATGATTGATTTAAAAAGGAATCTTTTCAAAATTGATGTCCGGGCACAAAAGGATGAAGAGAAAGTTTTCATGCGT
ACGGCGTGG

SEQ ID 500

LEKEAKQMIDLKRNLFKIDVRAQKDEEKVFMRTAW

SEQ ID 501

GTGACTACGATGATTGATTTTATTATTTCTATTGATGATTGCGCAGTTGAATTGGATAGTCGTCAATCTTGGAAAATTCGCTACCCCTTATCAACC
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TACGTTGATTTGAGTGAAGGTTGTCCGTCTCATGATACCTTAGAGCGTGTGATTAGTCTTGTTAATTCAGACCGTTTAAAAGAGCTTAAAGTTCAA
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AATGCGCAGTATTATCAGACTGTTGAAAAATCTAGGGGACAGATTGAAGTTAGAGAATACTGGGTGTCTTCCGATATCAAATGGTTGTGTCAAAAC
CATCCCAAATGGCATAAGTTACGTGGTATTGGGATGACTCGTAACACGATTGATAAGGATGGTCAGCTGAGTCAAGAGAATCGTTATTTTATCTTT
AGCTTTAAGCCGGATGTCCTCACATTTGCCAATTGTGTACGAGGTCATTGGCAGATAGAGAGTATGCACTGGTTATTGGACGTTGTTTATCATGAA
GATCATCATCAGACATTGGATAAAAGAGCCGCATTTAACCTAAATCTTATCCGAAAAATGTGCTTATATTTTCTCAAAGTGATGGTATTTCCTAAA
AAAGACCTCAGTTATCGTCGCAAACAACGGTATATTTCTGTCCATTTGGAAGATTATTTAGTCCAATTATTTGGAGAAAGAGGC

SEQ ID 502

MTTMIDFIISIDDCAVELDSRQSWKIRYPLSTILFLVFVCQLAGIETWKEMEDFIEMNEPLFATYVDLSEGCPSHDTLERVISLVNSDRLKELKVQ
FEQSLTSLDAVHQLISVDGKTIRGNRGKNQKPVHIVTAYDGGHHLSLGQVAVEEKSNEIVAIPQLLRTIDIRKSIVTIDAMGTQTAIVDTIIKGKA
DYCLAVKGNQETLYDDIALYFSDVNLLEELQENAQYYQTVEKSRGQIEVREYWVSSDIKWLCQNHPKWHKLRGIGMTRNTIDKDGQLSQENRYFIF
SFKPDVLTFANCVRGHWQIESMHWLLDVVYHEDHHQTLDKRAAFNLNLIRKMCLYFLKVMVFPKKDLSYRRKQRYISVHLEDYLVQLFGERG

SEQ ID 503

GTGACTACGATGATTGATTTTATTATTTCTATTGATGATTGCGCAGTTGAATTGGATAGTCGTCAATCTTGGAAAATTCGCTACCCCTTATCAACC
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TACGTTGATTTGAGTGAAGGTTGTCCGTCTCATGATACCTTAGAGCGTGTGATTAGTCTTGTTAATTCAGACCGTTTAAAAGAGCTTAAAGTTCAA
TTTGAGCAATCATTGACAAGCTTAGATGCCGTTCATCAACTGATTTCAGTGGACGGTAAAACGATTCGAGGCAATCGAGGTAAAAATCAGAAGCCT
GTTCATATTGTAACGGCTTATGATGGGGGTCATCATCTTAGTTTGGGACAGGTAGCGGTTGAGGAGAAAAGTAATGAAATTGTTGCCATTCCTCAG
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GACTATTGCTTAGCCGTCAAAGGAAATCAAGAAACACTTTATGATGATATTGCTCTTTATTTTAGTGATGTCAACTTATTGGAAGAACTCCAAGAA
AATGCGCAGTATTATCAGACTGTTGAAAAATCTAGGGGACAGATTGAAGTTAGAGAATACTGGGTGTCTTCCGATATCAAATGGTTGTGTCAAAAC
CATCCCAAATGGCATAAGTTACGTGGTATTGGGATGACTCGTAACACGATTGATAAGGATGGTCAGCTGAGTCAAGAGAATCGTTATTTTATCTTT
AGCTTTAAGCCGGATGTCCTCACATTTGCCAATTGTGTACGAGGTCATTGGCAGATAGAGAGTATGCACTGGTTATTGGACGTTGTTTATCATGAA
GATCATCATCAGACATTGGATAAAAGAGCCGCATTTAACCTAAATCTTATCCGAAAAATGTGCTTATATTTTCTCAAAGTGATGGTATTTCCTAAA
AAAGACCTCAGTTATCGTCGCAAACAACGGTATATTTCTGTCCATTTGGAAGATTATTTAGTCCAATTATTTGGAGAAAGAGGC

SEQ ID 504

VTTMIDFIISIDDCAVELDSRQSWKIRYPLSTILFLVFVCQLAGIETWKEMEDFIEMNEPLFATYVDLSEGCPSHDTLERVISLVNSDRLKELKVQ
FEQSLTSLDAVHQLISVDGKTIRGNRGKNQKPVHIVTAYDGGHHLSLGQVAVEEKSNEIVAIPQLLRTIDIRKSIVTIDAMGTQTAIVDTIIKGKA
DYCLAVKGNQETLYDDIALYFSDVNLLEELQENAQYYQTVEKSRGQIEVREYWVSSDIKWLCQNHPKWHKLRGIGMTRNTIDKDGQLSQENRYFIF
SFKPDVLTFANCVRGHWQIESMHWLLDVVYHEDHHQTLDKRAAFNLNLIRKMCLYFLKVMVFPKKDLSYRRKQRYISVHLEDYLVQLFGERG

SEQ ID 505

GTGGAACAGCCTATTTATTTATTGGATGACCCCAAACAGGAAATTTATCTCTTATTATGCATAGCAGCTATTGATAATGAAACGCATTTGAAAGCT
CTATCGCATTTGACAACAATACTTCGTGATAATAATAATGTTAAAGCTTTGTTAGCTTCACGTAGGTATCAAGATATTGAAATGATTATAAAACAG
GAGGAT

SEQ ID 506

MEQPIYLLDDPKQEIYLLLCIAAIDNETHLKALSHLTTILRDNNNVKALLASRRYQDIEMIIKQED

SEQ ID 507

ATGTTAAGAATTGGAACAGCATGTGGATCAGGTTTAGGTTCAAGTTTTATGGTACAAATGAATATTGAGTCTATTTTGAAGGATTTGGGGGTTTCT
GATGTTGAAGTTGAACATTATGATTTAGGTGGAGCAGATCCAAGTGCAGCAGATGTTTGGATTGTTGGTCGTGATTTGGAGGATTCAGCTGGTCAC
CTGGGGGATGTTCGTATTTTAAACAGTATCATTGATATGGATGAATTGAGAGAATTAGTGACAGGTATTTGCCAAGAAAAAGGCTTAATC

SEQ ID 508

MLRIGTACGSGLGSSFMVQMNIESILKDLGVSDVEVEHYDLGGADPSAADVWIVGRDLEDSAGHLGDVRILNSIIDMDELRELVTGICQEKGLI

SEQ ID 509

TTGAAAAAGGAGACGAATCACATGATTAAAATTGTAACGGTTTGTGGAAACGGTATTGGTAGTAGCTTGTTACTTCGCATGAAAGTAGAAGCTATC
GCCTCTAGTTTGGGTATTGATGTGGATGCAGAATCCTGTGATTCCAATGCGGCTGTTGGAAAGGGTGCAGATTTGTTTGTTACCGTTAAAGAATTT
AAAGATATTTTTCCAGAGGATGCCAAGGTTTGTATCGTTAAAAGCTATACCAATCGTAAAAAAATTGAAGAAGATTTGGTTCCGGTTCTCAAGGAA
ATGAGTGGCAAGGAA

SEQ ID 510

LKKETNHMIKIVTVCGNGIGSSLLLRMKVEAIASSLGIDVDAESCDSNAAVGKGADLFVTVKEFKDIFPEDAKVCIVKSYTNRKKIEEDLVPVLKE
MSGKE

SEQ ID 511

ATGACAGTAGTGCCAGTCACAATCATGACTATCATACTAACCAATCCACCAACAAAACTTGAGATAAAACCAATCAATACTGCATTAGGTGCA

SEQ ID 512

MTVVPVTIMTIILTNPPTKLEIKPINTALGA

SEQ ID 513

ATGAAAGGTCTATTGGATTTTTTAGTTAATATTGCCAGCACGCCAGCTATTTTAGTCGCCTTGATAGCCATTATCGGTTTAGTACTGCAGAAAAAA
GGCGTTCCTGATATTGTAAAAGGTGGAATAAAAACATTTGTTGGCTTCTTAGTGGTTTCTGGAGGTACAGGGATAGTCCAAAATTCCTTGAATCCA
TTTGGAAAAATGTTTGAACATGCTTTTCATTTGGTGGGGGTAGTTCCTAATAATGAAGCCATTGTAGCAGTAGCTCTTACGAAGTATGGCTCAGCA
ACTGCTTTGATTATGTTAGCGGGAATGATTTTTAATATTTTAATTGCTCGTTTTACAAAATTTAAATATATTTTCTGACAGGACATCATACATTG
TATATGGCTTGTATGATTGCTGTTATTTTTGCCGTAGCAGGCTTTACTTCGTTCTCGCTCATCCTTTTTGGAGGTCTAGCGTTAGGGATTATTATG
AGCGTATCTCCTGCATTTGTGCAAAAATACATGATTCAACTGACAGGTAATGATAAGGTGGCACTTGGGCACTTTGGTTCTTTAGGCTATTGGTTG
AGTGGATTTATTGGTGGAATTGTTGGAGATAAATCAAAATCAACAGAAGATATTAAATTTCCAAAGAGTTTATCATTTTTACGTGACAGTACCGTA
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CTTGTTTATGCCCTCCAACTAGCTGGGCAATTTGCGGCAGGTGTATTCGTTATTTTAGCAGGTGTACGCCTTATCCTAGGTGAAATTGTACCAGCC
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TGTGGGGCAACGGCAGGTGTTATCGGTAATGCTTCTGGTGGTGTGAGAGGAGCGACTATTGGTGCATTTGTTCAAGGTATCCTCATCAGTTTCTTG
CCGATTTTCTTGATGCCTGTACTAGGTGGACTTGGTTTCAAAGGGTCAACATTCTCAGATGCTGATTTTGGTTTGACCGGTATCATTCTTGGCGCT
CTTAATCATGTCGGCGGTGCGATAGCTATTGTTATTGGTATTGTAGTTATCTTAATTGGACTTTTTGGCATTTCATTTGTTGGAAAATCAACCCAT
AAGGAAGGT

SEQ ID 514

MKGLLDFLVNIASTPAILVALIAIIGLVLQKKGVPDIVKGGIKTFVGFLVVSGGTGIVQNSLNPFGKMFEHAFHLVGVVPNNEAIVAVALTKYGSA
TALIMLAGMIFNILIARFTKFKYIFLTGHHTLYMACMIAVIFAVAGFTSFSLILFGGLALGIIMSVSPAFVQKYMIQLTGNDKVALGHFGSLGYWL
SGFIGGIVGDKSKSTEDIKFPKSLSFLRDSTVSITISMAIIYLIVAVFAGEAYIAKEISNGVNGLVYALQLAGQFAAGVFVILAGVRLILGEIVPA
FKGISEKLVPNSKPALDCPIVYPYAPNAVLIGFISSFVGGLVSMIVMIVTGTTVILPGVVPHFFCGATAGVIGNASGGVRGATIGAFVQGILISFL
PIFLMPVLGGLGFKGSTFSDADFGLTGIILGALNHVGGAIAIVIGIVVILIGLFGISFVGKSTHKEG

SEQ ID 515

ATGGAAGCATTATTATCATTTATTCGAGATATTTTAAAAGAACCTGCATTTTTAATGGGCTTGATTGCCTTTGCAGGGTTGGTGGCTTTGAAAACA
CCTGCTCATAAGGTGTTGACAGGAACCTTGGGGCCGATTTTGGGATACCTTATGCTTGTTGCAGGGGCGGGTGTTATTGTGACCAATTTGGACCCT
CTTGCCAAACTCATTGAGCACGGTTTTAGCATCACTGGCGTAGTGCCAAATAACGAAGCCGTCACTTCTGTCGCTCAAAAGATTCTGGGTGTGGAA
ACTATGTCCATCTTGGTGGTTGGGTTATTGCTCAATTTGGCTTTTGCTCGTTTTACCCGCTTCAAATACATTTTCTTAACAGGACATCACAGCTTC
TTTATGGCTTGTCTCTTGTCCGCCGTGCTTGGAGCTGTTGGTTTCAAAGGAAGTCTTTTGATTATCTTAGATGGGTTCCTCTTGGGAGCTTGGTCA
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TCTGCCTGGGTTGGTAGCAAGGTTGGCAAAGACAGTAAAGATACCGAAGACCTTCAGATTTCTGAAAAATGGAGTTTCTTGCGCAACACCACCATT
TCAACAGGACTTATCATGGTGATTTTCTACTTGGTGGCAACAGTGGCTTCTGTTTTGAGGAATGCTTCAGTAGCAGAAGAATTAGCAGCAGGTCAA
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CCAGCCTTCCAAGGTATTGCTAACAAATTAATTCCAAATGCTATTCCAGCCGTGGATTGTGCGGTATTCTTCCCTTATGCGCCAACCGCTGTTATC
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TTCTTCTGCGGTGCAACAGCAGAGATTTTTGGAAATTCAACAGGTGGTCGTCGCGGTGCGATGATTGGTGCTTCGCTAATGGCTTATTACTCGCCT
TCTTGCCAGCCATGCTTCTACCTGTACTTGGTAAACTTGGTTTTTCAAACACGACCTTTGGAGATGTGGATTTCGGTGTTT

SEQ ID 516

MEALLSFIRDILKEPAFLMGLIAFAGLVALKTPAHKVLTGTLGPILGYLMLVAGAGVIVTNLDPLAKLIEHGFSITGVVPNNEAVTSVAQKILGVE
TMSILVVGLLLNLAFARFTRFKYIFLTGHHSFFMACLLSAVLGAVGFKGSLLIILDGFLLGAWSAISPAIGQQYTLKVTDGDEIAMGHFGSLGYYL
SAWVGSKVGKDSKDTEDLQISEKWSFLRNTTISTGLIMVIFYLVATVASVLRNASVAEELAAGQNPFIFAIKSGLTFAVGVAIVYAGVRMILADLI
PAFQGIANKLIPNAIPAVDCAVFFPYAPTAVIIGFASSFVGGLLGMLILGVAGGVLIIPGMVPHFFCGATAEIFGNSTGGRRGAMIGASLMAYYSP
SCQPCFYLYLVNLVFQTRPLEMWISVF

SEQ ID 517

ATGACATCACCAGAAGAAAGATATTCATCTCTAAGACGATTTGCAACGGAGATTCGTTTAAATACTCTAGAAACGCTAAACCATTTAGGATTCGGT
CACTATGGGGGTAGTTTATCAATTGTTGAGGCTTTGGCTGTTCTGTATGGTGATATTATGGATATAAATCCTGAAAAATTCAAAGAAAGTGATCGG
GATTATATGGTCTTATCAAAAGGACATGCTGGTCCAGCCTTGTATAGTACACTCTATTTAAAAGGTTTTTTTGATAAAACATTCCTTCATTCGCTC
AATACAAACGGTACCAAACTACCTTCGCATCCTGACCGCAATTTAACTCCTGGTATAGATGTAACGACAGGCTCGTTAGGTCAAGGCATTAGTATT
GCAACGGGAATTGCTTATGCTCAAAAGATTGAGAATTCAAGCTATTATACTTATACTATTGTAGGTGATGGTGAATTAAATGAAGGACAATGTTGG
GAGGCTATACAATTTGCTGCGCATCATCAACTGCACCATTTAATTGTTTTTGTAGATGATAATAAAAAACAATTAGATGGTTTGACAGCTGATATT
TGTAATCCTGGAGACTTTGTTGCTAAATTTGAAGCTTTTGGATTTGATGCAGTACGTGTAAAAGGAGATGACATTGAGGCAATTGACAAAGCTATT
AAAACTTTTCAAGATTCAAATAGTGTCAGACCAAAATGTATTGTTTTAGATAGCATCAAGGGACAAGGTGTGAAAGAGTTGGAGGAGTTAGCTTCT
AATCATCATTTACGACCAGATTTACAACAAAAAACAATGTTAGAGCGAGCGTTGATAAGCTTGAGAGAAAGTTTGGAGGTGGTAGAA

SEQ ID 518

MTSPEERYSSLRRFATEIRLNTLETLNHLGFGHYGGSLSIVEALAVLYGDIMDINPEKFKESDRDYMVLSKGHAGPALYSTLYLKGFFDKTFLHSL
NTNGTKLPSHPDRNLTPGIDVTTGSLGQGISIATGIAYAQKIENSSYYTYTIVGDGELNEGQCWEAIQFAAHHQLHHLIVFVDDNKKQLDGLTADI
CNPGDFVAKFEAFGFDAVRVKGDDIEAIDKAIKTFQDSNSVRPKCIVLDSIKGQGVKELEELASNHHLRPDLQQKTMLERALISLRESLEVVE

SEQ ID 519

GTGGCCACTGTGTCAACAGGCTCTCTTATATTCATCGTCAAAAAGAATCCACCAATGATGTCCAAACTAGTTTTTTTCTGGCAAAATAGAGAAAAA
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GAGGTTTTACTTATGACATTTGATGCAATTGACCAGTTGGCAGTAAACACTGTCCGCACCCTATCAATGGATGCCATTCAAGCGGCAAATTCTGGA
CACCCAGGACTTCCAATGGGGGCAGCACCTATGGCCTATGTTCTTTGGAATCACTTCATGAACATCAATCCCAAAACAAGCCGTAATTGGTCAAAC
AGAGACCGTTTTATCCTATCAGCAGGTCATGGAAGTGCCATGCTTTATAGCTTGTTACACTTAGCTGGTTATGATTTATCTGTAGAAGATTTAAAG
AACTTCCGTCAATGGGGTTCTAAAACACCAGGTCACCCAGAAGTGAACCACACAGACGGTGTCGAAGCAACCACAGGACCTCTTGGTCAAGGGACC
GCAAATGCCGTTGGGATGGCCATGGCAGAAGCTCATCTAGCAGCTAAATTTAACAAACCAGGCTTTGACATCGTTGATCACTACACATTTGCTTTG
AATGGTGACGGTGACCTTATGGAAGGGGTCAGCCAAGAAGCAGCAAGTATGGCAGGACATTTAAAACTTGGGAAATTGGTCTTGCTATATGATTCA
AACGACATCTCTCTTGATGGTCCAACCTCTATGGCTTTCACAGAAGATGTGAAAGGACGTTTCGAAGCTTATGGTTGGCAACATATCCTTGTGAAA
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CAAGATTTTGAAGTGCCTGCTGAAGTAACAGAGCGCTTTGCTCAAGGTCTTCAAGCGCGTGGTGAAAAAGCAGAACAAGCCTGGAATGACTTGTTT
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GAAGGCATTCATGTGCGTGTCGTATCTATGCCATCACAAAATATCTTTGACGAACAGTCAGCAGAGTATAAAGAAAGCATCCTACCAGCAGCTGTG
ACTAAACGTCTCGCTATCGAAGCAGGTTCAAGCTTTGGCTGGGCAAAATATGTCGGCCTATCAGGAAAAACATTGACCATTGACACTTGGGGTGCT
TCAGCTCCAGGAAATCGTATCTTCGAAGAATATGGTTTCACTGTGGCAAATGCAACTGAGTTATACAAATCACTC

SEQ ID 520

VATVSTGSLIFIVKKNPPMMSKLVFFWQNREKEFRDFGGFSEKSVYFCDTIDNRKRLILVVINREVLLMTFDAIDQLAVNTVRTLSMDAIQAANSG
HPGLPMGAAPMAYVLWNHFMNINPKTSRNWSNRDRFILSAGHGSAMLYSLLHLAGYDLSVEDLKNFRQWGSKTPGHPEVNHTDGVEATTGPLGQGI
ANAVGMAMAEAHLAAKFNKPGFDIVDHYTFALNGDGDLMEGVSQEAASMAGHLKLGKLVLLYDSNDISLDGPTSMAFTEDVKGRFEAYGWQHILVK
DGNDLEEIAAAIEAAKAETEKPTIIEVKTIIGFGAEKQGTSAVHGAPLGAEGIAFAKKAYQWTHQDFEVPAEVTERFAQGLQARGEKAEQAWNDLF
AAYEAEYPELAAEYQKAFTNEAAQVELEAHELGSSMASRVSSQQAIQQISEQVASFWGGSADLSASNNTMVKAETDFQPGHYEGRNIWFGVREFAM
AAAMNGIALHGGTRVYGGTFFVFSNYLLPAVRMAALQNLPTVYVMTHDSIAVGEDGPTHEPIEQLASVRSMPNLNVIRPADGNETNAAWKRAIAET
DRPTMLVLTRQNLPVLEGTKELAEDGLSKGAYILSEAKGDLDGILIATGSEVKLAMDTQEALEAEGIHVRVVSMPSQNIFDEQSAEYKESILPAAV
TKRLAIEAGSSFGWAKYVGLSGKTLTIDTWGASAPGNRIFEEYGFTVANATELYKSL

SEQ ID 521

ATGAGATGTTCAACCAAAGAAATGAGGCTTGTCTATCGTGATTTCCTCCTTCAAGCTAATCAAGAAAATAAACAAATTACCGTTTTAGAAGCCGAT
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GCAGGGCTCGCCATTAAAGGTTACAAGCCATACCTTCATACTTTTGGTCCTTTCGCGTCAAGGCGTGTCTTTGATCAAGTATTCTTATCGTTAGGT
TACTCACAATTATCAGCTACGATTATTGGCTCAGATGCAGGAATTAGCGCAGAAATGAATGGCGGAACTCATATGCCTTTTGAAGAGTTAGGTCTA
CTAAGGTTAATTCCCAAAGCGACTATTTTTGAGGTTAGTGATGATATTCAGTTTGAAGCAATTTTAAAACAAACATTAAGTATTGATGGCCTAAAA
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TTAGAGGAGTATGGACTCGCTGTTAAAGATATAGTACAGCATTGCAAATCAATTTATAAATCA

SEQ ID 522

MRCSTKEMRLVYRDFLLQANQENKQITVLEADLSSSMSTNALASEFGKRYINLGIMEAEMVGLAAGLAIKGYKPYLHTFGPFASRRVFDQVFLSLG
YSQLSATIIGSDAGISAEMNGGTHMPFEELGLLRLIPKATIFEVSDDIQFEAILKQTLSIDGLKYIRTIRKAPTAVYEGREDFSKGFIQLRQGKDI
TLVASGIMVSRAIEAADYLKELGIEASVIDLFKIKPLPEELKPLLIDQSIVTIENHNRIGGIGSALCEWLSMEKDTTVSRMGIDERFGQVGQMEYL
LEEYGLAVKDIVQHCKSIYKS

SEQ ID 523

ATGCTAGATAAAATTAAAACAATACCTTTCCAAGCTCGCATAACGACCACCCCTTTATTTTTAGTAAGGATAAAATACCACAAGATACTTATACAA
AACTTAAAAATTTCAGAAAATAACAAAAAGGCAACTCCAATGTTGCCTTTTTGTTATGATTTA

SEQ ID 524

MLDKIKTIPFQARITTTPLFLVRIKYHKILIQNLKISENNKKATPMLPFCYDL

SEQ ID 525

TTGACAAGTTTATCGCTAACATTCCTCTTATCAACCAAATTTAGGATACTTGAAAGTTACTTTCAAGGTATTGAAAATATGTATTTTTACCACAAG
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SEQ ID 526

MTSLSLTFLLSTKFRILESYFQGIENMYFYHKVMAVFSMILLLLHKIGLGQGGHGSEFAKTIGSAGLYLFLSIVFVAYFGNFLKYEIWRFIHRFVY
LAYILGLVHTFMILGDRILGNTLLSLIVLGYAVIGVISGFYIIFLYSRMRFRRVGYVQKVTHLNHDTTEIEIAMKRPYRYDYGQFTFFKIYQAGFE
SAAHPFSISGGHDRVIFLTVKASGDYTKSIYKQLKVGTKIALDRAYGHMLFDKDKKEQVWIAGGIGITPFISFIRENSILTKRVDFFYTFSNQDNL
IYQDMLESYAKANPNFKLHLNNSSLKGRLDFSQSVFEGQPTIFMCGPTSMTSTYAKVFRQKDAKSRLVYEGFSFRDSWLSIFLLKTFDKVYSNLIK

SEQ ID 527

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AACTTATTAGCATACCTACGTCGTACAGATGTTAACCGTTACCGTGAATTGATTCAATCACTTGGACTTCGTCGT

SEQ ID 528

MAISKEKKNEIIAQYARHEGDTGSVEVQVAVLTWEINHLNDHIKQHKKDHATYRGLMKKIGHRRNLLAYLRRTDVNRYRELIQSLGLRR

SEQ ID 529

ATGGCAATCTCAAAAGAGAAAAAAAAATGAAATCATTGCTCAATATGCACGTCATGAAGGCGATACAGGTTCAGTTGAAGTTCAAGTAGCAGTTCTT
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AACTTGTTGGCATACCTACGTCGTACAGATGTTAACCGTTACCGTGAGTTGATCCAATCTCTTGGACTTCGTCGT

SEQ ID 530

MAISKEKKNEIIAQYARHEGDTGSVEVQVAVLTWEINHLNSHIKQHKKDHATYRGLMKKIGHRRNLLAYLRRTDVNRYRELIQSLGLRR

SEQ ID 531

ATGGAGAATAATATGTCAAAACAAGTCTTTGAAATGATTTTTGCTGGAAAAAAATTAGTTGTTGAAACTGGCCAAGTGGCTAAACAAGCAAATGGA
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TACGAAGAAAAAATGTATGCTGCTGGGAAATTTCCGGGTGGCTTTAACAAACGTGAAGGGCGTCCAAGTACGGATGCTACCTTAACAGCACGTCTT
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SEQ ID 532

MENNMSKQVFEMIFAGKKLVVETGQVAKQANGSVVVRYGDSTVLTAAVMSKKMSTGDFFPLQVNYEEKMYAAGKFPGGFNKREGRPSTDATLTARL
IDRPIRPMFAEGFRNEVQVINTVLSFDENASAPMAAMFGSSLALSISDIPFNGPIAGVQVAYVDGNFIINPTAQEQEASALELTVAGTKEAINMVE
SGAKELSEEIMLEALLKGHEAVCELIAFQEEIVTAIGKEKAEVELLQVDPELQAEIIATHNIALQAAVQVEEKKAREAATEAVKEVVIGEYEARYA
EHEEYDRIMRDVAEILEQMEHAEVRRLITEDKIRPDGRRVDEIRPLDAEIDFLPQVHGSGLFTRGQTQALSVLTLAPMGEAQIIDGLTPEYKKRFM
HHYNFPQYSVGETGRYGAAGRREIGHGALGERALEQVLPRLEEFPYAIRLVAEVLESNGSSSQASICAGTLALMAGGVPIKAPVAGIAMGLISDGT
NYTVLTDIQGLEDHFGDMDFKVAGTREGITALQMDIKIEGITPQILEEALAQAKKARFEILDVLHGAIAEPRPQLAPTAPKIDMIKIDVDKIKVVI
GKGGETIDKIIAETGVKIDIDEEGNVSIFSSDQAAIDRTKDIIASLVREAKVGEVYHAKVVRIEKFGAFVNLFDKTDALVHISEIAWTRTANVADV
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SEQ ID 533

ATGTCAAAACAAACCTTTACAACAACATTTGCAGGGAAACCCCTTGTTGTTGAAGTTGGTCAAGTCGCTAAGCAAGCCAATGGGGCAACCGTTGTT
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SEQ ID 534

MSKQTFTTTFAGKPLVVEVGQVAKQANGATVVRYGDSTVLTAAVMSKKMATGDFFPLQVNYEEKMYAAGKFPGGFMKREGRPSTDATLTARLIDRP
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LATIMRDVAEILEQMEHAEVRRLITEDKIRPDGRKIDEIRPLDAVVDFLPKVHGSGLFTRGQTQALSVLTLAPMGETQIIDGLAPEYKKRFLHHYN
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LTDIQGLEDHFGDMDFKVAGTREGITALQMDIKIAGITPQILEEALAQAKKARFEILDVIEATIAEPRPELAPTAPKIDTIKIDVDKIKVVIGKGG
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EDVDVKVIKIDEKGRVDASMKALIPRPPKPEKKEEKHD

SEQ ID 535

ATGACAAGTACAAACGAGTTAGACATTAGATTGCGTGCTTTTATCAATGCACCGGATAATTTTTTAGATAGTATAGGTCTTGTGAATGCCTTGCAC
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TTCAAAGAGGAGCAAGAAAGTGCTCGAGATATGTTTGGGAGAGTCGTCGTAGTTTAGACGTTCTTGATGAAGCTATTTCACATGGCTTAGCAGGA
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GATGATACCTTTGGAGTAGCCATCAATCCATTTGATGAACAACAAGTTTTAGTTGATTGGTCTGATGTAGAAAACGAT

SEQ ID 536

MTSTNELDIRLRAFINAPDNFLDSIGLVNALHHSTVWASKEPYAIQVDGQEVVPVFTDITDLNHFKEEQESARDMFWESRRSLDVLDEAISHGLAG
LVYNLKKEGDFGNSTIFYCEDMVQFMNNYTTILNQLLNEDNIVADIMDKTYLVPAFVHPREEGSFDRLFPTMSTPEGKSYVPVFSNLLSFEKWYNH
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SEQ ID 537

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SEQ ID 538
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SEQ ID 539
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SEQ ID 540
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YYSSKL
SEQ ID 541
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SEQ ID 542
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SEQ ID 543
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SEQ ID 544
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SEQ ID 545
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SEQ ID 546
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SEQ ID 547
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SEQ ID 548
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SEQ ID 549
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SEQ ID 550
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SEQ ID 551
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SEQ ID 552
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SEQ ID 553
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SEQ ID 554
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SEQ ID 555
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CGC
SEQ ID 556
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SEQ ID 557
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SEQ ID 558
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SEQ ID 559
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SEQ ID 560
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SEQ ID 561
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SEQ ID 562

MTFKILTDSTSDLDEKWAQEHNVDIIGLTIELDGKTYETVGDEKITSDFLLERMQEGAKPTTSQINVGQFEEVFSTYAENDHALLYLALSSHLSGT
YQSATIAREMVLDKYPDAQIEIVDTMAASCGEGVLAMLATKERQEGKSLEEVKQKIESLLPKLNTYFLVDDLNHLMRSGRLSKGAAIIGSVAKIKP
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SEQ ID 563

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ATTAATGTGGGAGAGTTTGAGAAGGTTTTTCGTGAACATGCTAGGAACAACAAAGCACTGCTTTATCTTGCTTTTTCTTCGGTTTTATCGGGTACC
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SEQ ID 564

*MTFTIMTDSTADLNQTWAEDHDIVLIGLTILCDGEVYETVGPNRISSDYLLKKMKAGSHPQTSQINVGEFEKVFREHARNNKALLYLAFSSVLSGT*
YQSALMARDLVREDYPDAVIEIVDTLAAAGGEGYLTILAAEARDSGKNLLETKDIVEAVIPRLRTYFLVDDLFHLMRGGRLSKGSAFLGSLASIKP
LLWIDEEGKLVPIAKIRGRQKAIKEMVAQVEKDIADSTVIVSYTSDQGSAEKLREELLAHENISDVLMMPLGPVISAHVGPNTLAVFVIGQNSR

SEQ ID 565

TTGTTGATGAAAGTTTTTGGAAAATGTTTTTGTTGCTGGCGCATTTGCCCTCATAGGAATAACTATTTTATTGATGCTTTTACTAGGAAGGTTGAT
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AAGGACAGA

SEQ ID 566

MLMKVFGKCFCCWRICPHRNNYFIDAFTRKVDIATYFSRGDDAILAVIGISLIAMGISVYYHKYKDR

SEQ ID 567

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SEQ ID 568

MFTPFVRPRNLSNTLVDRNIHTCKQKRIRIGEIMNKTTFMAKPGQVERKWYVVDAADVPLGRLSAVVASVLRGKNKPTFTPHTDTGDFVIVINAEK
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SEQ ID 569

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CTTTCTGCAGTAGTTGCTAGCGTACTTCGCGGAAAAAACAAACCAACTTTCACACCACATACTGATACAGGTGATTTTGTTATCGTTATCAACGCT
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GTCTTCGTTGGCGGTGAGCATACTCACGCAGCACAACAACCAGAAGTACTTGACATCTCAGGACTTATC

SEQ ID 570

LFTPFERPRNLPNTFDGTEHPSPCKQILRIRIGEIMNKTTFMAKPGQVERKWYVVDAADVPLGRLSAVVASVLRGKNKPTFTPHTDTGDFVIVINA
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SEQ ID 571

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GTTAACGTTGTAGGTGGTGGATATGCAGGTCAATCAGGTGCGATCCGTCATGGTATCTCACGTGCACTTTTAGAAGTTGACCCAGATTTCCGCGAT
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SEQ ID 572

MAQAQYAGTGRRKNAVARVRLVPGTGKITINKKDVEEYIPHADLRLVINQPFAVTSTQGSYDVFVNVVGGGYAGQSGAIRHGISRALLEVDPDFRD
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SEQ ID 573

ATGGCACAAGCACAATATGCAGGTACTGGCCGTCGTAAAAACGCTGTTGCACGCGTTCGTTTGGTTCCAGGTACTGGTAAAATCACTGTTAACAAA
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TCATTGAAACGCGCTGGCCTTCTTACACGTGACGCACGTATGGTTGAACGTAAAAAACCAGGTCTTAAGAAAGCTCGTAAAGCTTCACAATTCTCA
AAACGT

SEQ ID 574

MAQAQYAGTGRRKNAVARVRLVPGTGKITVNKKDVEEYIPHADLRLIINQPFAVTSTEGSYDVFVNVVGGGYGGQSGAIRHGIARALLQVDPDFRD
SLKRAGLLTRDARMVERKKPGLKKARKASQFSKR

SEQ ID 575

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SEQ ID 576

MSIHKYPSKKAKNGYLYFVKIYMVKDSQRADHIKRGFRTRKEAKDYEARLIYLKASGKLEEFIKPTHKTYNEIFEKWYQAYQDMVEPTTASRTLDM
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KHYALFRLLAYSGLRKGELYALKWADIDFQTETLSVDKSLGRLDGQAIEKGTKNDFSVRKIKLDSETISILQEWKSISQKEKAQLAVAPLSIEQDF
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SEQ ID 577

ATGGAAAGGTTTATGATCATGAAAATAACAGAACATAAGAAGAAAAACGGTACAATCGTTTATCGTGCTAGTATTTATCTAGGCATTGACCAAATG
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AATAATTTA

SEQ ID 578

MERFMIMKITEHKKKNGTIVYRASIYLGIDQMTGKRVKTSITGRTRKEVNQKAKHAQFDFLSNGSTIKRKVVIKTFKELSHLWLETYKLTVKPQTY
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HLETSQHKRYNLYFDAVLYQLLLSTGLRIGEACALEWGDIDLENGTIAINKTYNKNLKFLSTAKTQSGNRVISVDKKTLRSLKLYQMRQRQLFNEV
GARVSEVVFATPTRKYFNASVRQSALDTRCKEAGIERFTFHAFRHTHASLLLNAGISYKELQYRLGHANISMTLDTYGHLSKGKEKEAVLYYEKAM
NNL

SEQ ID 579

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AATTCAAAAATAGCAAATTCAACAATCAAAGATACAAATTTATTAAGTTTTTTGAACAAGTCAAAAAGGATATGGGTCAAGATTATTTTTCTACT
CTTGAAACCCTTGAAAAAGTTAGCAAAAAAACTCTTTTCAACTCTCCCATACGTGACAGACTTGAGGAAATTAAGCAAGAAAAAATCAAGCTTAAC
CAGAAAATTGATGAACTTGAAGCAGAGGCTAAAAATCTTCGAAAAACTCTTGATAAAGAAGTAAAAGAGAGATTAGAACTTTTAAAAAAA

SEQ ID 580

MYNRLKELRKDKGLTQADLAKVINTNQSQYGKYENGKTSLSIENSKILADFFGVSIPYLLGLDNNSKIANSTIKDTNLLSFFEQVKKDMGQDYFST
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SEQ ID 581

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ATTGAGAGAGGAGAGGTTGCCTTAATGGCAGATGTTCTTGTGCAGTTTTATAAACTCTATAACGTCAGTATTGATTATTTATTAGGGCAAACAGAT
TATCCGTATCGTTTTCATAATAAA

SEQ ID 582

MYPRIRNLREDNDFTQKFVANLLSFSHANYAKIERGEVALMADVLVQFYKLYNVSIDYLLGQTDYPYRFHNK

SEQ ID 583

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GATTATATGGTTTCTCCATTTGTTCGAAAACGAGTTAAACGTGAAATGACTGAAGAACAACGAGAGGAAGCAAGAAAAAGAATGGCAAGATTACAT
TCTAAGTCTGAAATA

SEQ ID 584

MAYTLEERETIVRYDEMDNCWYFESNVRKHITKIMKTIDSCQILGQEKEDDRIIWIHAKLTNLDDYMVSPFVRKRVKREMTEEQREEARKRMARLH
SKSEI

SEQ ID 585

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GCAGGCATGCCACATATGGTTATTGACGGAGTGACTCTGTACGATAAGCGCAAGGTCGCTCAATGGCTACAACAATTTGAAAGA

SEQ ID 586

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SEQ ID 587

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SEQ ID 588

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SEQ ID 589

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SEQ ID 590

MIKIYFGKDITLNQAIQSRLDSYQIDYQAFSSKDIDAKTLMEWLFRSTDIFELLSTKMLKYKLNTQITLSQFVRKILKDVNSTLKLPIVVTDEVIY
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SEQ ID 591

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SEQ ID 592

MCTSEVHLLHPFFGKFGWSKMKMVRLRRGRLGATPPRMSFYVGLCADKKIGAVRRPPKRKEVCLKLKVSLDNITMTAYIKSKKYLAMKQLIETHLA
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TKEFRSSTGTLETKYLGAPRSEKQVRLYNKKKEQLQNGTDKDKDFASQFKHWWRLEFQLRSRSIDEIFEVIDTIIFKPFNLKGLSIETQIYLTALI
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SEQ ID 593

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SEQ ID 594

MLKIQYYQGVTRSKMRIKDYADSLGVSSQSIYKRIRSPKYKERLKGHLYRDNQKVENLDLIGIKILEDYHFENDVIELEKTLGDIQEEFEQEKKGM
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SEQ ID 595

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AATAGT

SEQ ID 596

MSYVVARMAKYKSGQLTAIYNHNERIFKNHSNKEIDVEKSHLNYELTNRDQAQNYHKQIKEHINENRLSTRGVRKDAILCNEWIITSDKTFFDSLD
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SEQ ID 597

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SEQ ID 598

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SEQ ID 599

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SEQ ID 600

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SEQ ID 601

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SEQ ID 602

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SEQ ID 603

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SEQ ID 604

LDYKKYQIIYAPDVLEKLKEIRDYISQNYSSTSGQRKMEQIISDIEKLEVFPEVGFDADEKYGSKIIHYHSTKGYTLSKDYIVLYHIEGEENRIVI
DYLLPTQSDYIKLFK

SEQ ID 605

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SEQ ID 606

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SEQ ID 607

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SEQ ID 608

MTTVKKNRAVTFQANKELVSEAMTVLNKKNLTLSSALRLFLQNVVVTNEVDLLTEEELEKEKLFKQFQAEINKNIEDVRQGKFYTSEEVRAELGL

SEQ ID 609

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AAA

SEQ ID 610

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K

SEQ ID 611

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SEQ ID 612

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SEQ ID 613

ATGGCTAAGCATCCTGAATATTTTGTGAATTTTCGACATAAAGAGGATAATGTAACTTGGTGGAACGATTTTAATAAACTAGATGATAAAGATTAT
GGTACCGTGAAATGGGTAAATGGTAAAAGTCATAAAATAGAGAGTTGGAAATTTACTGATGATGGTAAGTTAAAAGATGAAAAAGGTAACATCGTA
AATCCTAAGTCACCAGCTGTTCAGTCTGTTCTTTATGAAGAAGTTCATTTTCAAAAAGCTAAAGCTAAATTAAAAAAATCTGGAGGCAAACTTAGT
CATAGTGAAAAAGTATATTTAGATTCTGAACAGGCTATATTTATTGCTAACGGTTTAACCACGGCATCTCAAACAGCTTCTGATGATATCAAGAAG
AATGCTGAATTAGTTAAAGAAAAAGCATCAGAACTATTTGCAAAAACTAAAGTGATGCCTCCTGGTATAACAGATTTAAGTCCGGAAGAATTAGCT
GATACATATAGTGAGGGCGGAGTTAGAGAGGACACCATAGTAACACCAATTGAAACTTTCTTTGATGAAAAAGTTACTAATGCACAAGAGATTACA
ACTTCATATATTAATCTTCAAAAACAAATTGAATCTGGTGTCCAAAAATTGCTAGAAGAGGACTCCAAATTAGCAGGAGAATTTAAGGAATGGTCA
CAGTAC

SEQ ID 614

MAKHPEYFVNFRHKEDNVTWWNDFNKLDDKDYGTVKWVNGKSHKIESWKFTDDGKLKDEKGNIVNPKSPAVQSVLYEEVHFQKAKAKLKKSGGKLS
HSEKVYLDSEQAIFIANGLTTASQTASDDIKKNAELVKEKASELFAKTKVMPPGITDLSPEELADTYSEGGVREDTIVTPIETFFDEKVTNAQEIT
TSYINLQKQIESGVQKLLEEDSKLAGEFKEWSQY

SEQ ID 615

ATGGTCACAGTACTAGATCAAAATGAAAACAAAATTAATAGTCTAAAAATAAACCTAGGGAAATTGGAAGATAATTATCATCGCGAAAATATGGAG
ATAGAAGATAAATTATATAGCCTTGAGGATAAAAAGAACGAGTTAGAGACTTATTTACAAGAAGTCTATGAAGAGACAAGTCACCTTTTGAGACAA
AATGATTCAGATGGTTCGACTTTTATGAGTTTAAATCGAATAATTGAAAGTTATCAAATGGAATTAATTGATGAATATGAAAACTATAAACAGACT
ATCATTGTCCAAGAGGAAAATAGTCGGACACAGTTTCTAAAAGACCGAGTAAAATTAGAAAATGACATTTCTAGTTTAGAAGGAAGAAAATACTAC

SEQ ID 616

MVTVLDQNENKINSLKINLGKLEDNYHRENMEIEDKLYSLEDKKNELETYLQEVYEETSHLLRQNDSDGSTFMSLNRIIESYQMELIDEYENYKQT
IIVQEENSRTQFLKDRVKLENDISSLEGRKYY

SEQ ID 617

ATGAGTTTAATAGGCGCTGTATTGAAAGGAACCAAAGAAGACAAAGAATTCAAAAAGCAAATTCAAAGAGCTTTAGTAAGGATTGTCTATGCCCCT
GAAATAGTAGAAGAAGCTGATTCTATTAAGATGACTTATAGTGACAAGATTGATAATGTTTCTGAGACGGCCAAATCATCAATTAAAACGATAGCA
AATCAAATAGATTCAGGACTTGTAGGACAATTTGGGGAAAAAGTAAAGGCACAGGTAGATTTAAATAAAGGTAGTTATGATGATTTA

SEQ ID 618

MSLIGAVLKGTKEDKEFKKQIQRALVRIVYAPEIVEEADSIKMTYSDKIDNVSETAKSSIKTIANQIDSGLVGQFGEKVKAQVDLNKGSYDDL

SEQ ID 619

ATGAAGGATAACAAAGTTTATTATTTACATTTTGGTAAAGCAATAGATAAAAATGAAGCTAAAAATGATAAGTATCTCAATCAAATTATAAATAAT

SEQ ID 620

MKDNKVYYLHFGKAIDKNEAKNDKYLNQIINN

SEQ ID 621

ATGATGGAGGAATTTTGTATGGTAAGTACTCAATATATGAAAGTAACCTTACGAGAAAAATTCCCAGATAAATTAACATATGTTGATTTAGAAGAA
CTTGTGATA

SEQ ID 622

MMEEFCMVSTQYMKVTLREKFPDKLTYVDLEELVI

SEQ ID 623

GTGAATGTGACTCCTCAAGAAAAATGTCGGAAGAAGACCTTTGCTTTTTGTCGGATTACCTCTTTCAAAAGGATAGTTGGGAAATTAGTGACTATA
TTT

SEQ ID 624

MNVTPQEKCRKKTFAFCRITSFKRIVGKLVTIF

SEQ ID 625

ATGTTTAAATATGTCCCTATTTTTAGGGAATTTCGACTTAATCGACAGTTTTCTCTTAAACAGGTTGCTTCAAATGAACTTTCTGTTTCTCAGTTA
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ATGAAGCAAGCTATTTTTTGCTTCCAAGCAATTGGTTCTAAACATCATGTTGAAAATTTTCAGGAACACTTTAATAGGGTAACAAGATTA

SEQ ID 626

MFKYVPIFREFRLNRQFSLKQVASNELSVSQLSRFERGESDLSLTKFLGALEAIDLSISEFMDRVNKYQKSDQISLMSQMAQYHYQRDVAGLEKMI
SVEEGKLKKDSSDIRCRLNIVLFRGMICECDSSRKMSEEDLCFLSDYLFQKDSWEISDYILIGNLYRYYNTRHICQLVKEVINQKEYYRDIYTNRN
VVEATLLNVVETLIERRALEEATFFLEKVEALLNNERNAYHRIILLYEKGFLAYAKGDSRGIQSMKQAIFCFQAIGSKHHVENFQEHFNRVTRL

SEQ ID 627

GTGAAAGTGGGAAAAATGGAAAAAGAACTCGGAAAAACCTTAAGGCGATTACGTAAGGGTAAGCAGGTTAGCATTTCTTTTTTAGCAGATGAATAC
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GACGAATTTGTTTCGGCTCATTCCAAGACGCATACGCATTTTTTCACGCTCTTAAGTCAGGCGAGAAAATGTTATGCTGAGAAAAACGTGGTTAAA
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CAAGAAGAATTGACTCGCCTCACAGATTATTTATTTAAAGTGGAACAGTGGGGATATTATGAAATCATTCTTCTGGGGAATTGCTCGCGCTTCATG
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CAGATTTTTAAGTATCTTGGAGAGGACTCATTGTATTATAGTTATAAGGAACATTACCGTCAAATAGTGCTGGGAGGTAAGGGGGATGAGGACTGG
TCTGAGGCAGATTTA

SEQ ID 628

VKVGKMEKELGKTLRRLRKGKQVSISFLADEYLSKSQISRFERGESEITCSRLLNLLDKLNITIDEFVSAHSKTHTHFFTLLSQARKCYAEKNVVK
LTKLLKDYAHKDYERTMIKAILFSIDSSIAPSQEELTRLTDYLFKVEQWGYYEIILLGNCSRFMNYNTLFLLTKEMVASFAYSEQNKTNKMLVTQL
SINCLIISIDHSCFEHSRYLINKIDLLLRDELNFYEKTVFLYVHGYYKLKQEEMSGEEDMRQALQIFKYLGEDSLYYSYKEHYRQIVLGGKGDEDW
SEADL

SEQ ID 629

ATGAATATTAATGGTATAAAATTACTATCTAGTCGAGCAGTCAGTAAACTTGGTGATGTGTTTTATGATTATGGAAATAGTACTTGGATTGCTTCG
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CGCTTTCAACGAAGAAAAATTTTACTAATAACAGATGCTATCTGTGCTATCATGTGTTTCTTACTTTCTTTTATTGGAGATGATAAAGTAATGGTG
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GAAAAGGTAGCGATAAAAAATATTTTAGCTGATATTGCAGATGGATTTACTTACATCAAAAAAGAAAAAGAAATTATGTTTTTTCTAATTATTGCT
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AATATTCATTTTTTCAGTCAGGTACAAATCAGGGTCGATGAAGCGTATATGGGGCGTGTGATGTCGACTATATTTACTATTGCTATTATGTTTATG
CCTATAGGAACACTATTTATGACTATCTTTTCATTTGCCTTATCAAATGTTAGCTTTATTGTTATAGGATGTGCCATTGCTATATTGGGAGGATTA
GGATTTAGCTATAGTAAAAAACAATTT

SEQ ID 630

MNINGIKLLSSRAVSKLGDVFYDYGNSTWIASMGGLGQKILGIYQIVELLVSIVLNPFGGALADRFQRRKILLITDAICAIMCFLLSFIGDDKVMV
YGLIVANAILAVSNAFSSPAYKSYIPEIVDKADIITYNANLETIVQIISVSSPVLGFLIFNNFGIRITLIVDAITFLISFLFLYAIKVERVQLSKQ
EKVAIKNILADIADGFTYIKKEKEIMFFLIIAALLNTFLAMFNYLLPFTNSLLKTSGAYATILSISAIGSIIGALIARKIKSSINSMLSMLVFSSL
GVIVMGFPSLFELPIWIPYSGSFLFNSLLTMFNIHFFSQVQIRVDEAYMGRVMSTIFTIAIMFMPIGTLFMTIFSFALSNVSFIVIGCAIAILGGL
GFSYSKKQF

SEQ ID 631

ATGAACAATAGGAAAAAAAATATTCAATATTTAGTGTATAGTAAAGTTATATATCGAATTGGCGATGTTATGTTTGATTTTGCTAACAATACTTTT
CTTGCTGGGCTTAATCCAGCGTCTCTATCATTAGTTGCAGTATATCAGTCTCTAGAAAGTGTCATAGGTGTTCTATTTAATTTATTTGGTGGAGTC
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ACAATAACTATTCTTTTTATGCCTATTGGGACTGGCTTTTTCTCGGTGGCATTAAATCCTAACAATAGCTTTAATCTTTTTATTATTGGTTCGTGC
ATTACTACATTGTCATTAGTATTTAGAATATTATTTAAAAAGTATAATATTCGT

SEQ ID 632

MNNRKKNIQYLVYSKVIYRIGDVMFDFANNTFLAGLNPASLSLVAVYQSLESVIGVLFNLFGGVIADSFKRKKIIITTNILCGTACLVLSFLTKEQ
WLVYAIVLTNVILAFMSAFSSPSYKAFTKEIVKKDSISQLNSLLETTSTVIKVTVPMVAIFLYKLLGIHGVLLLDGLSFLIAALLISFILPVNDEV
VIKEKVTIREIFNDLKIGFKYVYSHKSIFIITVLSALVNFFLAAYNLLLPYSNQMFGEISTGLYGTFLTAEAIGGFIGAILSGFVNKELSSMRLIL
FLSLSGLMLMLAPPFYIMFHNAIILALSPALFSLFLSIFNIQFFSLVQKDVDNDFLGRVFGIIFTITILFMPIGTGFFSVALNPNNSFNLFIIGSC
ITTLSLVFRILFKKYNIR

SEQ ID 633

ATGGGAATCGCAAATGTCATCCAAACCATTCCTTCTTTAGCTATGATCTCTATCATTATGTTAGGTCTAGGGCTAGGTATTAAAACAGTAGTTGCA
ACTGTCTTTCTTTATTCTCTTCTGCCAATCATCACAAATACTTACACTGGTATTAGAAATGTTGACTCCGACTTACTAGATGCTGCTAAAGGAATG
GGCATGACTAAGCGTCAACGTTTATTTATGGTTGAGTTACCACTATCTATTTCCGTTATCATGGCTGGACTTAGAAATGCCCTTGTTGTAGCAATT
GGTATTACAGCCATTGGTGCTTTCGTCGGGGGAGGCGGACTTGGAGATATCATCATAAGAGGAACTAATGCAACAAATGGTGGTGCTATTATCTTA
GCAGGATCTCTTCCAACAGCCCTTATGGCAATTTTCTCTGATTTAATCCTAGGCGGTATCCAACGCATGCTTGAACCAAGAAAA

SEQ ID 634

MGIANVIQTIPSLAMISIIMLGLGLGIKTVVATVFLYSLLPIITNTYTGIRNVDSDLLDAAKGMGMTKRQRLFMVELPLSISVIMAGLRNALVVAI
GITAIGAFVGGGGLGDIIIRGTNATNGGAIILAGSLPTALMAIFSDLILGGIQRMLEPRK

SEQ ID 635

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ACTAGCTTCTTATATGAAGCCCTTAAATCTGGAGATATTGATATGTATCCTGAATTTACAGGAACCATAACATCAAGTCTTTTACGCGACAAACCA
CCTTTGTCTAATGACCCTAAGCAGGTCTATGAGGATGCTAAAAAAGGCATTGCTAAGCAAGATAAACTGACCCTTCTCAAGCCATTTGCTTACCAA
AATACGTATGCTGTTGCTATGCCAGAAAAATTGGCTAAGGAATATCAGATTGAAACCATTTCTGATTTAAAAGCGCATGCTGATACTTAAAGGCC
GGTTTTACTTTGGAATTTAAGGACAGAGCAGATGGCTATAAGGGAATGCAATCTCAATATGGATTACAGCTATCTGTGGCGACGATGGAGCCAGCT
CTTCGTTATCAAGCAATTCAATCAGGAGATATCCAAGTAACAGATGCTTACTCTACGGATGCTGAAATTACGAAATACCATTTGAAAGTTTTAAAG
GATGATAAACAGTTGTTTCCACCTTATCAGGGAGCTCCTTTGATGAAAACTTCCTTATTAACAAAACATCCAGAATTAAAAGGCATTCTTAATCAA
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SEQ ID 636

MLLWSIYLEVMSMPSLFVTFQNRFNEWLAALGEHLQISLLSLMIALLIGVPLAALLSRSKRWSDIMLQVTGVFQTIPSLALLGLFIPLMGIGTLPA
VTALVIYAIFPILQNTITGLNGIDPSLVEAGIAFGMTKWERLKTFEIPIAMPVIMSGVRTSAVMIIGTATLASLIGAGGLGSFILLGIDRNNANLI
LIGAISSALLAIIFNSLLQYLEKASLRRIMISFGITLLALLASYTPMALSQFSKGKDTVVIAGKLGAEPDILINLYKELIEDQSDISVELKSNFGK
TSFLYEALKSGDIDMYPEFTGTITSSLLRDKPPLSNDPKQVYEDAKKGIAKQDKLTLLKPFAYQNTYAVAMPEKLAKEYQIETISDLKAHADTLKA
GFTLEFKDRADGYKGMQSQYGLQLSVATMEPALRYQAIQSGDIQVTDAYSTDAEITKYHLKVLKDDKQLFPPYQGAPLMKTSLLTKHPELKGILNQ
LAGKITEKEMQDMNYEVSVKGADANKVARDYLLKTGLIQK

SEQ ID 637

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YWMYWMYTYCMAMMWWAWKGKWRK

SEQ ID 638

MLKKSHFLQIFTLCLALLTISGCQLTDTKKSGHTTIKVAAQSSTESSIMANIITELIHHELGYNTTLISNLGSSTVTHQALLRGDADIAATRYTGT
DITGTLGLKAVKDPKEASKIVKTEFQKRYNQTWYPTYGFSDTYAFMVTKEFARQNKITKISDLKKLSTTMKAGVDSSWMNREGDGYTDFAKTYGFE
*FSHIYPMQIGLVYDAVESNKMQSVLGYSTDGRISSYDLEILRDDKKFFPPYEASMVVNNSIIKKDPKLKKLLHRLDGKINLKTMQNLNYMVDDKLL*
EPSVVAKQFLEKNHYFRXXXXXXXXXXFXXFXXXXXXXXX

SEQ ID 639

ATGGTCAATTTCTTATCACAGTATGGCATGCAAATATTAGTAAAAACATGGGAACAAGTCTATATCTCATTCTTTGCTATAGCACTTGGGATTGCA
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GCCTTATTAGCTTTAATGATTCCATTGTTTGGAATTGGAAAAATCCCAGCTATCGTTGCTTTATTTATTTATTCCTTGCTTCCTATACTAAGGAAT
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CTTGGTGATCTCATTTTTAGCGGGTTAAATCTTTTTCAGTCCAAATTAATTCTAGGGGGCACAATTCCTGTTATTATCCTGTCACTTATTATAGAT
TATCTTTTAGGATTACTGGAAACAGCTCTAACGCCCAGAACAACAAGAAGGGAGGCT

SEQ ID 640

*MVNFLSQYGMQILVKTWEQVYISFFAIALGIAIAVPLGVVLTRFPKVAKIIIAIASMLQTIPSLALLALMIPLFGIGKIPAIVALFIYSLLPILRN*
TYIGMNNVNPTLKDCAKGMGMKPIQSIFQVELPLATPIIMAGIRLSTIYVIAWATLASYIGAGGLGDLIFSGLNLFQSKLILGGTIPVIILSLIID
YLLGLLETALTPRTTRREA

SEQ ID 641

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GTAACCGATAACGGTAAATTAATTGGTTTTATTGACTTAGAATCTCTAAGCAGTAAATATAAGAAAGATCGACTTGTTTCTGATATCTTAAAACAT
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SEQ ID 642
MGQEPIIEYQNINKVYGENVAVEDINLKIYPGDFVCFIGTSGSGKTTLMRMVNHMLKPTNGTLLFKGKDISTINPIELRRRIGYVIQNIGLMPHMT
IYENIVLVPKLLKWSEEAKRAKARELIKLVELPEEYLDRYPSELSGGQQQRIGVIRALAADQDIILMDEPFGALDPITREGIQDLVKSLQEEMGKT
IILVTHDMDEALKLATKIIVMDNGKMVQEGTPNDLLHHPATSFVEQMIGEERLLHAQADITPVKQIMLNNPVSITAEKTLTEAITLMRQKRVDSLL
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SEQ ID 643
ATGATACGTTTTAATAATGTTTCTAAAACTTTTGGTCAGACAAAGGTTTTGCAAGAGCAGACCTTTCAAATTAATGATCGTGAATTTTTTGTGCTG
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ACCCACCCTGCTAATGCTTTTGTGGTCAATTTATTTGGAGGTGATGAGCATGCC
SEQ ID 644
MIRFNNVSKTFGQTKVLQEQTFQINDREFFVLVGPSGSGKTTLLKMINCLIEPSSGDILLNNVPQTELDLREMRLSIGYVLQQIALFPNLTVAENI
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SEQ ID 645
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SEQ ID 646
MMGTSGLEPPTSRLSGVRSNHLSYAPKLLLGFYFLIK
SEQ ID 647
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TGGCACATTTATGAA
SEQ ID 648
MIYKIYILRKENMMRKYIKWLIPISIFGMILGGCQMNSEHKIQSNEVKNSKQSEVKKDKKMTKKEQLAYLKEHEQEIIDYVKLHNNQIESVQFDWS
SVKVEQSGNGTPQGGDYNLSLRGKFNHLQNSKLIVDFYLAHKNDIPNIKSMGMLNKPYIHKNGIWHIYE
SEQ ID 649
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TTTGATATAGTTAGTATGCTTAATCGTGAAAAGCCA
SEQ ID 650
MSNWNLDNFDNLHSSLAESAYNSRPNSFPELFETDSVTEVKFSQPSEDNKGQITQGGTNLPNDGIVYLQPDKSLKSIDENVKVLIPDVNGGYHTEH
YVTHSYQKGVLTDDKAGFNAYYLSDTEKIDSTTKHTYLAIRGSDGIGLDTLNDWVSNNAMFAVSNKYIPQAKLANKAMKEKIAELKGKAPGAIIDV
TGHSLGTIVSSQAVVNLSYAELENVGQVVLFDGPDVSRSLEKMEGISAKKIQEAGKHVTYYVNPFDIVSMLNREKP
SEQ ID 651
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GCACAAAATTTAACAGCTCAAGATGAGCAACTAGCTGGTGATATTGTCACGAACTTATCC
SEQ ID 652
MLYMATQLAESDVSEKVSATKKHISEAKDTIVEISTSTISSAEIMAMHLDQSEVDALVSDIKMSTVWNDGVETSDYEALDHYKTKMTTFTTNLVTV
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SEQ ID 653
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CTTGAAGGCCAGTCAGCTCAAGCAGCATCTGATTTCTTGACACAACTTCCAAAACCAGAGTTAGATAATCCAGTCAAT
SEQ ID 654
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SEQ ID 655
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TATAATGATAGAGTAGATGAATTGTATCAGAAGGCTAAGCAAAACGAAGCAAAAAAAGGA
SEQ ID 656
MIDTKKLQELDQEYDQNLRNIYRNREQLEDDFHLFMARTDSLKESVYQATLGQGWELPQEAHAHLYNMDDNKDTFISEFNEYMEKLEEKEIDLRRV
YNDRVDELYQKAKQNEAKKG
SEQ ID 657
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SEQ ID 658
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SEQ ID 659

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CTTGAGGGACGGAGA

SEQ ID 660

MGDFMNNKNKWTIILLIFTIIVIDVSLLFGGNRLSLPIKLLILLVTSIAEFCSIFIMIKVPTPQKYKKEPFGLKAKFYSIVLFLSTILYTIGIWNV
TPASPYNVKESILGVGILIQVVFFIYFLLKKINESPDERFYSNLALSASLMFLISIMLLILIAIYLNIYGTLELKSGYLYIMVGLLLLMFAVTYYF
LEGRR

SEQ ID 661

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AGAGAAACAATTGGTCATTTAGAAAATAACAGGTATAATCCTTCTCTAGAGATGGCACTTAAAATTGTTAAGATTTTCGACATGAAGATAGAAGAT
ATTTTTCAATTAAGGAAAGAGGAT

SEQ ID 662

MGKETKIISSLKQVREDIGMTQQELAIRIGVRRETIGHLENNRYNPSLEMALKIVKIFDMKIEDIFQLRKED

SEQ ID 663

TTGAATAAATTTTTTTTAGAATCAGAGAGACTTATTATAAGGCCACTAGAAGAAAGTGATTATGATAGTTGGTATACTAGTTTTATGAATCGTGGA
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GAAAGTGACATAGTATATATATTTGGTGTTTTTCTAAAAAGCGGTGAGCACGTAGGAATGTTAAATATTGTTACCCTTGCAAGAGCAGATATGCAA
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SEQ ID 664

MNKFFLESERLIIRPLEESDYDSWYTSFMNRGPSLTPFDDGILDMSMCDINWFKNLVNLQRKEWESDIVYIFGVFLKSGEHVGMLNIVTLARADMQ
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SEQ ID 665

ATGAATAATTTGGATACACTATATTGTAAATTAGCAATGTGCAACACAGTACTAACGGAAAGATTACGACTCCAGCCTGTTGAATTAACTAATGTA
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AATGTTTGTATGAAATCACCATTAGGAATTTATGCAATGATTGAAAAAGAATCACAGAAGATGATAGGTATTATTGAATTAGAAATCAGAGATGAA
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CATCTAGACTTGGAAAGAATTTATGCTAGATTTGACATTAATAATAAAAAATCTGGAAATGTTATGGAACGGATAGGTATGAAAAAAGAAGGCGAG
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SEQ ID 666

MNNLDTLYCKLAMCNTVLTERLRLQPVELTNVNDFLEFSSDSETVFYMQRYKANTVEEAQVVLANVCMKSPLGIYAMIEKESQKMIGIIELEIRDE
FSAEFGYILNKNYNGKGYMTEACSKLMSIGFEHLDLERIYARFDINNKKSGNVMERIGMKKEGELRHLAKNPKGEWKTRAYYSILKEEYFNKVNTK

SEQ ID 667

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SEQ ID 668

MDIWTKLAVFAFFETPKVILRPFRYEDHWDFYSMVNDTKNLYYVFPEQKTKAASDYLLVHSFIKFPLGQWAIEDKATHQVIGSIRIEHYDAKTRCA
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SEQ ID 669

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ACAAAA

SEQ ID 670

MGDVVENFTEGKNPKIDTLNGKTVRIEKINPDHFEDLFQVYGELSTEDSLTYISFSKFNSKNEFDVFFQTLLKSEDPYYLAIVDNNTGKVLGTFSL
MRIDTKNRVVEMGWVVYSSKLKQTRIATEAQYLVMKYVFEELCYRRYEWKCDSLNAPSNNSAKRLGFTFEGTFRQAVVYKGRNRDTNWYSILDKEW
PEKKTRFEKWLDDSNFAVNGYQIRSLSSIEQKTK

SEQ ID 671

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SEQ ID 672

MIKTKFSDPLEQLAKKRKRKTLFKTVVLALITVLLVVGIAFKGFTYLTSKNGQKTYHNFELLSEIAYPNISYDSLYYQPSGQFTGKVHADRFKDID
GVQIPYSSFEENYSISGTFGTNADEKSEKNGLYDRGTRQKVPQFFNKNVKYKKGEAKTTPTNDLKYVNKLNNDLIEIAITFDKSYSYKEIKTMIPN

NIKQNWLWIGTSTELDTSYWPTKYQFGTDPETLNTPQIFIDKIKENLKGNSKVYFNNINIYSDLEKYAKKYDKVNNSDKLKFSGIILTGKAENFKQ
LKEKEWVHASSIGANIEYKPYYKLDKE

SEQ ID 673

ATGATGAAAAAATATATAAAATGGTTAATTCCCATATCTATTATTGGGATGTTACTAGTAGGCTGTCAAATGAATAGGGGACCTAAAAGTCAGTCA
AACGAAGTAAAAAATAGCAAGCAATCAGAAGTGAAGAAAGGTAAAAATATGATAAAAAAGAACAGT

SEQ ID 674

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SEQ ID 675

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GACAAGCTTTTGGTCTTTATTCTCGAGTTAATCGTACAAACTATTGGACGCCCCTTCTTTACAGAATTATCTACATTTTCTACTAAAGAGGAACTA
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SEQ ID 676

MKNNIIFSIEQYINDQEMPKGKQKVILSAIELFASQGFHGTSTAQLAKNAEVSQATIYKYFETKDKLLVFILELIVQTIGRPFFTELSTFSTKEEL
IHFFVQDRFKFIEKNNDLIKILMQELLINSETSTIFTKLINSTDPNITKIFNCLSEGNSLNKMEILRAVIGQFITFFIQLYILNIKPENLEEELKQ
IEKQILKLLS

SEQ ID 677

ATGCCGTATGATAACATATATCCAAATACAATATCACTACGTTTAACAGGAGTTGCAAGGAGTCGATCAAGTGTACCAGAAGTACGCTCTTTTAAT
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SEQ ID 678

MPYDNIYPNTISLRLTGVARSRSSVPEVRSFNKAIPEIKKTKKKTINPISIGIIFAKKPVFLFP

SEQ ID 679

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SEQ ID 680

MRIIAITEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSANSNTKVKIGTINVNTKVVSNLDNIKHIQVRSFKFNSSAKKALKSNKIDALISEDN
KSYTVFYANTDSSKTTLTRQAFKTAVNTMNSKELISQVKILANKNPKLAQSLQTRSKYIKEKYNYGNKNTGFFAKMIPILMGFMVFFFVFLISGMA
LLKERTSGTLDRLLATPVKRSDIVFGYMLSYGILAIIQTIVIVLSTIWLLDIQVVGSIFSVIIVNFILALVALSLGILMSTLAKSEFQMMQFIPLI
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SEQ ID 681

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SEQ ID 682

MICFIKTLFVKIKRKKTSYVTFFLMPILTTLLALSLSFSNNNQAKIGILDKDNSQISKQFIAQLKQNKKYDIFTKIKKEHIDHYLQDKSLEAVLTI
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GSTSVIYSGILADKSSQLYHRLMLSNLSRFRYMLSYVCVGFVAFTIQIVIMLSLLKVFNISFFVPTSLLLIIFFLFSLLAIGFGLLIGAITQNSQQ
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SEQ ID 683

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SEQ ID 684

MEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTALVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKV
VDLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKDEGHSIFITTHVMDEAELTSKVALLLRGNIIAFDTP
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SEQ ID 685

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AACCATTTGAATTTAGAAGAAATTTTCTTACACTTAACAGGTAAGAAGTTACGAGAT

SEQ ID 686

MSFVQLTNVVKSYKNGKKAVNDVSLSIEAGNIYGLLGPNGAGKSTLINLILGLIPLSSGKITVLGQSQKTIRKISSQIGYVPQDIAVYPDLTAYEN
VELFGSLYGLKGAQLKKQVLKSLEFVGLHSQAKQFPSQFSGGMKRRLNIACALVHSPKLIIFDEPTVGIDPQSRNHILESIRLLNKEGATVIYTTH
YMEEVEALCDYIFIMDHGQVIEEGPKFELEKRYVANLANQIIVTLTDSRHLELADKPDWSLIEDGEKLMLKIDNSDMTSVVHQLTQANITFSEIRH
NHLNLEEIFLHLTGKKLRD

SEQ ID 687

GTGAGTAAACACTCACTCACTGAGAGAGGAGCAAAAAGTTATCATGAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATGCCTCAGAAAC
CGTTTTAAA

SEQ ID 688

MSKHSLTERGAKSYHEKSHRFKKTTKSICLRNRFK

SEQ ID 689

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TTT

SEQ ID 690

MKAQAIVTSQGRIVSLDIAVNYCHDMKLFKMSRRNIGQAAKILADSGYQGIMKMYSQAQTPRKSSKLKPLTLEDKTYNHTLSKERIKVENIFAKVK
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SEQ ID 691

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TACCGCACTTATGAACAAATTGCGGCTGATTTTGGCATTCACGAAAGCAACTTAATCCGTCGAAGTCAATGGGTTGAATCAACTCTTATTCAAAGT
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SEQ ID 692

MNYEASKQLTDVRFKRLVGVQRTTFEEMLAVLKTAYQRKHAKGGRTPKLSLEDLLMATLQYMREYRTYEQIAADFGIHESNLIRRSQWVESTLIQS
GFTISKTHLSAEDTVIVDATEVKINRPKKIN

SEQ ID 693

ATGGATAAACTGAAAAAATTACAAAAAGAAAATACGCTATTAGAAGGAAGAATTGATAACTCTAATAACCAAACCTATACAGATATGATTGTCTAT
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AAATCGAAAGAAAAGAAATATTTCTTTCGATATATATTTCTAATTCTTTCGCTTATCATAGCTTATATCCTTATAGGAAAATATTATCATCTTCCT
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SEQ ID 694

MDKLKKLQKENTLLEGRIDNSNNQTYTDMIVYLRGASISPYHQELIRNDIVNMLLEAQERQASLVSVFGEDRHDFINQVIKSTPKISKKEETLQRW
DLAILLLTIQMIIFLGGYLITEALQQSVPDLIPITLLDVLFAIFISIIAVKIADTIIYATYNFDKSKEKKYFFRYIFLILSLIIAYILIGKYYHLP
FINIPLWIYLIILGLSFSLHIIVKKYLNKHY

SEQ ID 695

GTGAGTATGAAAATAGATAAAAAAGAACTTTTAGCACTTATTGCTAGTATTATTTTTATTAATTTTTGCTTCTGTTACGTTTTTCTTATTTAAAGAT
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AAGAAACCTTCAGAAAAATTATTGAAGGATGTCGAACTTGCTTTAAATAAATTGTCCAATTCTTCTAAAAAAGAAGCTTTGCAAAAACGTTTTAAG
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GAAAATGTGTTAAAAGCTGAAGCAGCAGTCAATAAGTTAACTGTCAAAGAATCTAAAGAAGCTTTACAAAAACGTATTGATACTGTTAAGACACAA
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GTTAATCAGAATGTAGCACCAACTTATGAGCAACCGCAAGCGAATAATACACCAGTTACTCCAGGGGTTAACAATACTGTTCCGACTCCAGGAACT
GGTACTGTACCTGCTACTAATGGGACAGGTGTTGCTCAG

SEQ ID 696

MSMKIDKKELLALIASIILLIFASVTFFLFKDHGTTQMDTVESSVNHVSDSQLTEAQDMLDKFEKKPSEKLLKDVELALNKLSNSSKKEALQKRFK
KAKDKYLKDEADKKATKDATDLVEILEQAPSEENVLKAEAAVNKLTVKESKEALQKRIDTVKTQYGLIGNQTPSSSVAETTEQGTANPASQDTSSY
VNQNVAPTYEQPQANNTPVTPGVNNTVPTPGTGTVPATNGTGVAQ

SEQ ID 697

ATGGCTACGATGAAACAATATCATAAAGGAGATTCCATGACTAAATCACAAAAAGAGGCGCTTTATTGGATGTTGAGTGTTCTAACTATCACTCTA
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ACCTCTTCAGAACCTTCCGACTCAGGAGACAAGCAATCATCAAAAGAG

SEQ ID 698

MATMKQYHKGDSMTKSQKEALYWMLSVLTITLIGGSCLIFGSHPQTQDKVAKHSKSAASLLKKAVKAVNDADRLATAAAIQEAQKAVDKLAESSKK
KTLQEQLNVAKAKQEQEDAATQAVKAAEETLNQNLKDIAQKAVNDLSNKGKKAALQSRLDAILPAKPIIDEFPRQSGEITDNSYWTPFPGDVSDTY
DNSQSPTLDPSSESSASDVTPQPSHPDPIPPQTSSEPSDSGDKQSSKE

SEQ ID 699

TTGCCCGCTACTGCCGCAACTGATTTAGACGCCTCTTCTAGTCGCTTTGTATCTGAAGTTAGGGTTGTCGGCAAGAAAGATGTGACTCCAGTAGAT
AGTAAGCCAGCACTCATTCGCAAAATTCCTTCTGAATCACAATCCATAACATCAGCGCCAGCAAAACCA

SEQ ID 700

MPATAATDLDASSSRFVSEVRVVGKKDVTPVDSKPALIRKIPSESQSITSAPAKP

SEQ ID 701

ATGAGAGTGAATGGGGGGAAGAAGATGACGAAGTACATCAAGGCTGACCGATTCTTTTATGCTGATCATGTAAAGGAAAACGGTTATTTAGAAATA
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SEQ ID 702

MRVNGGKKMTKYIKADRFFYADHVKENGYLEIKDNHFGKWIENISGQEEILDYSGYQIAPGLVDTHIHGFAGADVMDCDSEGILRMSAGLLSTGVT
SFLPTTLTSDTKRLEEASKSVAAVAGKEQGAKIQGIYFEGPYFTEEYKGAQNPIYMRNPNLEEFAQWQKAAKGLITKIALAPEREGVEEFVSAITK
QGVTVALGHSNGTYKEAKKAVKAGASVWVHAYNGMRGLTHREPGMVGAVYNLPNTYAELICDGHHVDPVACDILMTQKGHNHVALITDCMAAGGAP
DGDYMLGELPVVVSNGTARLXXLIN

SEQ ID 703

ATGACATGCTATCTTAAAGCAGATTGTTTTTATTACCCAACAGAGGTGAGACCGGCTGGCTACCTAAGTCTTCATGATGGTGTTTTTGGGGAGTGG
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SEQ ID 704

MTCYLKADCFYYPTEVRPAGYLSLHDGVFGEWTEIVPADAQIIDYTGYQIAPGLVDTHIHGYAGADVMDNSAQGIHQMSEGLLATGVTSFLPTTLT
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HSNGTYQEAKEAVQAGASVWVHAYNGMRGLTHREPGMVGAVYNLPNTYAELICDGHHVSPIACDILMQQKGHDHVAMITDCMRAGGSPDGDYLLGE
FSVVVANGTARLKESGNLAGSILKLKDGLRNVVAWGIATPAEAIHMATYVPAVSVGIDDVCGQIKAGHAADFIVLDKDLTLVATYLNGQKAFDA

SEQ ID 705

GTGAATAGAGAGGTTACTATGTCAATAGAATCAGATTTTTTCCGGAAAAAACGTTTTATTTTTTCATCGCTTGAGGAGTTTGGATTTATCAAATCT
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GTTGATTATCCATTTGCGAAGCACCCACAATATGCTTCCTATCGTGTGTCAGGTAAATGGTATGCTCTGCTTTTTCCATTGAAGATGGGGAAACTA
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AAT

SEQ ID 706

MNREVTMSIESDFFRKKRFIFSSLEEFGFIKSDQEYIYCQTFMDNDFKAIITISLDGKIAGKVIDSALEEEYLPLRAANYNGSFVGEVRSAYMAIL
GDISDSCCKDLLFTKDQSNRLAEKIAKTFEDSVDYPFAKHPQYASYRVSGKWYALLFPLKMGKLENVPAQLSEDEVEVLNIKVNPQDMEILLQKEG
IYPSYHMSKKTWVSIVLDNTLSDIEIFKLVSDSRKLVSHNKKSNSEPEFWIIPANPKFYDXXLIN

SEQ ID 707

ATGAGTTTAGCAACTGACTATTTTAGCCGACAGACCCCCATAGTTGAAAAGCTAATGGCTTACGGTTTTGAGAAGCGAGACAACGGTTATTTCTAT
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GATTATTTGCCTTTACAACAAGCAGCCTGGCAAGGAACCTATACTGGGCAGGTTAGAGCGGCCTATTTGGAACTTTTGGAGCGCTTATCAGTAGCC
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GAGTATTTTAAAGAGAACAAC

SEQ ID 708

MSLATDYFSRQTPIVEKLMAYGFEKRDNGYFYNERFMEGEFEAQLRIDEAGNIWDRVIDCDLEEDYLPLQQAAWQGTYTGQVRAAYLELLERLSVA
CFEATPFQSMQANRLAKHITKEWSDPMDYPFEKHPDLATYRVGGKWYAMIFSLLADKLDQIPERLVGQTCEVMTVKVNPKAFPQLLQQEGIYPAYH
MSKKNWISIILDDKVTDDKLWTLVTQSRQLVNPNGLSNPNGPDYWVIPANLKYYDIDAEFAANDVILWTQKAGIAVGDYVLIYITAPVKSIRYVCQ
VLETDIPNEGYRKNPNIDKLMRLRKCQQYKDGLLSFDLMKKHGVAAVRGPRRLSPQLIAFLKEKEYFKENN

SEQ ID 709

TTGCGAGACTTCACTAGAAAGAGATTTATTCCCATGACCCAGTTTACCACAGAATTACTTAACTTCCTAGCTCAAAAACAAGATATTGATGAATTT
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ACCGGTAATAGTCGTAATGGTGCTTATACACGTCGATTTGAGACCAAGTATGGTGTTGTTAATTTGTTGATCCCTAGAGATCGAAACGGGGAGTTC
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CGCGCGATCAATGTAGAGGAAGCAAAGCAAGCCTTAGATAGCTTTATCAATGAGTGGAAACCACACTACAAGAAGGTAATAGAGACCTTAGAATCA
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CGTCAAACCAAAAAGAAAGTCGTCTTTCCCAATGAAGAATCCCTAGAACGCTATCTCGTCACACTATTTAGTGATTACAACTTCAAGCAAGGACAA
CGAATCCACAAAGGTTTTGGCCAATGTACGGACACACTTGAAAGCCTATTTGAT

SEQ ID 710

MRDFTRKRFIPMTQFTTELLNFLAQKQDIDEFFRSSLETAMNDLLQVELSAFLGYEPYDKAGYNTGNSRNGAYTRRFETKYGVVNLLIPRDRNGEF
SPALIPSYGRRDNHLEEMVIKLYRTGVTTREISDIIERMYGHHYSPATVSNISKATQENVASFHERSLEANYTVLYLDGTYLPLRRGTVSKECIHI
ALGVTSYGHKAILGYDIAPNENNASWSDLLERFKGQGVQQVSLVVSDGFNGLDQLIQQAFPMAKQQRCLVHIGRNIASKVKRADRALILEQFKTIY
RAINVEEAKQALDSFINEWKPHYKKVIETLESIENLLIFYEFPHQIWGSIYSTNLIESLNKEIKRQTKKKVVFPNEESLERYLVTLFSDYNFKQGQ
RIHKGFGQCTDTLESLFD

SEQ ID 711

ATGACTCAGTTTACCACAGAATTACTTAACTTCCTAGCACAAAAACAAGATATTGATGAATTCTTTCGCTCCTCTTTAGAAATAGCTATGAATGAC
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SEQ ID 712

MTQFTTELLNFLAQKQDIDEFFRSSLEIAMNDLLQVELSAFLGYEPYEKEGYNTGNSRNGTYSRQFETKYGLVNLIIPRDRNGEFSPVLLPSYARR
EDHLEEIVIKLYQTGVTTREISDIIKRMYGDHLFLSGSLVTKRL

SEQ ID 713

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GCACTTAATCGTGTTGAAAAGGTAGATTCTCCGAAACACCTCTTATTATCATTAGTGACTGCTTTCTCAAAGCAATATTTTGATGTTTTAGATACT
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SEQ ID 714

MFSSDFGFEIINVDDLSLQEERFLPSELLAYARDENESSFVRDIEGHLALVYQLLDTQGHVDDVRHVPRVIPVTLFLKEDGLFVLANHKNINLVKK
ALNRVEKVDSPKHLLLSLVTAFSKQYFDVLDTISEERDKLINDLRKRPNKSNLARLANLQSGTVHLMMGTKQNFEMLTDLQNIEQDKENTRNEKMQ
LQDAIIEARQLSNMCSLNSQVFQELSSYNNVLSNNLNDNVTTLTIISIGISIIAMVTSFYGMNVKLPFDSVDAVWVLIILITTIITIMLSIVMYI

SEQ ID 715

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SEQ ID 716

MKQMFLSSAIEFKEIETFEPGAWIKLVNPSQEESMKIADQFNIDISDLRAPLDVEETSRIAVEDDYTLIIVDVPIYEERNNKSYYITMPLGIIVTE
NAVITTCLHDMTLFDHFHNRRVKNFYTFMKTRFVFQILYRNAELFLTALRTIDRQSERLEAQLEAATRNEELIDMMELEKSIVYLKASLKFNERIV
KKLSSSTSSLKKYIEDEDLLEDTLIETQQAIEMAGIYENVLNAMTETTASIINNNQNTIMKTLALMTMALDIPTVIFSAYGMNFQNNWLPLNGLEH
AFWYITLIAMLLSSFVVIYFIRKKWF

SEQ ID 717

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SEQ ID 718

MSKVRYGVVSTAKVAPRFIEGVRLAGNGEVVAVSSRTLESAQAFANKYHLPKAYDKLEDMLADESIDVIYVATINQDHYKVAKAALLAGKHVLVEK
PFTLTYDQANELFALAESCNLFLMEAQKSVFIPMTQVIKKLLASGEIGEVISISSTTAYPNIDHVTWFRELELGGGTVHFMAPYALSYLQYLFDAT
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SEQ ID 719

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SEQ ID 720

MKLAVLGTGMIVKEVLPVLQKIDGIDLVAILSTVRSLTTAKDLAKAHHMPLATSKYEAILGNEEIDTVYIGLPNHLHFAYAKEALLAGKHVICEKP
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FGRPKTVQYLANVEKGIDTSGMLVMDYEQFKVVCIGAKDCTAEIKSTIQGNKGSLAVLGATNTLPQVQLSLHGHEPQVINHNKHDHRMYEEFVAFR
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SEQ ID 721

ATGTCAAAAGAACTATCACCAAAATACAATCCTGCCGAGGTTGAGGAAGGCCGTTATCAAACTTGGCTTGACCAAGATGTTTTCAAGCCATCAGGG
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SEQ ID 722

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SEQ ID 723

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SEQ ID 724

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KDVEGAFYHMNYMLEDGSRALQVATTRPETMFGDVAVAVNPEDPRYKDLIGKNVILPIVNKLIPIVGDEHADPEFGTGVVKITPAHDPNDFEVGQR
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VLLYTLDKILRLLHPIMPFVTEEIYAQYAQGSIVTVDYPVVRPAFENEAAHKGVESLKDLIRAVRNARAEVNVAPSKPITILVKTADSELEDFFNS
NINYIKCFTNPEKLEISSAIAAPELAMTSIITGAEIYLPLADLLNVEEELARLDKELAKWQKELDMVGKKLGNERFVANAKPEVVQKEKDKQADYQ
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SEQ ID 725

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AATGATTCAAGAGATGTAGTATTTCTAGAAAAGATTCAAATAGTTTTTCAATCTCACAACCAAGAGGTATTATTTGTAGAATTAGAAACAGAGCTA
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SEQ ID 726

MWRYALWFTAKRVGEKKKMNIIIIGAQASGKMTIGQEIAKQTGMTLFHNHDSIDFVLRFMPWSPDSIALTESIRFKFFETFAKTGQEMIFTIVIDF
NDSRDVVFLEKIQIVFQSHNQEVLFVELETELSERLKRNRTENRLKHKPSKRDIKWSESDICSTMDYAIFNPEVAPEALTYYHKINNTCLTATETA
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SEQ ID 727

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GAGAAC

SEQ ID 728

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IQAVFQSYDQEVLFVELKTDIEERLKRNRTENRLKHKPLKRNIEWSEQDIQSTMAYAVFNPEEPPKTLTHYQKINNTQLTAAETAQLIIQKMTHIK
EN

SEQ ID 729

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SEQ ID 730

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HRHEDDIFEIGYLLHPDYWGQGIVPEAASALVEIGFTLLGLHKIELGCYDYNKQSQAVARKLGFTLEANIRDRRDAQGKRCGDMRFGLLRSEWEKK
RR

SEQ ID 731

TTGCATAAAATTGAGCTGGGTTGCTACGACTACAACAAGCAAAGTCAGGCAGTGGCTCGCAAATTAGGCTTTACCTTAGAAGCCAATGCCCGTGAC
CGTAAGGACGTTCAAGGTCGCCGCTGTGGCGACATGCGTTTTGGGTTACTGAGAAGTGAGTGGGAGGAGCAGAAACAAAAA

SEQ ID 732

LHKIELGCYDYNKQSQAVARKLGFTLEANARDRKDVQGRRCGDMRFGLLRSEWEEQKQK

SEQ ID 733

TTGAAACAAAACGAGTTGCGGATGTTATCATCCGAATTTGGGTGGTACCGCGGAAATCGTAACACGAAATTCGTCCCTGTCAGAATTGACAGGGAT
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SEQ ID 734

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SEQ ID 735

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SEQ ID 736

MGFQNTSKLIYSSKIRLLSQGKSNYFAKTTPLSTNCLIAAGPIPFSAKTSASLTFANASRLTRPASFKTSCLLAVKPSKRSTAFGASGAVFFGNAT
SCKV

SEQ ID 737

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SEQ ID 738

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SEQ ID 739

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TTTAAAAAA

SEQ ID 740

VAKQKNRKKALKLEMKRNGLLKKAGQVFDKAVESVETAVDKTISAGKNLVEKGSQTVENLTASKERLTLDEFAGQPVVAGIRSDLVETLYAEGIHS
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SEQ ID 741

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TATCATAACCAAAAATCTTTCCATGATTTGCCTGATGGTCTTTTTGGACAACGTCATTAT

SEQ ID 742

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SEQ ID 743

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SEQ ID 744

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SEQ ID 745

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SEQ ID 746

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SEQ ID 747

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CAAGTGCTTTTAGAT

SEQ ID 748

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QVLLD

SEQ ID 749

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TTGCTTCTG

SEQ ID 750

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LLL

SEQ ID 751

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TTTTATTATAATGCTTCTGGTAAGGAGACATATTATAAAGAAGGTAGCAAGGCTTTAGAAAAAGCATTAAGAGATAAAGAA

SEQ ID 752

MKKKLLGLMILAISTVFLVACSTNSLNVKYYKVYDGEKMLVLEINDESGIYHNEGNFVVTNIDTKSKSFVLKGGSAKYTVLYDVKSDGKLNVDLGN
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SEQ ID 753

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ACAAAATTAAAGGGAATACGAGTTAAGGCTAGTGATCCAGAAAGTGTAAATGCGTTTTTTGGAGATGAAGATTTTTCAGAATATGAGGAATATTTT
AAA

SEQ ID 754

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K

SEQ ID 755

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GATGTCGGGAAATTCTATTTCCAA

SEQ ID 756
MSLQKRRITMAKTGTLNLRVDDSVKSAADDILKRLGIPMSTAIDMFLNQIILTGGIPFDVSLPEAPQRVNVDYMSQEKFYDKLITSFEDAKTCNPQ
DVGKFYFQ

SEQ ID 757
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TCTGTTTCTAAGAAAAAAGAGGAT

SEQ ID 758
MTYPDGSKDTVDVTVKVVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVKV
VDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVKVVDPRTDADKNDPAGKDQ
QVNVGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVKVVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNL
PDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDTVDVTVKVVDPRTDADKNDPAGKDQQVNGKGNKLPATGENATPFFNVVALTIMSSVGLL
SVSKKKED

SEQ ID 759
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SEQ ID 760
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VAASSEETPSPSTPAAPETPEEPAAPSPSPESEEPSVAAPSEETPSPETPEEPAAPSQPAESEESSVAATTSPSPSTPAESETQTPPAVTKDSDKP
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SEQ ID 761
GTGACTGTTAAGGTTGTCGATCCACGTACAGATGCCGATAAGAATGATACAGCAGGTAAAGATCAGCAAGTCAATGTAGGTGAGACACCGAAGGCA
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AAAGTTGTTGAAACTTACCCANNNNNT

SEQ ID 762
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SEQ ID 763
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CCGGGAGACAAACCAGCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATCTG

SEQ ID 764
MYRAIQNKVKENIMFRRSKNNSYDTLQTKQRFSIKKFKFGAASVLIGISFLGGFTQGQFNISTDTVFAAEVISGSAVTLNTNMTKNVQNGRAYIDL
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KWDEGSRDKVLISLDDIKTDIDNNPKTQSDIANKITEVTNLEKILVPRIPDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFETPVDT
ATPGDKPAKVVVTYPDGSKDTVDVTVKVVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDG
SKDTVDVTVKVVDPRTDADKNDPAGKDQQVNVGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTYPDGSKDL

SEQ ID 765
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SEQ ID 766

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LKKKLTETQINASEQDYFIDRLSQLPFFSLSQIRELLIVTNYCLTGVVKDKLSEPLHYYTKGWSNSFDLDKIKQFSKQNMSSYKYQYHFENNILKA
VKSGSEFLLKETVEQFSNSIVPIISGDELRSEKNYSIMIYDRLSQATIQAGLDIETAYRARDRFIKENESTISLNEVLKLRDTAILFYTQQVHSLK
KHLETPHSQTIVAVIRYLENNLNRFIKTEEIAKECHMSESKLRKLFKQEKHITIQQYFLNLKIEAAKQLLDENKKVEEVSNLLGFSTSSNFSRTFK
KIVGISPLEYKQKPKTI

SEQ ID 767

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AGTATCGCTACGTTATTATTATCTGACGATCCCTATTTTTTATTACGCTTTAGAAGTGAATTAGAACACGATGTTTACCCTAGATTGCGTGAGGAG
TATATTACAAAGGTGGACATTCCTGAAGATTTCTTAAAACAATTTCTTTTATCCAGTTTTATCGAGACCTTAAAGTGGTGGCTTCATCAAAGACAG
AAAATGACTGTTGAAGATTTACTAAAATATTATTTAACTATGGTAGAGAGG

SEQ ID 768

MSYMVKDRQIQKTKVAIYNAFISLLQENDYSKITVQDVIGLANVGRSTFYSHYESKEVLLKELCEDLFHHLFKQGRDVTFEEYLVHILKHFEQNQD
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SEQ ID 769

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AGCATTGCGACGTTGTTACTTTCTAATGATCCCTATTTTTTATTAAGATTTAAAAACGAACTAGAACATGATGTTTACCCTAACTTGCGCTGCAAG
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AGGATGTCTGCAAATGAACTATTAAAGTATTATTTAGAGCTCATAAAA

SEQ ID 770

VSDMTKDRQIKKTKTAIYSAFIALLQKKEYSKITVRDMITLANVGRSTFYAHYESKEMLLKELCEELFHHLFRQKRNVTFEDYLVHILKHFEQNKD
SIATLLLSNDPYFLLRFKNELEHDVYPNLRCKYIDKTTIPEVFLKQFVLSSFIETLKWWLHQRQRMSANELLKYYLELIK

SEQ ID 771

ATGGAATCTGGAACACCATCTAAAAAAAGTTTCAGGGTTGATAGTAATTTAGGAAGTGCTTTAGATAAGATGAAAGTAGATATGGCAACTGATAAT
AATGGATCAAGGATATACAACGGTTTCCAATTTAAGATAAGAGATATAACAATAATAGCTAACCACCCTAGAATATCTTCCAAAAAA

SEQ ID 772

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SEQ ID 773

ATGACATCAAACAAAAAAGTGGCTATCGCTTTTATATTAAATATCAGCTTTTCCGTCCTTGAATTCATCTTTGGAAGTCTATTCTTCTCAGGAGCT
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SEQ ID 774

MTSNKKVAIAFILNISFSVLEFIFGSLFFSGAILADAVHDFGDAIAIGISATLEKKSKKDEDTIFSLGYKRFSLLGALITSLILISGSILVMIENI
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SEQ ID 775

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TTTTCACTAGGCTATAAGCGATTTAGCCTTTTAGGAGCGCTAACGACAAATCTAATACTTATTAGCGGGTCATTATTAGTAATGATTGAAACGATA
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GAAGTCAAC

SEQ ID 776

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EVN

SEQ ID 777

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AATGGTCATGTTAAACCTGCTGTCAATCAAATCTTAGCTCACATCGGAAATACACCTTTCGACTTGATTGATTACTGTCAAAGTAAAGGTATTCAA
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SEQ ID 778

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SEQ ID 779

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SEQ ID 780

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RLGLDYVDLYLIHWPNPKALRNTWKEANAQAWQYMEEAVEAGLIKSIGVSNFMVHHLEALQETAKITPAINQIRLAPGCYQKEVVDYCKANEILLE
AWSPLGQGEIFDNETMQQLANKYDKTVAQVALAWSLAEGFIPLPKSVHDERIKENMAIFDVSLTQEDKKTIRYLSGMSAIPNPDTTSF

SEQ ID 781

GTGATTTTGTTATTGTTCCCTTTACACATGGCTGTGGCCAATGTCCGTCTTGTAAGGCTGGATTTGATGGAAATTGTACAAATCATCAAGCTGCAA
AAAATG

SEQ ID 782

MILLLFPLHMAVANVRLVRLDLMEIVQIIKLQKM

SEQ ID 783

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SEQ ID 784

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NRIIAMSRHKDRQELALTFGATDIVEERGDEAVKRVLDLTNQAGADAVLECVGTEQSVDTATQIARPGAVIGRVGIPQNPDMNTNNLFWKNIGLRG
GIASVTTFDKSVLLDAVLTHKINPGLVFTKSFVLDDIQKAYEAMDKRDAIKSLVIVD

SEQ ID 785

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SEQ ID 786

MNWLITSQPYKKLNMKAATYLSTGNLQLIDKPKPVIIKPTDAIVQLVKTTICGTDLHILGGDVPACKEGTILGHEGIGIVKEVGDAVTNFKIGDKV
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GLAALLTVQFFSPANIIMVDLSQNRLEAAKTFGATHTICSGSSEEVKAIIDDITNGRGVDISMECVGYPATFDICQKIISVGGHIANVGVHGKPVD
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SEQ ID 787

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TGGCATGGTGCTAAAAAAGATTCTGAATTTGCACATATTGCGATTACAGCTGGTAAGAGTGAGTTTTATGAAGCTGTTAGTGATGAAGAATATTCA
AGACTAGGT

SEQ ID 788

MQETTKSIFPKGEKNPYGEFFIGQSYLAALAKSPDGNVSVGNVTFEAGCRNNWHVHLDGYQILLVTEGSGWYQEEGKEAVSLKPGDVIVTDKGVRH
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SEQ ID 789

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CAATTTGCCAAACAAAACGGAGTTACTAAAGAAGAAATTGCTGACATTATCACTCACCTCGCTTTTTATGTTGGATGGCCAAAAGCTTGGTCAGCC
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SEQ ID 790

MKEKQTAGRRQLEEFAPEFARYNDDILFGEVWAKEDHLTDKTRSIITISALISGGNLEQLEHHLQFAKQNGVTKEEIADIITHLAFYVGWPKAWSA
FNKAKEIWI

SEQ ID 791

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SEQ ID 792

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SEQ ID 793

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SEQ ID 794

MLSFQIVEKPAMILAGVTLENVKSNQEGIQQAIGICKTQPDFRFDYSATYQVETSVQAPKGLEIIRIPSATYAVISVKGPMPSSLQETWRKIIQGF
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SEQ ID 795

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ACT

SEQ ID 796

MITQEMKEIINSQLAMVATVDAKGQPNIGPKRSMRLWDDKTFIYNENTDGQTRINIEDNGKIEIAFVDRERLLGYRFVGTAEIQTEGTYYEAAKKW
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SEQ ID 797

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AACAGTGAAAGTAAC

SEQ ID 798

MITQEMKDLINNQLAMVATVDAKGQPNIGPKRSMRLWDDKTFIYNENTDGQTRINIEDNGKIEIAFVDRERLLGYRFVGTAEIQTEGAYYEAAKKW
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SEQ ID 799

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SEQ ID 800

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SEQ ID 801

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SEQ ID 802

MKKHLKTVALTLTTVSVVTHNQEVFSLVKEPILKQTQASSSISGADYAESSGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQEL
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SEQ ID 803

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SEQ ID 804

MTQSDAYLSLNAKTRFRDRTGNYHFTSDKEAVEQYMIEHVEPNTMVFTSLIEKLDYLVSNNYYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGA
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SEQ ID 805

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SEQ ID 806

MSQTNASYLSLNALTRFKKPDGSYHFDSDKEAVRRYLEEHVSPNQMAFNSLEDKLAYLINEGYYEQAIFDAYPNDLIKEAFHYAYQQGYRFLNLMG
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SKRGGGVALCLTNLREIGAPIKGIENQATGIVPVMKLLEDSFSYANQLGQRQGAGAVYLHAHHPEVLTFLDTKRENADEKIRIKSLALGLVIPDIT
FQLAKENKDMALFSPYDIKRAYGKDMSDISITEEYDKLLANPAIKKTYISARKFFQLIAELHFESGYPYLLFDDTVNKRNPHAKKGRIVMSNLCSE
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SEQ ID 807

ATGGATAGTACAGTGAAGGTGGTCTATTTTTCATCGAAATCTAACAATACCCATCGTTTTGTTCAAAAGTTGGCTTGTTCTAACCAGCGTATTCCA
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CAAGTTGTACAGTTTTTAAATGTTCGACAAAATCGGGAACATTGCCAAGGGGTTATTTCTTCTGGAAATACCAATTTTGGTGACACTTATGCCATT
GCTGGACCTATTATTGCTCGAAAATTAAATGTTCCTTTGCTTCATCAATTTGAATTACTGGGAACACAAGAAGATGTTACAAGGGTAAAGGAGTTA
CTTTGCCAATTCACTAGAAAGGATAAA

SEQ ID 808

MDSTVKVVYFSSKSNNTHRFVQKLACSNQRIPSDGSSILVTEDYILIVPTYAGGGDDTKGAVPKQVVQFLNVRQNREHCQGVISSGNTNFGDTYAI
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SEQ ID 809

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TCTCAT

SEQ ID 810

MAELIIVYFSSKSNNTHRFVQKLGLPAQRIPVDNRPLEVSTHYLLIVPTYAAGGSDAKGAVSKQVIRFLNNPNNRKHCKGVISSGNTNFGDTFALA
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SEQ ID 811

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SEQ ID 812

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KHSQTDHEQVIYANFAFMVAIHARSYGTIFSTLCTSQQIEEAHEWVVDTESLQARSRILIPFYTGDDPLKSKVAAAMMPGFLLYGGFYLPFYLSAR
GKLPNTSDIIRLILRDKVIHNYYSGYKYQQKVAKLSVEKQAEMKTFVFDLLYQLIDLEKAYLYELYDGFDLAEDAIRFSIYNAGKFLQNLGYDSPF
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SEQ ID 813

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SEQ ID 814

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SEQ ID 815

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SEQ ID 816

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SEQ ID 817

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SEQ ID 818

MNINILLSTYNGERFLAEQIQSIQRQTVNDWTLLIRDDGSTDGTQDIIRTFVKEDKRIQWINEGQTENLGVIKNFYTLLKHQKADVYFFSDQDDIW
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SEQ ID 819

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SEQ ID 820

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SEQ ID 821

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SEQ ID 822

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QVVKNYNNDLASTLGSTRFEKTRWDGKDKDGKVVANGTYTYRVRYTPISSGAKEQHTDFDVIVDNTTPEVATSATFSTEDRRLTLASKPKTSQPVY
RERIAYTYMDEDLPTTEYISPNEDGTFTLPEEAETMEGATVPLKMSDFTYVVEDMAGNITYTPVTKLLEGHSNKPEQDGSDQAPDKKPETKPEQDG
SGQAPDKKPETKPEQDGSGQTPDKKPETKPEQDGSGQTPDKKPETKPEKDSSGQTPGKTPQKGQPSRTLEKRSSKRALATKASTKDQLPTTNDKDT
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SEQ ID 823

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TATCTAGAAGATAATATTCCTCATCTTGATATGGTTTTATTA

SEQ ID 824

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SEQ ID 825

ATGGATGTCTCCTCAATTGACGAATCAAGGACGCCACATGTTCCAAAAACAATTAAACTTTCCATTCCAAATACTATAATATCTTCCAAGATTGCT
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SEQ ID 826

MDVSSIDESRTPHVPKTIKLSIPNTIISSKIATQAEAPT

SEQ ID 827

ATGAATGTGGTTTTAAAACAGCGAATTCCTTTAAAAATTAAACGAATGGGAATTAATGGTGAAGGAATAGGTTTTTATAAAAAAACACTAATCTTT
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SEQ ID 828

MNVVLKQRIPLKIKRMGINGEGIGFYKKTLIFVPGALKGEEVFCQISSVRRNFAEAKLLKINKKSKNRVEPPCSIYKECGGCQIMHLQYDKQLEFK
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IAGVRTVMIRRAQASGEVQLIFITSKRLDFDDVVIELVREFPELKTVAVNINASKTSDIYGQITEVIWGQESINEEVLDYGFSLSPRAFYQLNPKQ
TQILYSEAVKALDVKEDDDLIDAYCGVGTIGLAFAGKVKSVRGMDIIPEAIQDAKENALYMGFTNTHYEAGKAEDIIPRWYSEGFRANALIVDPPR
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SEQ ID 829

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SEQ ID 830

MVVKVKQKIPLKIKRMGINGEGIGFYQKTLVFVPGALKGEDIFCQITAVKRNFAEAKLLTVNKASKNRVKPACSVYETCGGCQIMHLAYPKQLDFK
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IAGIRTIMVRKAQASDQVQIIVVSSKEVRLANFIGELTKAFPQVKTVALNSNRSKSSEIYGDETEILWGQEAIHEEVLDYGFALSPRAFYQLNPQQ
TEVLYGEVVKALDVGSKDHIIDAYCGVGSIGFAFAGKVKSVRGMDIIPEAIEDAQKNAKAMGFDNAYYEAGKAEDIISKWYKQGYRADAVIVDPPR
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SEQ ID 831

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TATTTA

SEQ ID 832

MKITKIEKKKRLYTLELDNTENLYITEDTIVHFMLSKGMIINAEKLENIKKFAQLSYGKNLGLYYISFKQRTEKEVIKYLQQHDIDSKIIPQIIDN
LKSENWINDKNYVQSFIQQNLNTGDKGPYVIKQKLLQKGIKSKIIESELQAINFQDLASKISQKLYKKYQNKLPLKALKDKLMQSLTTKGFDYQIV
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SEQ ID 833

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TATTTA

SEQ ID 834

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SEQ ID 835

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GCTCAGATGAACTATCCTACCGATATTGATTATATATTAAAGGAAAATGTAAAAATATTGGTAGAATGGATAAATGAGAATAAAGGCCCCTTTTCA
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SEQ ID 836

MRLPKEGDFITIQSYKHDGSLHRTWRDTMVLKTTENALIGVNDHTLVTENDGRRWVTREPAIVYFHKKYWFNIIAMIRETGVSYYCNLASPYILDP
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SEQ ID 837

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SEQ ID 838

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SEQ ID 839

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TTTGTAGTAGTTACTAAGAAA

SEQ ID 840

MKKNKELNVLREKQVRKESRKTMVLFTGATVEEAIEKGLQELNISRLRAHIKVVSREKKGFLGFGKKPAKVEIEGITDEVTDINESVALKNIKNVP
SSVDVVEEYIEEVDETLEKEDVSQPELPKIDDKNVVTTSEAIEKIDLLPNIEVAAAQVTKYVENIIYEMDLDATIETTTSKRQINLQIETPEAGRI
IGYHGKVLKSLQLLAQNYLHDRFSKSFSVSINVHDYVEHRTETLIDFSKKIARRVLETNEPYHMDPMSNSERKTVHKTIATIEGVESYSEGNDPNR
FVVVTKK

SEQ ID 841

ATGGTATTATTTACAGGAAAAACAGTCGAAGAAGCTATCGAAACAGGACTTCAAGAGTTAGGGTTATCACGCCTTAAAGCGCATATCAAAGTCATT
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GAATCTGGTCAAGATTACACCATGGATCCCATGAGTAACAGTGAGCGTAAAATCGTTCATAAAACCGTTTCATCCATTGAAGGGGTTGATAGTTAT
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SEQ ID 842

MVLFTGKTVEEAIETGLQELGLSRLKAHIKVISKEKKGFLGFGKKPAQVDIEGISDKTVYKADKKATRGVPEDINRQNTPAVNSADVEPEEIKATQ
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ETPEAGRVIGYHGKVLKSLQLLAQNFLHDRYSKNFSVSLNVHDYVEHRTETLIDFTQKVAKRVLESGQDYTMDPMSNSERKIVHKTVSSIEGVDSY
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SEQ ID 843

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SEQ ID 844

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SEQ ID 845

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SEQ ID 846

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ELQRKYAGKDTQTRMKLAEESQALYKKYGVNPYASLLPLLIQMPVMIALFQALTRVSFLKTGTFLWVELAQHDHLYLLPVLAAVFTFLSTWLTNLA
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SEQ ID 847

TTGAGTCTTTTAGGTTATTTATGGTATAATAAAACCAATTTAGATAAATGGAGCACTATTTTGAAAAAAACCTATCGGGTAAAAAGTGATAAGGAT
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TCTGTTAGTAAGAAATTAGGAAATGCTGTTGTTCGTAACGCTATTAAAAGAAAAATTAGGCATGTTTTACTCTCTCAGAAAACAGCGCTGCAAGAT
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ATC

SEQ ID 848

MSLLGYLWYNKTNLDKWSTILKKTYRVKSDKDFQMIFSRGKNVANRKFVIYYLEKEQKHFRVGISVSKKLGNAVVRNAIKRKIRHVLLSQKTALQD
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SEQ ID 849

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CATGTTATCATGGCATTAGGGCATCAGCTGAAGTCAGAGGATTTCGTGGTGATTGCCCGTAAGGGTGTCCACTCTTTGGAGTATCAAGAGCTTCAA
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SEQ ID 850

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QNLHHVLKLAQLLEKGFESEEKH

SEQ ID 851

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SEQ ID 852

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YTNTDVVGVETAGALKNIIAVGAGALHGLGYGDNAKAAIITRGLAEITRLGVQLGADPLTFSGLSGVGDLIVTGTSVHSRNWRAGDALGRGEKLED
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SEQ ID 853

ATGACAAAACAAAAAGTAGCTATTTTAGGACCTGGTTCTTGGGGAACTGCCCTTTCTCAGGTTCTTAATGACAATGGCCATGACGTCCGTTTATGG
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CTTGATTTAGGTCAAGCCCTATCAGATGTTGATGCGGTGCTTTTTGTTGTGCCAACTAAAGTAACACGATTAGTTGCTAGACAAGTTGCCGCCATT
TTAGATCATAAAGTAGTGGTCATGCATGCCTCAAAAGGTCTAGAACCAGAGACCCACGAACGTTTATCAACTATCCTAGAAGAAGAAATTCCAGCT
CATTTTCGTAGTGAAGTGGTCGTTGTATCAGGTCCTAGTCATGCTGAAGAAACTATCGTTCGCGATATTACTCTCATCACGGCAGCCTCAAAAGAT
ATTGAAGCTGCAAAGTATGTTCAGTCCCTCTTTAGTAACCACTACTTCCGACTTTATACCAATACCGACGTCATCGGAGTTGAAACAGCTGGTGCC
CTCAAAAACATTATTGCTGTTGGAGCAGGAGCTCTCCATGGACTTGGGTATGGAGATAATGCCAAAGCAGCGGTAATTACTCGTGGGTTAGCTGAA
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TCACGTAACTGGCGGGCTGGAGCTGCCCTTGGACGTGGTGAAAAATTAGAAGATATTGAACGCAACATGGGTATGGTTATCGAAGGTATCGCAACA
ACTAAGGTAGCCTATGAAATTGCCCAAGACCTCGGAGTTTACATGCCAATTACAACAGCTATTTATAAGTCCATCTACGAGGGCGCTGATATCAAA
GAAAGCATCCTCGGCATGATGTCAAATGAATTTCGTTCTGAAAATGAATGGCAT

SEQ ID 854

MTKQKVAILGPGSWGTALSQVLNDNGHDVRLWGNIPDQIEEINTKHTNRHYFKDIVLDKNITATLDLGQALSDVDAVLFVVPTKVTRLVARQVAAI
LDHKVVVMHASKGLEPETHERLSTILEEEIPAHFRSEVVVVSGPSHAEETIVRDITLITAASKDIEAAKYVQSLFSNHYFRLYTNTDVIGVETAGA

LKNIIAVGAGALHGLGYGDNAKAAVITRGLAEITRLGVKLGADPLTYSGLSGVGDLIVTGTSVHSRNWRAGAALGRGEKLEDIERNMGMVIEGIAT
TKVAYEIAQDLGVYMPITTAIYKSIYEGADIKESILGMMSNEFRSENEWH

SEQ ID 855

ATGAAAGTCAGAAAAGCAGTTATCCCTGCCGCTGGTTTAGGAACACGTTTTTTACCTGCTACTAAAGCTTTAGCTAAAGAAATGCTTCCAATCGTT
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GACCACTTTGATTCAAATTTTGAATTAGAATATAACCTAAAAGAGAAAGGGAAAAACGAACTTCTCAAACTTGTTGATGAAACAACTGGCATTCGA
CTCCATTTTATTCGACAAAGTCATCCTCGTGGGCTTGGAGATGCTGTGCTACAAGCAAAAGCCTTCGTTGGTAATGAACCTTTTGTTGTTATGCTA
GGTGATGATCTAATGGATATTACCAATAATAAAGTTATTCCTCTCACCAAACAATTAATTAATGACTTTGAAGCTACTCATGCATCAACAATTGCT
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CCTGGTGCAGGAAATGAGATTCAACTAACCGATGCTATCGATACTTTAAATAAAACGCAACGTGTTTTTGCTAGAAAATTTACAGGAGACCGTTAC
GACGTTGGTGACAAGTTTGGTTTTATGAAAACATCTATTGATTATGCTCTTCAACACCCACAAGTTAAAGATGACTTGAAGAAATATATCATTGAT
TTAGGAAAATCTCTAGAAAAAACATCTAAGAAG

SEQ ID 856

MKVRKAVIPAAGLGTRFLPATKALAKEMLPIVDKPTIQFIVEEALKSGIEDILVVTGKSKRSIEDHFDSNFELEYNLKEKGKNELLKLVDETTGIR
LHFIRQSHPRGLGDAVLQAKAFVGNEPFVVMLGDDLMDITNNKVIPLTKQLINDFEATHASTIAVMEVPHEDVSAYGVIAPQGEGVNGLYSVNTFV
EKPSPEEAPSNLAIIGRYLLTPEIFNILETQKPGAGNEIQLTDAIDTLNKTQRVFARKFTGDRYDVGDKFGFMKTSIDYALQHPQVKDDLKKYIID
LGKSLEKTSKK

SEQ ID 857

ATGACCAAAGTCAGAAAAGCCATTATTCCTGCTGCAGGTCTAGGAACACGTTTTTTACCTGCTACCAAAGCTCTTGCCAAAGAGATGTTGCCCATC
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GAGGACCATTTTGATTCAAACTTTGAATTAGAATACAACCTCCAAGCTAAGGGGAAAAATGAACTGTTGAAATTAGTGGATGAAACCACTGCCATT
AACCTTCATTTTATCCGTCAAAGCCACCCAAGAGGGCTGGGAGATGCTGTCTTACAAGCCAAAGCCTTTGTGGGCAATGAACCCTTTGTGGTCATG
CTTGGAGATGACTTAATGGACATTACAAATGCATCCGCTAAACCTCTCACCAAACAACTCATGGAGGACTATGACAAGACGCATGCATCCACTATC
GCTGTGATGAAAGTTCCTCATGAAGATGTGTCTAGCTATGGGGTTATCGCTCCTCAAGGCAAGGCTGTCAAGGGCCTTTACAGTGTAGACACCTTT
GTTGAAAAACCACAACCAGAAGATGCGCCTAGTGATTTGGCTATTATTGGTCGTTACCTCCTAACCCCTGAAATTTTTGGTATTTTGGAAAGACAG
ACCCCTGGAGCAGGTAACGAAGTGCAACTCACAGATGCTATCGATACCCTCAATAAAACTCAGCGTGTCTTTGCACGAGAATTTAAAGGCAATCGT
TACGATGTTGGGGATAAATTTGGATTCATGAAAACATCTATCGACTATGCCTTAGAACACCCACAGGTCAAAGAGGACTTGAAAAATTACATTATC
AAACTAGGAAAAGCTTTGGAAAAAAGTAAAGTACCAACACATTCAAAG

SEQ ID 858

MTKVRKAIIPAAGLGTRFLPATKALAKEMLPIVDKPTIQFIVEEALKSGIEEILVVTGKAKRSIEDHFDSNFELEYNLQAKGKNELLKLVDETTAI
NLHFIRQSHPRGLGDAVLQAKAFVGNEPFVVMLGDDLMDITNASAKPLTKQLMEDYDKTHASTIAVMKVPHEDVSSYGVIAPQGKAVKGLYSVDTF
VEKPQPEDAPSDLAIIGRYLLTPEIFGILERQTPGAGNEVQLTDAIDTLNKTQRVFAREFKGNRYDVGDKFGFMKTSIDYALEHPQVKEDLKNYII
KLGKALEKSKVPTHSK

SEQ ID 859

ATGATTTTTTTATGTTATGATAGAAATCTGTTTTTATGTGACTATAACTTATTAGGAGGTTCATTCTCGGTGAACAGAAAAATTATTGGCTTAACT
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GATTATTTCCAGTCATCTAATGAATCAGATCATGCTAATAACCTTGATACGGCAGCCTCTAGTGGTTATAATTTAATTTTTGGTATTGGATTTGGT
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GTCAAAAAAGCTAAAGAGGATATTGTTTCAGGGAAAATACAAGTTCCTATGAAA

SEQ ID 860

MIFLCYDRNLFLCDYNLLGGSFSVNRKIIGLTLLSLSVLTLTACGNRSDKSANKSDIKVAMVTNQGGVDDKSFNQSAWEGLQKWGKKKGLTKGNGF
DYFQSSNESDHANNLDTAASSGYNLIFGIGFGLHDTIEKVSENNKDVKYVIVDDIIKGKENVASVTFADNEAAYLAGVAAAKTTKTKTVGFIGGME
GVVVKRFEAGFKAGVKSIDPAIKVAVSYAGSFTDAAKGKTIAATQYATGVDVIYQAAGGTGAGIFSEAKTENETRKESNKVWVIGVDRDQSQEGNY
VSKDGKKANFVLASTIKEVGKSLQSVAELTEKKQYPGGKVTVFGLKDSGVDIKEHQLSSEGSVAVKKAKEDIVSGKIQVPMK

SEQ ID 861

ATGAACAAGAAATTTATTGGTCTTGGTTTAGCGTCAGTGGCTGTGCTGAGTTTAGCTGCTTGTGGTAATCGTGGTGCTTCTAAAGGTGGGGCATCA
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GGTAAAGAAATGGGCCTTCAAAAAGGAACAGGTTTCGATTATTTTCAATCTACAAGTGAATCTGAGTATGCAACTAATCTCGATACAGCAGTTTCA
GGAGGGTATCAACTGATTTATGGTATCGGCTTTGCATTGAAAGATGCTATTGCTAAAGCAGCTGGAGATAATGAAGGAGTTAAGTTTGTTATTATC
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AAAACAAAAACAGTTGGTTTCGTGGGCGGTATGGAAGGAACTGTCATAACTCGATTTGAAAAAGGTTTTGAAGCAGGAGTTAAGTCTGTTGACGAT
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GCAACTACAAATGTTTCAAAAGAAGCTGTTAAAGCTATTAAAGAAGCGAAAGCAAAAATTAAATCTGGTGACATTAAAGTTCCTGAAAAA

SEQ ID 862

MNKKFIGLGLASVAVLSLAACGNRGASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAWEGLQSWGKEMGLQKGTGFDYFQSTSESEYATNLDTAVS
GGYQLIYGIGFALKDAIAKAAGDNEGVKFVIIDDIIEGKDNVASVTFADHEAAYLAGIAAAKTTKTKTVGFVGGMEGTVITRFEKGFEAGVKSVDD
TIQVKVDYAGSFGDAAKGKTIAAAQYAAGADVIYQAAGGTGAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVG
KAVQLINKQVADKKFPGGKTTVYGLKDGGVEIATTNVSKEAVKAIKEAKAKIKSGDIKVPEK

SEQ ID 863

ATGTCTATGAAGAAGTTCGCTAAAGAGTATCCGACGACAGTACTCTTGGTCAGTCTGACAACCCTTGTTTTTTTATTGATGCAACTAACTTATGGA
AGTCAAGCGGAGTCTAGCCAAGTTATTTTTCAATTTGGTGGAATACAAGGTGATTATCTAAAAGCATATCCAACAAATCTATGGAGACTAATAAGT
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AAACAAAATGGTTCTTTATTATTTAAAACTTGGCAAAGTATTTTAGCTTTAATGATATTTATTATTGTATCGATCAGCTTAATAGGTCTATCGTTG
GTA

SEQ ID 864

MSMKKFAKEYPTTVLLVSLTTLVFLLMQLTYGSQAESSQVIFQFGGIQGDYLKAYPTNLWRLISPIFVHIGWEHFLLNGLALYFVGQMGESIWGSL
RFLILYILSGLMGNIFTLFFTPHVVAAGASTSLFGVFSAIAIAGYFGKNPYLKQVGKSYQVMILLNLFFNIFTPGVSLAGHVGGLVGGVLVAIFLT
KQNGSLLFKTWQSILALMIFIIVSISLIGLSLV

SEQ ID 865

ATGATATTGCTGTTTAGGAGGTTTATCTTAGATGACACAGTTATTAAAACGATATCCTATTACTATTTTCCTTTTAGGGTTAACAGGCTTAATTTT
TATAGCAATGCAAGTGGTATATGGACATTTAGCAACTGGTGCTCAAGCTATTTATCAAGTTGGAGGTATGTTTGGATTACTAGTAAAAGCAATGCC
AGACCAGTTGTGGCGATTGGTGACTCCGATATTTATTCATATCGGCTTTGGTCATTTTTTTGTCAATGGATTAACACTATATTTTGTTGGTCAAAT
CGTCGAAGACCTCTGGGGCTCACGCCTTTTTTATTACTTTATGTTTTATCAGGTGTTATGGGCAATGCCTTTACTTTTTGGTTGACTCCTGAAACA
GTAGCTGCAGGAGCATCGACGTCGTTATTTGGACTTTTTGCTGCTATTGTAGTATTGAGTTTTTTGGGTAAGAACCAAGCGTTGAAAGATTTGGGC
AAGTCATACCAGACGTTAATTGTAGTCAATTTACTGATGAATCTTTTTATGCCAAACGTGAGTATGGCAGGCCATATTGGCGGTGTCGTGGGTGGT
GCGTTACTGAGTATAGTTTTTCCAACTAAGATGAGAGTGATAACAGTGAAGAAAACCAAGCGAATGTTGGCTTTAGTGAGCTATGGTATTATTTTG
GTTGGTGTGTTAGTGCTTGGGTTTTTA

SEQ ID 866

MILLFRRFILDDTVIKTISYYYFPFRVNRLNFYSNASGIWTFSNWCSSYLSSWRYVWITSKSNARPVVAIGDSDIYSYRLWSFFCQWINTIFCWSN
RRRPLGLTPFLLLYVLSGVMGNAFTFWLTPETVAAGASTSLFGLFAAIVVLSFLGKNQALKDLGKSYQTLIVVNLLMNLFMPNVSMAGHIGGVVGG
ALLSIVFPTKMRVITVKKTKRMLALVSYGIILVGVLVLGFL

SEQ ID 867

ATGGAAAAGAAATTATTAAGAAAAGAAGTTTTGATAACCTTAAAATCTCAACCTCAAGCTTACAAATCAGAAGTTGACTGTAAACTTTTAGAGGCT
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TTATGTGATGGCAAACGTGTCCTTGTTCCCAAAACTTATCCAAAAGGTAAAATGATTTTTGTGGACTATCAAAAAGATAACTTGAGGACAACACCG
TTTGGCTTATTAGAACCTGTTAATGATAGAGCTGTTGAAAAAGCTAGTATAGACTTAATTCATGTGCCCGGACTTATCTTTAACAATAAAGGTTTT
CGTATAGGTTATGGTGCAGGTTATTTTGATCGCTATTTGAGTGATTTTGAAGGTGATACTATTAGTACTATTTATAGGTGTCAGAGACAGGATTTT
GTAGAAGAGAAGCATGACGTAGCAGTTAAGGAGGTATTATGTCTA

SEQ ID 868

MEKKLLRKEVLITLKSQPQAYKSEVDCKLLEAFIKTKAYQNSCVIATYLSFDYEYNTQLLIKQALCDGKRVLVPKTYPKGKMIFVDYQKDNLRTTP
FGLLEPVNDRAVEKASIDLIHVPGLIFNNKGFRIGYGAGYFDRYLSDFEGDTISTIYRCQRQDFVEEKHDVAVKEVLCL

SEQ ID 869

ATGGACCTCCCAGAAAACTATGACAAAGAAGAATTTTCTCGCATTCAAAAAGCCGCTGAAAAGATTAAATCAGATAGCGAAGTACTCGTGGTTATT
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CAGATTCTTTATGCTGGAAATTCTATTTCATCTACTTACCTTGCCGATTTAGTTGAATACGTCCAAGATAAAGAATTCTCAGTAAATGTCATTTCA
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GGTGTACTCCTTGCTCATACAGATGGTGGGGTTCCAAATATGTTTGTAACGCTTCCTACACAAGACGCTTACACCCTTGGTTACACTATTTACTTC
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CTAGGTAAACCTGGATTCGAAGAGCTTAGCGCTGAATTGAATGCACGTCTT

SEQ ID 870

MDLPENYDKEEFSRIQKAAEKIKSDSEVLVVIGIGGSYLGAKAAIDFLNNHFANLQTAEERKAPQILYAGNSISSTYLADLVEYVQDKEFSVNVIS
KSGTTTEPAIAFRVFKELLVKKYGQEEANKRIYATTDKVKGAVKVEADANNWETFVVPDNVGGRFSVLTAVGLLPIAASGADITALMEGANAARKD
LSSDKISENIAYQYAAVRNVLYRKGYITEILANYEPSLQYFGEWWKQLAGESEGKDQKGIYPTSANFSTDLHSLGQFIQEGYRNLFETVVRVEKPR
KNVTIPELTEDLDGLGYLQGKDVDFVNKKATDGVLLAHTDGGVPNMFVTLPTQDAYTLGYTIYFFELAIGLSGYLNSVNPFDQPGVEAYKRNMFAL
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SEQ ID 871

ATGTCACATATTACATTTGATTATTCAAAAGTCCTCGAGTCATTTGCGGGACAACATGAAATTGATTTTTTACAAGGCCAAGTAACAGAAGCTGAC
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CTC

SEQ ID 872

MSHITFDYSKVLESFAGQHEIDFLQGQVTEADKLLREGTGPGSDFLGWLDLPENYDKDEFARILTAAEKIKADSEVLVVIGIGGSYLGAKAAIDFL
NHHFANLQTAKERKAPQILYAGNSISSTYLADLVEYVQDKEFSVNVISKSGTTTEPAIAFRVFKELLVKKYGQEEANKRIYATTDKVKGAVKVEAD
ANNWETFVVPDNVGGRFSVLTAVGLLPIAASGADITALMEGANAARKDLSSDKISENIAYQYAAVRNVLYRKGYITEILANYEPSLQYFGEWWKQL
AGESEGKDQKGIYPTSANFSTDLHSLGQFIQEGYRNLFETVIRVDNPRKNVIIPELAEDLDGLGYLQGKDVDFVNKKATDGVLLAHTDGGVPNMFV
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SEQ ID 873

GTGAAACATTTAACAAATCAAAAGGAGTCTCAAATGACTGAAAAAACTAAAGCAGTAGAAACTACAGATGTTGCTCTTGCAATTGATACATTGGTT
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CATGGAGAACTTGCTCTTCATGCAGTAGAAGAAACTGGTCGTGGTGTCTTTGAAGATAAAGCGACAAAAAATTTATTTGCATGTGAACACGTCGTT
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CGCCTTCCGATGGTAGATCACATGCAAGAAATCATCGAAGATGCTTATTATGGTTATGAGGAACGTCCAGGACGTCGTAAG

SEQ ID 874

MKHLTNQKESQMTEKTKAVETTDVALAIDTLVQNGLKALDEMRQLNQEQVDYIVAKASVAALDAHGELALHAVEETGRGVFEDKATKNLFACEHVV
NNMRHTKTVGVIEEDDVTGLTLIAEPVGVVCGITPTTNPTSTAIFKSLISLKTRNPIIFAFHPSAQESSAHAARIVRDAAIAAGAPENCVQWIEQP
SIDATNALMNHDGIATILATGGNAMVKAAYSCGKPALGVGAGNVPAYVEKSANIRQAAHDIVMSKSFDNGMVCASEQAVIIDKEIYKEFVEEFKSY
HTYFVNKKEKALLEEFCFGAKANSKNCAGAKLNPNIVGKSAVWIAEQAGFTVPEGTNILAAECTEVSEKEPLTREKLSPVIAVLKAESTEDGVEKA
RQMVEFNGLGHSAAIHTKDADLAREFGTRIRAIRVIWNSPSTFGGIGDVYNAFLPSLTLGCGSYGRNSVGDNVSAINLLNIKKVGRRRNNMQWFKV
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TGMDVLTHATEAYVSQMANDYTDGLALQAIKIVFDYLERSVKDADFEAREKMHNASTMAGMAFANAFLGISHSMAHKIGAQFHTVHGRTNAILLPY
VIRYNGTRPAKTATWPKYNYYRADEKYQDIAKLLGLPAATPEEAVESYAKAVYDLGTRLGIKMNFRDQGIDEKEWKEKSRELAFLAYEDQCSPANP
RLPMVDHMQEIIEDAYYGYEERPGRRK

SEQ ID 875

ATGACTGAAGGACATAATACTGTTGAAACAACCTCTGTTTCTGTGACAATTGATGCTCTTGTTCAAAAAGGTTTAGCTGCTCTTGAAGAGATGCGT
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ACAGGTCGCGGTGTCTTTGAAGATAAAGCAACAAAACATCTATTTGCTTGTGAGCATGTGGTTAATAACATGCGCCATCAAAAAACAGTAGGAATT
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ATTGAAGATGCTTACTATGGTTATGCTGAACGTCCAGGACGACGTAAG

SEQ ID 876

MTEGHNTVETTSVSVTIDALVQKGLAALEEMRKLDQEQVDYIVAKASVAALDAHGELAKHAYEETGRGVFEDKATKHLFACEHVVNNMRHQKTVGI
IEEDDVTGLTLIAEPVGVICGITPTTNPTSTAIFKSLISLKTRNPIIFAFHPSAQESSAHAARIVRDAAIAAGAPENCVQWVETPSLEATNALMNH
DGIATILATGGNAMVKAAYSCGKPALGVGAGNVPAYVEKSANIRQAAHDIVMSKSFDNGMVCASEQAVIIDKEIYDDFVAEFKSYHTYFVNKKEKA
LLEEFCFGAKANSKNCAGAKLNPNIVGKPATWIAEQAGFTVPEGTNILAAECKEVSENEPLTREKLSPVIAVLKSESREDGVEKARQMVEFNGLGH
SAAIHTADAELAKEFGTRIRAIRVIWNSPSTFGGIGDVYNAFLPSLTLGCGSYGRNAVGDNVSAINLLNIKKVGRRRNNMQWFKVPSKTYFERDSI
QYLQKCRDVERVMIVTDHAMVELGFLDRIIEQLDLRRNKVVYQIFAEVEPDPDITTVMKGTELMRTFKPDTIIALGGGSPMDAAKVMWLFYEQPEV
DFHDLVQKFMDIRKRAFKFPELGKKTKFVAIPTTSGTGSEVTPFAVISDKANNRKYPIADYSLTPTVAIVDPALVLTVPGFIAADTGMDVLTHATE
AYVSQMANDFTDGLALQAIKIVFDNLEKSVKTADFEAREKMHNASTMAGMAFANAFLGISHSMAHKIGAQFHTVHGRTNAILLPYVIRYNGTRPAK

TATWPKYNYYRADEKYQDIAKLLGLPASTPEEAVESYAKAVYDLGCRVGIQMNFKAQGIDENEWKEHSRELAYLAYEDQCSPANPRLPMVDHMQEI
IEDAYYGYAERPGRRK

SEQ ID 877

GTGCATTATAGTGATAGCGATACTACAGGGGCTGATTTATATGTTAGTAACGTCAAAAAAGCTATTCAAAAATCAGCTCAACGAGCTGCAAAA

SEQ ID 878

MHYSDSDTTGADLYVSNVKKAIQKSAQRAAK

SEQ ID 879

ATGAGAATAAAATGGTTTTCGTTTGTTAGGGTAACAGGACTTTTACTGGTTTTACTCTACCACTTTTTTAAAAATGTATTTCCAGGAGGTTTTATT
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CTCTTTGTTCATACGTGGAGCTTAGCTATTGAAGTTCATTTTTACTTGTTTTGGGGTGTATTTGTTTGGTTATTAGCTAGACGCAAGGAGACTCAG
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TCCCTGATTTATTTTTCGAGTCTTTCTCACAGTTTTCCCTTCTTTTTAGGGGCGATGTTTGCCACGATAACAGGTATTAACGAGACTACTGTTCGA
TTTCAAAAAAATGTACGTTTATGGCCGCGCCAGTATGTCCTTGCTGCTATGATTGGAGCATTTACACTTTTGCTTGTGCTAACGGTCACATTGGAT
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CCAGATGTACAAGAGCCTAAAGCTATCACTTATATAGCTGATATTAGCTATGGGATTTACCTCTTCCATTGGCCATTTTACATTATTTTTAGCCAA
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AGAAAACCAAACCTGCTTGGTTTAGAAATTGACTGTTCTCCTTACTATAAGTGGATTGTAGGAGGGTCTCTCGCCTTAGCATTATTAACTTTAGGA
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CTAGCTGCAGGAGACGCTAATGCTTTGAGTGACGTAGGTATTATTGGTGATTCTGTAGCATTACGCTCTAGTGCAGCATTCTCACAAATTATGCCA
CAAGCGCAACTGGATGCAGCGGTCAGTCGGAATTTTAAAGAAGCTTTCGATTTATTTAATAACCAAATTAAATCTAAGAGTCTATCTAAGACTGTT
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TCTCCATATAATGCCAAAAATGCCAGTCAGGTTGCAGAAGCTAGAGACTATGGTCTTAAATTGTCCAAAAAATACAAGTATGTCACTATTGCAGAC
TGGTATAAAGTTGCTGTTGAACATCCAGATATTTGGTATGGCAGTGATGGTGTTCATTATAGTGAAGATAGTCAAGGAGCAGAACTATATGTCTCC
ACAATCCAGACTGCTGTTGAGAAGTCAGCTAAAAAACCAGCTAAA

SEQ ID 880

MRIKWFSFVRVTGLLLVLLYHFFKNVFPGGFIGVDIFFTFSGYLITALLIDEYTKKESIDIIGFLKRRFYRIVPPLVLMILLTIPFTFLIKKDFIA
NIGSQITAVLGFTTNIYEILTGSSYESQFIPHLFVHTWSLAIEVHFYLFWGVFVWLLARRKETQKQLRGLLFLISLGIFAISFLSMFIRSFMTSNF
SLIYFSSLSHSFPFFLGAMFATITGINETTVRFQKNVRLWPRQYVLAAMIGAFTLLLVLTVTLDFNHITTYLFGFALASLFASIMIYAARVLHEQT
PDVQEPKAITYIADISYGIYLFHWPFYIIFSQLMSHILAVILTVFFSILFATVSYYIVEPLVQGRKPNLLGLEIDCSPYYKWIVGGSLALALLTLG
TCMIAPKVGKFEKQLLVSSLQQAQSNMERTHTLAAGDANALSDVGIIGDSVALRSSAAFSQIMPQAQLDAAVSRNFKEAFDLFNNQIKSKSLSKTV
VLAVGVNSLDNYSQAVQSFIEALPKGHRLVLVSPYNAKNASQVAEARDYGLKLSKKYKYVTIADWYKVAVEHPDIWYGSDGVHYSEDSQGAELYVS
TIQTAVEKSAKKPAK

SEQ ID 881

ATGAGAATAAAATGGTTTTCTTTGGTACGTATAACAGGACTACTACTTGTTTTACTTTACCATTTCTTTAAGAATAGTTTTCCAGGAGGATTTGTT
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TGTCGTAGACGTTTTTACCGTATTTTCCCACCATTAGTATTGATGGTTTTGGTGACAATACCTTTTGTATTTCTGGTTAAAAGCGATTTTAGAGCA
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TCAACGATATATTTCTCTACATTATCACATATATTTCCGTTCTTTTTAGGAGCGATGGTGGCTACAATATCTGGTATTCGAGAGATTACCGGACGA
TTCAAGNNNNNT

SEQ ID 882

MRIKWFSLVRITGLLLVLLYHFFKNSFPGGFVGVDIFFTFSGFLITALLIDEFSKTKKIDFVSFCRRRFYRIFPPLVLMVLVTIPFVFLVKSDFRA
SIGSQIMTALGFTSNFYEILTGGNYESQFIPHLFVHTWSLSIEVHFYVLWGLTVWLLSKRSKDQKQLRGTLFLISMGIFGVSFLTMFVRAFFVDNF
STIYFSTLSHIFPFFLGAMVATISGIREITGRFKXX

SEQ ID 883

ATGAAGAATTTTAAAATAACACGAACTCATCTAGAAATATTATCTTTGATAATTATTGTTGTTTTTGGTTTATCAGTATTTACCTTAACGACTTCT
AGTCAAGGAGTCTTTAGCTATGATGGCGGCAAGATAAAATATGTGGGCTCTATTGTTAATCACCATATGACTGGTAAAGGTAAATTAACCTATGAG
AATGGGGATTACTATAAGGGCGATTTTGTAAATGGAGTCTTTGAAGGGAAAGGAACATTTGTTTCAGTTCATGGCTGGTCTTATACAGGTGACTTT
AAAAAAGGTCAACCTGATGGACAAGGTCGCCTCAATGCTAAAAATAAGAAAGTCTATAAGGGGACATTTAAACAGGGGATTTATCAAAAA

SEQ ID 884

MKNFKITRTHLEILSLIIIVVFGLSVFTLTTSSQGVFSYDGGKIKYVGSIVNHHMTGKGKLTYENGDYYKGDFVNGVFEGKGTFVSVHGWSYTGDF
KKGQPDGQGRLNAKNKKVYKGTFKQGIYQK

SEQ ID 885

ATGATAGATATGCAAGATATAGTAAAAAAATGGAGTATTACACGGGCGAAGTTGGAAATTGTCTCGGTGATTGTCATATTGGTTTGTGCAATTTCT
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GAAGGGAAGCTTGTCTACCCCAACGGTGATATCTATGAGGGTACTTTTAAGGATGGCCTATTTGAAGGAAAAGGAACTTTTACTGCTAAGACGGGC
TGGTTATATAACGGGGAGTTTCATAAAGGACAAGCAAATGGCAAAGGTGTGTTAAAAGCAAAGAATAATAAAGTCTATAAAGGGATTTTTAAACAG
GGGATATTTCAAAAA

SEQ ID 886

MIDMQDIVKKWSITRAKLEIVSVIVILVCAISVFSVRISNKTSLTYDKGRMHYTGYVINHKMNGEGKLVYPNGDIYEGTFKDGLFEGKGTFTAKTG
WLYNGEFHKGQANGKGVLKAKNNKVYKGIFKQGIFQK

SEQ ID 887

ATGACAAGATTTTTAGATAGTGATGCAATGGGTGACGAAGAATTGGTAGAACGTACACTTCGTCCGCAGTATTTAAGAGAGTATATTGGACAAGAT
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ATTTTAAATGATTTAGAACCAGGTGATGTTCTTTTTATTGATGAAATTCATCGTATGCCGATGGCGGTTGAAGAGGTACTTTATAGTGCAATGGAA
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GCAGGTATGTTATCTAATCCCTTACGTGCTCGCTTTGGTATTACAGGGCATATGGAGTATTATGAAGAAAATGATTTGACAGAAATTATTGAGCGT
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AAACGTGTTCGAGATTATGCTCAAATCATGGGAGATGGTTTGATAGATGACAATATTACAGATAAAGCATTAACGATGTTAGATGTTGATCACGAG
GGGCTTGATTACGTCGATCAAAAAATCTTAAGAACCATGATTGAAATGTATAATGGAGGTCCTGTTGGTTTAGGAACTCTATCCGTTAATATTGCT

GAAGAACGAGATACTGTTGAAGACATGTACGAACCTTATTTAATTCAAAAAGGTTTTATTATGCGTACCCGTACCGGTCGTGTAGCTACGGTTAAG
GCATATGAACATTTAGGTTATCAGCGATTTGATAAA

SEQ ID 888

MTRFLDSDAMGDEELVERTLRPQYLREYIGQDKVKDQLKIFIEAAKLRDESLDHVLLFGPPGLGKTTMAFVIANELGVNLKQTSGPAIEKSGDLVA
ILNDLEPGDVLFIDEIHRMPMAVEEVLYSAMEDFYIDIMIGAGETSRSVHLDLPPFTLIGATTRAGMLSNPLRARFGITGHMEYYEENDLTEIIER
TADIFEMKITYEAASELARRSRGTPRIANRLLKRVRDYAQIMGDGLIDDNITDKALTMLDVDHEGLDYVDQKILRTMIEMYNGGPVGLGTLSVNIA
EERDTVEDMYEPYLIQKGFIMRTRTGRVATVKAYEHLGYQRFDK

SEQ ID 889

GTGCTGTTGACTGGTGGCGATTATAATAAAAGTAGGCCACTGCTCTCTTTTACTTTATGTTATAATAGTCTTATGGCTAGAATTTTAGACAATAAT
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TTTATAGAAGCAGCTAAAAGACGTGACGAATCTTTAGACCATGTTTTATTATTTGGACCTCCAGGACTGGGAAAAACAACAATGGCATTTGTGATT
GCCAATGAATTGGGAGTTAATTTAAAGCAAACTTCAGGTCCTGCCGTTGAGAAAGCTGGAGATTTGGTAGCTATTTTAAATGAATTAGAACCAGGG
GATATTTTGTTTATTGATGAAATTCACCGCATGCCAATGTCTGTCGAGGAAGTACTATATAGTGCTATGGAAGACTTCTATATTGATATTATGATT
GGCGCTGGAGATACTAGTCGTAGTATTCATTTGGATCTGCCTCCATTTACATTGATTGGTGCTACTACACGTGCAGGCATGTTATCTAATCCCCTC
AGAGCTCGTTTTGGTATCACTGGTCACATGGAATACTATCAAGAAAAGGATTTGACAGAGATTGTGGAGCGTACAGCTACTATTTTTGAAATAAAA
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ATGTATGAACCCTACTTAATTCAAAAAGGCTTTCTCATGCGAACACGAACAGGTCGTGTAGCGACGCAAAAGGCTTATCGTCATCTTGGCTATCCC
TATCAAAACACT

SEQ ID 890

VLLTGGDYNKSRPLLSFTLCYNSLMARILDNNVMGNEEFSDRTLRPQYLHEYIGQDKVKEQFAIFIEAAKRRDESLDHVLLFGPPGLGKTTMAFVI
ANELGVNLKQTSGPAVEKAGDLVAILNELEPGDILFIDEIHRMPMSVEEVLYSAMEDFYIDIMIGAGDTSRSIHLDLPPFTLIGATTRAGMLSNPL
RARFGITGHMEYYQEKDLTEIVERTATIFEIKIDHEAARKLACRSRGTPRIANRLLKRVRDYAQIIGDGIITAQITDRALTMLDVDREGLDYIDQK
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SEQ ID 891

ATGTTAAAACATTTTGGTAGTAAAGTAAGAAATTTGAGAGTAACTAGAAATATTACTCGCGAAGATTTTTGTGGTGATGAAACTGAGTTATCTGTA
AGACAATTAGCTAGGATTGAAAGTGGACAGTCAATTCCAAACTTGACTAAAGCTCACTACATAGCTAAACAATTGAATGTAAAATTGGATATTTTA
ACAGGAGGAGAGAGCTTAGAATTACCTAAACGGTATAAAGAGTTGAAGTATTTGATTTTAAGAATTCCAACTTATGCAGATGCTGAACGATTAAAA
TTAAGAGAATGTCAGTTTGATCATATTTTCGAAGAATTCTATGATAATCTTCCAGAAGACGAGTGCTTAGCAATTGACAGTTTACAAGCTAAATTT
GAAGTCTATCAAACAGGAGACATTAATTTTGGTGTGGAGGTTTTATGCGAATGCTTTGATAAAGTAAAATATAAAGAAAAATATACTCTTAATGAT
TTGATTATCATAGATTTGTTTTTAACTTGTGCAGTTGTATCTAAATTTAACAATAGAGCATTTACTAAAGAAGTATTTCAAACTATATGTAAAACT
TTGATAAGTCAGAACCACAAACTTACAGCAGAAGATTTGTTTTGGTTTAATCATGTACTCCTGAATTGTGTATTTGTTGGACTTTGTTTAAATAGT
GAAGAGTGTCTTGCAGAAATGTTAGAAGTTAGCCGACAAACGATGGTGTCAACACATGATTTTCATAAAATGCCTTTATATTTTATGTACCAATGG
AAATACTTCATTACAATTGACAATGATATAAAGTCTGCAGAAAATGCTTACCAACAATCAATTATGTTTTCAAAAATGATTGATGACAAGCATCTA
ATTAAAAAATTAGAATTGGAGTGGCAAGAAGATATAACAGGACAT

SEQ ID 892

MLKHFGSKVRNLRVTRNITREDFCGDETELSVRQLARIESGQSIPNLTKAHYIAKQLNVKLDILTGGESLELPKRYKELKYLILRIPTYADAERLK
LRECQFDHIFEEFYDNLPEDECLAIDSLQAKFEVYQTGDINFGVEVLCECFDKVKYKEKYTLNDLIIIDLFLTCAVVSKFNNRAFTKEVFQTICKT
LISQNHKLTAEDLFWFNHVLLNCVFVGLCLNSEECLAEMLEVSRQTMVSTHDFHKMPLYFMYQWKYFITIDNDIKSAENAYQQSIMFSKMIDDKHL
IKKLELEWQEDITGH

SEQ ID 893

ATGTTAGAACATTTTGGTGGAAAAGTAAAAGTGTTAAGACTTGAAAAGAGGATTAGTCGCGAGGACTTGTGTGGGGATGAGTCTGAACTTTCTGTT
CGTCAATTAGCACGGATAGAACTAGGTCAATCCATACCAAGTTTAAGTAAGGTTATTTTTATTGCAAAAGCCTTAAACGTTAGTGTCGGTTACTTA
ACTGATGGTGCTGATTTAGAACTACCTAAGCGTTACAAAGAATTAAAATACCTTATCTTAAGGACACCAACTTACATGGATGATGGAAAATTACAA
GTACGAGAAGAGCAGTTTGATGAAATTTTTGAGGATTATTATGATAAATTACCAGAGGAAGAGAAAATAATCATTGATTGTTTACAGGCAACTTTA
GATACTTTATTGAGTGAGAATACTAACTTTGGCATTGACTTACTTCAAGAATATTTTAATCAAATAAAGACTAAGGTACGCTTTAGGCAAAATGAT
TTAATACTTCTAGAATTATATTTAGCTTATCTTGATATTGAGGGAATGGATGGACAATATTCAGATAAGATTTTTTATGATTCTTTATTAGATAAT
CTATCAGAACAATTTGAACAATTTGAATTAGATGAATTATTTATAGTTAATAAGATTATCATTGATATTTCATCACTAAGCTTAAAAAATAACCGA
CTTGATAATTTAGAAAAAGCGATTGAAATGAGTCAAAAAATTATGGCGAAAATTCAAGATTGGAATAGAATGCCTATTTTAAAACTAATAGAATGG
AAATATTTTTTAATCAAACAAAAAGATATAATAAAAGCAGAACAATCATTTATGAAGGCATGTTTGTTCGCCCAAATGACAGCTGATCAGTATTTG
GAAAACAAGTTAATTCAAGAGTGGGAAAAAGATGTTAAAAGTTAT

SEQ ID 894

MLEHFGGKVKVLRLEKRISREDLCGDESELSVRQLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPKRYKELKYLILRTPTYMDDGKLQ
VREEQFDEIFEDYYDKLPEEEKIIIDCLQATLDTLLSENTNFGIDLLQEYFNQIKTKVRFRQNDLILLELYLAYLDIEGMDGQYSDKIFYDSLLDN
LSEQFEQFELDELFIVNKIIIDISSLSLKNNRLDNLEKAIEMSQKIMAKIQDWNRMPILKLIEWKYFLIKQKDIIKAEQSFMKACLFAQMTADQYL
ENKLIQEWEKDVKSY

SEQ ID 895

ATGATCGAACGTTATTCACGCCCTGAGATGGCGGCAATTTGGACAGAGGAAAATAAATACCGTGCTTGGTTGGAGGTCGAGATTTTGGCTGACGAG
GCATGGGCTGAGTTGGGTGAGATTCCTAAGGAGGATGTGGCTAAGATTCGTGAGAAGGCGGATTTTGACATTGACCGCATTCTTGAGATTGAGCAG
GACACGCGTCACGATGTGGTGGCTTTCACTCGTGCGGTTTCTGAGACGCTTGGTGAGGAGCGCAAGTGGGTGCACTACGGTTTGACGTCGACTGAC
GTGGTGGACACTGCCTACGGTTACCTCTACAAGCAGGCTAACGATATTATCCGTCGTGACCTTGAGAATTTCACAAATATTGTGGCTGATAAGGCT
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TTTGTGGAACAATATGTTTGTGACAAATTGGGCATCCGTCCGCAAGAGATTTCAACACAGGTTCTTCCACGTGACCTCCACGCAGAATATTTTGCA
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AAAGGTCAGAAAGGTAGCTCTGCTATGCCTCACAAACGCAACCCAATCGGTTCAGAGAACATGACTGGGCTAGCGCGCGTGATTCGTGGTCACATG
GTGACGGCTTATGAGAACGTGGCACTTTGGCACGAGCGTGATATTTCGCACTCATCTGCTGAGCGTATCATCACACCTGACACAACGATCTTGATT
GACTACATGCTCAACCGTTTTGGCAATATCGTTAAGAACTTGACTGTCTTCCCGGAAAATATGATGCGCAATATGGAATCAACTTTTGGTTTGATT
TATAGTCAACGTGTTATGCTCAAATTGATTGAAAAAGGAATGACACGAGAAGAAGCTTATGACTTAGTTCAACCTAAGACAGCTTATTCCTGGGAC
AATCAAGTGGATTTCAAACCACTTTTAGAAGAAGACACCAAAGTTACCTCTTGTCTTACACAGGAAGAAATTGATGAACTATTTAATCCGATTTAT
TACACAAAACGTGTTGATGATATTTTTGAAAGACTAGGATTAGAAAAA

SEQ ID 896

MIERYSRPEMAAIWTEENKYRAWLEVEILADEAWAELGEIPKEDVAKIREKADFDIDRILEIEQDTRHDVVAFTRAVSETLGEERKWVHYGLTSTD
VVDTAYGYLYKQANDIIRRDLENFTNIVADKAKEHKFTIMMGRTHGVHAEPTTFGLKLATWYSEMKRNIERFEHAAAGVEAGKISGAVGNFANIPP

FVEQYVCDKLGIRPQEISTQVLPRDLHAEYFAVLASIATSIERMATEIRGLQKSEQREVEEFFAKGQKGSSAMPHKRNPIGSENMTGLARVIRGHM
VTAYENVALWHERDISHSSAERIITPDTTILIDYMLNRFGNIVKNLTVFPENMMRNMESTFGLIYSQRVMLKLIEKGMTREEAYDLVQPKTAYSWD
NQVDFKPLLEEDTKVTSCLTQEEIDELFNPIYYTKRVDDIFERLGLEK

SEQ ID 897

ATGCTAGAACGTTATTCACGCCCTGAGATGGCGGCAATTTGGACAGAGGAAAATAAATACCATGCTTGGTTGGAGGTCGAGATTTTGGCTGACGAG
GCATGGGCTGAGTTGGGTGAGATTCCTAAGGAGGATGTGGCTAAGATTCGTGAGAAGGCGGATTTTGACATTGACCGCATTCTTGAAATTGAGCAG
GACACGCGTCACGATGTGGTGGCTTTCACGCGTGCGGTTTCTGAAACGCTTGGTGAGGAGCGCAAGTGGGTGCACTACGGTTTGACCTCGACTGAC
GTGGTGGACACTGCCTATGGTTACCTCTACAAGCAAGCTAACGACATTATCCGTCGCGATCTTGAGAATTTCACCAATATCGTGGCAGACAAGGCG
CGTGAGCACAAAATGACCATCATGATGGGTCGTACCCACGGTGTTCACGCCGAGCCAACGACTTTCGGTCTTAAGTTGGCGACTTGGTACAGCGAG
ATGAAACGTAATATTGAGCGTTTTGAACATGCTGCCGCAGGTGTGGAAGCTGGTAAGATTTCAGGTGCCGTTGGTAACTTTGCCAACATCCCACCT
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SEQ ID 898

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VTAYENVSLWHERDISHSSAERIITPDTTILIDYMLNRFGNIVKNLTVFPENMMRNMESTFGLIYSQRVMLKLIEKGMTREEAYDLVQPKTAYSWD
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SEQ ID 899

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SEQ ID 900

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EKSLIIKFLLTISFVFVIDFAMVRLLNFNIKFSTILACSAILLAWLYQNKSVTEPFLLKKLVIYFIFFIATLIGNLKNELSILETPLLFISIFFTM
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SEQ ID 901

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ATGTTCCCAAAGCCTCAACATCATCGTAAGGTGCCACAATCACCTCGC

SEQ ID 902

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SEQ ID 903

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SEQ ID 904

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SEQ ID 905

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SEQ ID 906

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FDLEISVIVSGNGKDVTVFPVQENIHRNNILSKTIVPARISDQLADKAKKTAVQIAKKLQLSGTLCVEMFTTADDIIVNEIAPRPHNSGRYSIEAC
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SEQ ID 907

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CTCATT

SEQ ID 908

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LI

SEQ ID 909

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SEQ ID 910

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RGIKIIIAGAGGAAHLPGMVAAKTTLPVIGVPVKSRALSGLDSLYSIVQMPGGVPVATMAIGEAGATNAALTALRILSIEDQNLADALAHFHEEQG
KIAEESSGELI

SEQ ID 911

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SEQ ID 912

MKLLVVGSGGREHAIAKKLLASKDVDQVFVAPGNDGMTLDGLDLVNIGISEHSRLIDFVKENEIAWTLIGPDDALAAGIVDGFNSAGLRAFGPTKA
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SEQ ID 913

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SEQ ID 914

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QSVVDTAVEMIVRPVLEGMVAEGRPYLGVLYVGLILTADGPKVIEFNSRFGDPETQIILPRLTSDFAQNIDDIMMGIEPYITWQKDGVTLGVVVAS
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SEQ ID 915

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SEQ ID 916

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SEQ ID 917

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SEQ ID 918

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SEQ ID 919

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SEQ ID 920

MIETMSLDDMREYLGQDQIPEDFDDFWKKQTMKYQGNIEYRLDKKDFNITFAQAYDLHFKGSNNSIVYAKCLFPKTNKPYPVVFYFHGYQNQSPDW
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SEQ ID 921

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TTTAAAAACAGGGGG

SEQ ID 922

MTRTVAIDIGGTMIKHGIVDNLGCIVEASELATEAYKGGPGILQKVCQIIDNYLAEGSIDGIAISSAGMVDPDEGCIFYSGPQIPNYAGTQFKKVL
EDTYQVRTEIENDVNCAGLAEAVSGSAKDSSIALCLTIGTGIGGCLIIDKTVFHGFSNSACEVGYMHLSDGDFQDLASTTALIADVAKAHGDEISR
WDGRRIFQEAKKGNEKCIASIDRMINYLGQGIANMVYVVNPEKVVLGGGIMAQKDYLQDKLSESLKRNLVTSLAEKTAIVFAQHENQAGMLGAYYH
FKNRG

SEQ ID 923

ATGAAGCATTATTTAGCAATTGATATTGGTGGTACTGCTATCAAGTATGGCTTGATTTCTGAAACAGGAGACCTGTTGGAAAAAGAGGAAATGGCC
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TCTTCTGCAGGAATGGTTAATCCTGATGAGGGAGAAATCTTTTATGCCGGCCCTCAGATTCCTAACTATGCTGGAACTCAGTTTAAAAAAGAGATT
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GCTCTTTGCTTGACAATTGGGACGGGAATCGGTGGCTGTTTATTGTTTAATTCCCAAGTTTTTCATGGTAGTAGTCATTCAGCTTGCGAAGTTGGT
TACCTTCATTTGTCAGATGGTCAGTTTCAGGATCTGGCATCTACCACAGCTCTTGTTCAAGAGGTGGTCTTAGCTTATGGCGATGACATTAGCCAA
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CTTGATAGCTACTTGGTTTCTAGTCTTGCCAAGAAAACTCAGCTGAAGTTTGCTAGTCATGGAAATAATGCTGGTATATTAGGAGCTTACTACCAT
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SEQ ID 924

MKHYLAIDIGGTAIKYGLISETGDLLEKEEMATEAYKGGPSILEKVKGLVKTYQDQMDLAGVAISSAGMVNPDEGEIFYAGPQIPNYAGTQFKKEI
EETFGLPCEVENDVNCAGLAEAISGSAKDYPVALCLTIGTGIGGCLLFNSQVFHGSSHSACEVGYLHLSDGQFQDLASTTALVQEVVLAYGDDISQ
WDGRRIFEQAKAGDAICIAAISKQVDYLGQGIANICYVVNPNVVVLGGGIMAQKDYLADKLKTALDSYLVSSLAKKTQLKFASHGNNAGILGAYYH
FKQKNERSCSFITLEKIENNLASS

SEQ ID 925

ATGAAAGATTTACAAAAATATCAAGGAATTATTCCTGCATTTTATGCTTGCTATGATGATAAGGGTGATATTTGTCCCGAACGAGTAAAAGCCCTG
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GCTGAAGCTATAGGTGTTGATGCTATTGCAGCAATTCCACCAATTTATTTTCGATTACCAGAGTATGCCATAGCAGATTATTGGAATACTATTAGT
CAAGCAGCACCACAAACTGATTTTATTATTTACAATATTCCTCAATTGGCAGGGGTTGCTTTGACATCGGATTTATATCGAAAAATGTTACAAAAT
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CAGTTAATTGTTGATAAAGATTTAGAAAAAGCGCGTGAACTTCAATTTACAATTAACGATATTATCACAAAGCTTTGTTCGGGTCATGGTAATATG
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SEQ ID 926

MKDLQKYQGIIPAFYACYDDKGDICPERVKALTNYFIDKGVQGLYVNGSSGECIYQSVADRKLVLENVMSVAKGKLTVIAHVACNNTKDSVELAMH
AEAIGVDAIAAIPPIYFRLPEYAIADYWNTISQAAPQTDFIIYNIPQLAGVALTSDLYRKMLQNPQVIGVKNSSMPVQDIQNFVAIGGENHIVFNG
PDEQFLGGRLMGAAAGIGGTYGVMPELYLTLNQLIVDKDLEKARELQFTINDIITKLCSGHGNMYAVIKAVLEINEQLTIGSVRLPLASVTEEDKP
IIKEAAEMIRHAKKQFC

SEQ ID 927

ATGACAGATCTTACGAAATACCAAGGCATTATTCCTGCCTTTTACGCTTGTTACGATGACCAGGGGAATATCAGCCCTGAGCGTGTGCGTGCCTTG
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TTAGAAAATGTCATGGCAGTCGCTAAGGGCAAGCTGACGATTATTAATCACGTTGCCTGCAACAACACTAAAGATAGTATTGAATTGGCAGCTCAT
TCAGAACGTTTGGGCGTGGATGCCATTGCAGCTATTCCGCCTATTTATTTCCGGTTACCAGAATATGCGGTTGCTGATTATTGGAATGCTATTTCT
TCGGCTGCTCCTCACACAGATTTTATCATCTATAATATTCCTCAACTGGCAGGGGTTGCCTTGACGCCAAGCCTTTATAAGACTATGTTGGCTAAT
AAGCGCGTGATTGGCGTTAAAAATTCATCTATGCCAGTGCAGGATATTCAAACCTTCTGTGCGATTGGTGGGGACGATCATATTGTTTTTAATGGC
CCAGATGAACAATTTCTAGGAGGGCGCTTGATGGGTGCTGCTGCAGGCATTGGTGGTACCTACGGGGCTATGCCAGAATTATTTTTAAGGCTGAAC
CAACTTATTGCTGACAAGGATTTAGAAAAGGCCAAGGCCCTTCAATATACTATTAATGAGATTATCGGTGTCCTTGTTTCTGCTCACGGCAATATG
TATGGGGTTATTAAAGAAGTACTTCGTATTAATGAGGGTCTTGATATTGGTTCTGTTCGATCACCTTTAGCTGAGTTGGTCGAGGAAGATAGGGTT
ATTTGCCAACGGGCTGCTGCTCTGATTAATCAGGCTAAGGAAACCTTT

SEQ ID 928

MTDLTKYQGIIPAFYACYDDQGNISPERVRALTQYYIDKGVQGLYINGSSGECIYQSVFDRQLVLENVMAVAKGKLTIINHVACNNTKDSIELAAH
SERLGVDAIAAIPPIYFRLPEYAVADYWNAISSAAPHTDFIIYNIPQLAGVALTPSLYKTMLANKRVIGVKNSSMPVQDIQTFCAIGGDDHIVFNG
PDEQFLGGRLMGAAAGIGGTYGAMPELFLRLNQLIADKDLEKAKALQYTINEIIGVLVSAHGNMYGVIKEVLRINEGLDIGSVRSPLAELVEEDRV
ICQRAAALINQAKETF

SEQ ID 929

GTGAAAAAAGCAAATCAATTAATAGCAGCGATTTTTGATGTTAACAACCCCTTTATGCAAGGTTGCAATGTTGTTTTTTGATCTGGCATTACTAAAC
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AGCATATACCTATTTCCTATGGCTGCCCGCTACGAAATGTCTCTTTTAGATACCGTGAAAAAGAGCTTTATAATGGCATGTTTAAACTTGAAATGG
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GCTTATACCGCCTTTGCTTACTTTAAAATTATTATTTTACAAAAACAATTTGCCTATTTCAGCAAACAACAAGGAGATTATCAA

SEQ ID 930

MKKANQLIAAIFDVNNPFMQGCNVVFDLALLNLLFMITCLPLVTIGAAKISLYRTLWQKLEGDQTNLLILYIKHLKKEWFQGMLLGLVELSILVVI
IFDLTILHYQIGFIVSFLKITCYAFLLLTVMTSIYLFPMAARYEMSLLDTVKKSFIMACLNLKWTGVLMFLLIMTWFIMVQSSLLFMLTVSAIFIF
AYTAFAYFKIIILQKQFAYFSKQQGDYQ

SEQ ID 931

TTGACATCGAAAAAACAGGGACTTTTACACTCTCTCTTCAAGCTTGATAGTAAATGGATGAGGGCTAGCGCAGCACTGTTTGATTTGCTCGTGTTT
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GTTAGTCAGCTTGTTACTACTTATAGCTCTCATTTTAAATATTACTTTAAAAGTGGGCTACGCCTTGGCCTTATTGAGCTTGGGATAATGACTATT
TGTCTCTTAGATCTTTTCTTAATTCGAAACCAATCAGGCCTAGTTTTTCAAGGGTTTAAAGTACTTTGCGTTGCTGTTTTATTTTTGGTGGTTATA
CTCTTTTTGTACGCTTATCCTCAGGCCGTCAAAAGAGACCTTTCCCTATCTACGCTGTTTAAGCGAAGCTTTTTATTAGCAGGACTCTTTTTTCCA
TGGAGTTTTGCTTTCTTGGCTTTTATTTGTCTCACGATATTTAGCCTACAATTGTCTCTGTTAACGTTATTTGGAGGCGTGTCTTTGCTAGCTATC
ATCGGCATCAGTAGTCTAACTTATCTCTACTTGATTATCATGGAATCTCTTCTTAGGCGATTCCCACTTAATAATGACATTGAA

SEQ ID 932

LTSKKQGLLHSLFKLDSKWMRASAALFDLLVFNLLFVLSCLPLLTIGVAKMALYASLLDWREGQVSQLVTTYSSHFKYYFKSGLRLGLIELGIMTI
CLLDLFLIRNQSGLVFQGFKVLCVAVLFLVVILFLYAYPQAVKRDLSLSTLFKRSFLLAGLFFPWSFAFLAFICLTIFSLQLSLLTLFGGVSLLAI
IGISSLTYLYLIIMESLLRRFPLNNDIE

SEQ ID 933

ATGATTTACGATCATTTATTGAATTTAACGCATTATAAAGATATTAATCCTAATTTAGATTTAGCGATTGATTATCTACTAAGTCATGATTTAAGG
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CATAAAAAATACCTTGATATACATTATGTCATTGAAGGACATGAAGTTATCAAATTGGGAAAAGGTGATAAGGTAGAGGTGGAGGAATACTTAGGC
GATATAGGATTTATCAAGTGCTCAGAAGAGACTTCTTTTGATTTGAGAGATAATTATATAGCCTTCTTTTTCCCAGAAGAAGCTCATCAGCCAAAT
GGTATGGGAAGTCTAGGTAATTATGTCAAAAAAGGGGTATTGAAAGTGTTAATGGCG

SEQ ID 934

MIYDHLLNLTHYKDINPNLDLAIDYLLSHDLRNLDIGTYHISPEVILMVQSNQLSESFDHIFEYHKKYLDIHYVIEGHEVIKLGKGDKVEVEEYLG
DIGFIKCSEETSFDLRDNYIAFFFPEEAHQPNGMGSLGNYVKKGVLKVLMA

SEQ ID 935

ATGAAAAAGAAAACATTCAGTGCTTATAACTTTTTAACGGCTCTTATCCTTTGTCTTTTGACAGTGCTTTTTATCTTTCCATTTTATTGGATTATG
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CAAAACCCAGCTTTGAGATGGCTTTGGAATAGTGTCTTTATCTCAATTATGACAATGTTCCTAGTTTGCTGTACATCGTCAATGGCAGGCTATGTT
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AGAATTATCAATTTTATGGGGATACATGATACCTTATGGGCGGTTATTTTACCTCTTGTTGGTTGGCCTTTTGGGGTCTTCTTGATGAAACAGTTT
TCTGAAAATATTCCAACAGAATTACTGGAATCAGCTAAAATTGATGGTTGTGGAGAGATTCGAACATTTATTAATGTAGCATTTCCAATTGTCAAA
CCTGGATTTGCTGCCCTAGCTATTTTCACATTTATCAATACTTGGAATGACTATTTTATGCAATTAGTTATGCTAACTTCTAGAAATAATCTGACC
ATTTCTCTTGGGGTAGCTACTATGCAGGCTGAAATGGCAACAAACTATGGCTTAATTATGGCAGGTGCAGCCTTAGCTGCTGTTCCTATTGTGACA
GTATTCTTAGTTTTCCAAAAATCCTTTACTCAGGGGATTACAATGGGAGCTGTTAAAGGA

SEQ ID 936

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAFKSQPDTIIIPPQWWPKAPTLENFKALTVQNPALRWLWNSVFISIMTMFLVCCTSSMAGYV
LAKKRFYGQKILFSLFIAAMALPKQVVLVPLVRIINFMGIHDTLWAVILPLVGWPFGVFLMKQFSENIPTELLESAKIDGCGEIRTFINVAFPIVK
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SEQ ID 937

ATGACGAAAAAGAAACTAACCGCATCAGATATCTTAACCACTGTGATGCTATGTGTTTTGACCATTTTGTTTATTTTTCCATTTTATTGGATTATG
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TCAGAAAATATTCCAACCGAGTTATTGGAATCCGCCAAGATTGATGGATGTGGCGAAATTCGTACCTTTTTCAATGTGGCTTTCCCTATTGTCAAA
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SEQ ID 938

MTKKKLTASDILTTVMLCVLTILFIFPFYWIMTGAFKAQADTIMIPPQWWPKAPTIENFKALVVQNPALKWLWNSVFISVATMFLVCGTSSLAGYA
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PGFAALAIFTFINTWNDYFMQLVMLTSRENLTISLGVATMQAEMATNYGLIMAGAAMAAVPIVTVFLVFQKSFTQGITMGAVKG

SEQ ID 939

ATGCGTACTAATAAGTTAAAGATGAGGGAAACGATGATAGCTTATGCTTTTCTAGCACCTATTCTCTTATTTTTCTTAATTTTTGTTTTTGCACCG
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CTTGCTATTATTATTATTTTGCTAACGACCTCAGTTGGTCAACCTATTATTCTATATATTGCGGCGATGGGAAATATTGATAATTCTCTTTGCGAA
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ACAATTAATTCATTTCAATGTTTTGCCTTAATCCAGCTCCTAACATCTGGTGGACCAAATTATTCAACAAGCACTTTGATGTATTATCTTTATGAA
AAAGCCTTTAAACTATCAGAATATGGCTATGCTAATACTATGGGAGTATTCCTAGCAGTAATGATTGCTTTAATAAGTTTTGCTCAATTTAAGATC
TTAGGAAATGATGTGGAATAT

SEQ ID 940

MRTNKLKMRETMIAYAFLAPILLFFLIFVFAPMVMGFVTSFFNYSMTQFTFIGLANYNRMFHDSIFMKSLINTVIIVIGSVPVVVFFSLFVAANTY
EKNVFSRSFYRCVFFLPVVTGSVAVTVVWKWIYDPMSGILNYILKSGHVIEQNISWLGDKHWALLAIIIILLTTSVGQPIILYIAAMGNIDNSLCE
AARVDGANEMQVFWQIKWPSLLPTTLYIAVITTINSFQCFALIQLLTSGGPNYSTSTLMYYLYEKAFKLSEYGYANTMGVFLAVMIALISFAQFKI
LGNDVEY

SEQ ID 941

GTGTTCCTAACAAGTGGCTTCTTTTCAATGCACATGTCAAATGGTCACTGGAAAGAAGCTTTTCTTTTTAGAAAAGTTGAACAGAAAAAAGAGGTA
TTTCAAGTGAACGTCAATAAATTAAAAATGAGAGAGACGCTCATCTCATACGCTTTCTTAGCTCCGGTCTTGGTTTTCTTTGTGATTTTTGTCTTG
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AAAATTTTAGGTAATGATGTGGAATAT

SEQ ID 942

VFLTSGFFSMHMSNGHWKEAFLFRKVEQKKEVFQVNVNKLKMRETLISYAFLAPVLVFFVIFVLIPMIMGFVTSFFNYSMTEFTFVGFANYARMFQ
DPIFMKSLINTLIIVIGSVPVVVFFSLFVAAKTYDKNVVARSFYRAVFFLPVVTGSVAVTVVWKWIYDPMSGILNYVLKYAHVIEQNISWLGDKHW
ALLAIIVILLTTSVGQPIILYIAAMGNIDNSLVEAARVDGATEFQVFWNIKWPSLLPTTLYIAVITTINSFQCFALIQLLTSGGPNYSTSTLMYYL
YEKAFKLSEYGYANTMGVFLAVMIAIISFAQFKILGNDVEY

SEQ ID 943

ATGAGTATCAAAAAAAGTGTGATTGGTTTTTGCCTCGGAGCTGCAGCATTATCAATGTTTGCTTGTGTAGACAGTAGTCAATCTGTTATGGCTGCC
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SEQ ID 944

MSIKKSVIGFCLGAAALSMFACVDSSQSVMAAEKDKVEITWWAFPTFTQEKAKDGVGTYEKKVIKAFEKKNPNIKVKLETIDFTSGPEKITTAIEA
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LKNKGYTPGSFFANGQGGDQGPRAFFANLYSAPITDKEVTKYTTDTKNSVKSMKKIVEWIKKGYLMNGSQYDGSADIQNFANGQTAFTILWAPAQP
KTQAKLLESSKVDYLEVPFPSEDGKPDLEYLVNGFAVFNNKDENKVKASKKFITFIADDKKWGPKDVIRTGAFPVRTSFGDLYKGDKRMMKISKWT
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SEQ ID 945

ATGAACATGAAGAAGTTAGCTTCATTAGCGATGCTTGGTGCATCTGTTTTAGGACTAGCAGCTTGTGGCGGAAAGAGCCAGAAAGAGGCTGGTGCA
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TGGACAAAATTCTACTCACCATACTATAACACGATTGATGGGTTTGCTGAAATGAGAACTCTTTGGTTCCCAATGGTTCAAGCCGTCTCTAATGGT
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SEQ ID 946

MNMKKLASLAMLGASVLGLAACGGKSQKEAGASKSDTAKTEITWWAFPVFTQEKAEDGVGTYEKKLIAAFEKANPEIKVKLETIDFTSGPEKITTA
IEAGTAPDVLFDAPGRIIQYGKNGKLADLNDLFTEEFTKDVNNDKLIQASKAGDTAYMYPISSAPFYMALNKKMLKDAGVLDLVKEGWTTDDFEKV
LKALKDKGYNPGSFFANGQGGDQGPRAFFANLYSSHITDDKVTKYTTDDANSIKAMTKISNWIKDGLMMNGSQYDGSADIQNFANGQTSFTILWAP
AQPGIQAKLLEASKVDYLEIPFPSDDGKPELEYLVNGFAVFNNKDEQKVAASKTFIQFIADDKEWGPKNVVRTGAFPVRTSYGDLYKDKRMEKIAE
WTKFYSPYYNTIDGFAEMRTLWFPMVQAVSNGDEKPEDALKAFTEKANKTIKKTQ

SEQ ID 947

ATGCCACATCTAAGTAAAGAAGCTTTTAAAAAGCAAATAAAAAATGGCATTATTGTGTCATGTCAAGCTTTGCCCGGGGAGCCTCTTTATACTGAA
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SEQ ID 948

MPHLSKEAFKKQIKNGIIVSCQALPGEPLYTESGGVMPLLALAAQEAGAVGIRANSVRDIKEIQEVTNLPIIGIIKREYPPQEPFITATMTEVDQL
ASLDIAVIALDCTLRERHDGLSVVEFIQKIKRKYPEQLLMADISTFEEGKNAFEAGVDFVGTTLSGYTDYSRQEEGPDIELLNKLCQAGIDVIAEG
KIHTPKQANEINHIGVAGIVVGGAITRPKEIAERFISGLS

SEQ ID 949

ATGCCTGATAAACCAACCAAAGAAAAGCTCATGGAGCAGTTAAAGGGTGGGATTATCGTTTCTTGTCAGGCTTTGCCAGGTGAGCCTCTCTATTCA
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CAAGCCATAACAGACCTACCAATTATCGGTATCATCAAAAAAGATTACCCGCCGCAAGAGCCTTTTATTACGGCAACGATGACCGAAGTGGATCAA
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TTGTCAGGCTACACCCCGTATAGCCGTCAGGAAGCAGGTCCTGATGTGGCATTGATAGAAGCTCTTTGCAAAGCAGGCATTGCTGTCATTGCCGAA
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GCAGAGCGTTTTATCGAAGCGCTCAAATCC

SEQ ID 950

MPDKPTKEKLMEQLKGGIIVSCQALPGEPLYSETGGIMPLMAKAAQEAGAVGIRANSVRDIKEIQAITDLPIIGIIKKDYPPQEPFITATMTEVDQ
LAALNIAVIAMDCTKRDRHDGLDIASFIRQVKEKYPNQLLMADISTFDEGLVAHQAGIDFVGTTLSGYTPYSRQEAGPDVALIEALCKAGIAVIAE
GKIHSPEEAKKINDLGVAGIVVGGAITRPKEIAERFIEALKS

SEQ ID 951

ATGAAAATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGTGTTCAAGCACAAGAAACAGATACGACGTGG
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TCAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGACAGTAACT
TACGATCAGAAGAGTCATACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTGGATTTGAAAACC
AATCAAGTTTCTGTTGCAGACCAAAAAGTTTCTCTCAATACAATTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCAATGAAG
ACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCT
CCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACCAGCT
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AAAGTAGAAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACT
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GGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAATATGGCA
GCAAATAACATTTCATATGTTATCTGGCAACAAAAGTTTTACTCAAATACAAACAGTATTTATGGACCTGCTAATACTTGGAATGCAATGCCAGAT
CGTGGTGGCGTTACTGCCAACCACTATGACCACGTTCACGTATCATTTAACAAA

SEQ ID 952

MKMNKKVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVT
YDQKSHTATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVSLNTISEGMTPEAATTIVSPMKTYSSAPALKSKEVLAQEQAVSQAAANEQVSPA
PVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATDSKLQAT
EVKSVPVAQKAPTATPVAQPASTTNAVAAHPENAGLQPHVAAYKEKVASTYGVNEPSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMA
ANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK

SEQ ID 953

ATGATTATTACTAAAAAGAGCTTATTTGTGACAAGTGTCGCTTTGTCGTTAGTACCTTTGGCGACAGCGCAGGCACAAGAGTGGACACCACGATCG
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GGTCAGGCAACGAATTTGACGGTTCAAGCACCTGCTTCTAGTCCAGCTAGCGTTAGTCATGTACCTAGCAGTGAGCCATTACCCCAAGCATCTGCC
ACCTCTCAACCGACTGTTCCTATGGCACCACCTGCGACACCATCTGATGTCCCAACGACACCATTCGCATCTGCAAAGCCAGATAGTTCTGTGACA
GCGTCATCTGAGCTCACATCGTCAACGAATGATGTTTCGACTGAGTTGTCTAGCGAATCACAAAAGCAGCCAGAAGTACCACAAGAAGCAGTTCCA
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GTCTCCTTTAATGCT

SEQ ID 954

MIITKKSLFVTSVALSLVPLATAQAQEWTPRSVTEIKSELVLVDNVFTYTVKYGDTLSTIAEAMGIDVHVLGDINHIANIDLIFPDTILTANYNQH
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TPKAAETTEVEPKTDISEAPTSANRPVPNESASEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATSNGLSYAPNHAYNPMNAGLQPQTAAFKE
EVASAFGITSFSGYRPGDPGDHGKGLAIDFMVPENSALGDQVAQYAIDHMAERGISYVIWKQRFYAPFASIYGPAYTWNPMPDRGSITENHYDHVH
VSFNA

SEQ ID 955

TTGAATAAATGGTTAGTTAAGGCAAGTTCCTTAGTTGTTTTAGGTGGTATGGTTTTATCTGCGGGTTCCCGAGTTTTAGCGGATACTTATGTCCGT
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CGCGTTGACAACAGTCAAGAACTGCTTTACAAA

SEQ ID 956

MNKWLVKASSLVVLGGMVLSAGSRVLADTYVRPIDNGRITTGFNGYPGHCGVDYAVPTGTIIRAVADGTVKFAGAGANFSWMTDLAGNCVMIQHAD
GMHSGYAHMSRVVARTGEKVKQGDIIGYVGATGMATGPHLHFEFLPANPNFQNGFHGRINPTSLIANVATFSGKTQASAPSIKPLQSAPVQNQSSK
LKVYRVDELQKVNGVWLVKNNTLTPTGFDWNDNGIPASEIDEVDANGNLTADQVLQKGGYFIFNPKTLKTVEKPIQGTAGLTWAKTRFANGSSVWL
RVDNSQELLYK

SEQ ID 957

ATGACTAAACGTGCTTTAATCTCAGTTTCTGACAAATCAGGAATTATTGACTTTGCAAAAGAATTGAAAAACTTGGGTTGGGATATTATCTCAACT
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ACCCTCCACCCAAACATTCACGGTGGGCTTCTGGCTCGTCGCGACGCTGACAGCCACCTTCAGGCTGCTAAGGACAACAATATTGAGTTGATTGAC
CTCGTGGTTGTCAACCTCTATCCCTTCAAGGAGACCATCCTTCGCCCAGACGTGACCTACGATTTGGCGGTGGAAAATATCGACATCGGCGGTCCA
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CAGGCTAAGGACCACCTTGACGGTGCCGTTCTAGCATCAGATGCCTTCTTCCCATTTGCGGACAACATTGAAGAAATCGCTGCCGCAGGGATCAAA
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TTTAGACAT

SEQ ID 958

MTKRALISVSDKSGIIDFAKELKNLGWDIISTGGTKVALDDAGVETIAIDDVTGFPEMMDGRVKTLHPNIHGGLLARRDADSHLQAAKDNNIELID
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QVGEAKPEKLTITYDLKQAMRYGENPQQDADFYQKALPTDYSIASAKQLNGKELSFNNIRDADAAIRIIRDFKDSPTVVALKHMNPCGIGQADDIE
TAWDYAYEADPVSIFGGIVVLNREVDAATAEKMHPIFLEIIIAPSYSEEALAILTNKKKNLRILELPFDAQAASEVEAEYTGVVGGLLVQNQDVVA
ENPSDWQVVTDRQPTEQEATALEFAWKAIKYVKSNGIIITNDHMTLGLGAGQTNRVGSVKIAIEQAKDHLDGAVLASDAFFPFADNIEEIAAAGIK
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SEQ ID 959

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TCAATGCTTCGCTCAGCCGCTAAAAATCACGCTAGCGTGACCGTTGTGGTTGACCCAGCGGATTATGCGACTGTTTTGGGAGAATTGGCTGACGCT
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CAGGCTAAAGACCACCTTGACGGTGCCGTTCTAGCATCAGATGCCTTCTTCCCATTTGCGGACAACATTGAAGAAATCGCTGCCGCAGGGATCAAA

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SEQ ID 960

MTKRALISVSDKSGIVDFAKELKNLGWDIISTGGTKVTLDDAGVETIAIDDVTRFPEMMDGRVKTLHPNIHGGLLARRDADSHLQAAKDNNIELID
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QVGEAKPEKLTITYDLKQAMRYGENPQQDADFYQKALPTDYSIASAKQLNGKELSFNNIRDADAAIRIIRDFKDRPTVVALKHMNPCGIGQADDIE
TAWDYTYKADPVSIFGGIIVLNREVDAATAKKMHPIFLEIIIAPSYSEEALAILTNKKKNLRILELPFDAQAASEVEAEYTGVVGGLLVQNQDVVA
ENPSDWQVVTDRQPTEQEATALEFAWKAIKYVKSNGIIITNDHMTLGLGAGQTNRVGSVKIAIEQAKDHLDGAVLASDAFFPFADNIEEIAAAGIK
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SEQ ID 961

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GCTATTGATGAGAAAGTTTACAACTCTTGCTTAGAAAAGGAATGGTCACAGGATTTAGTAGCAAATTACGCTACTTATCAGTACTATAAAAAACAA
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CATCCAGATTTTCGTCGGCGTGGTTTAGCAACAATAGTTGCAGCTCAGTTAATACTAACTTGTTTAGATAAGGGAATTTATCCTAGCTGGGATGCT
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SEQ ID 962

MKLVKNLEIVESIFGDWDETIIWSCVQGIMGEVFVDSLDQPKSSLAKLGRKSSFGFLAGQPTLFLLEVCSGEDIILVPQHKGWSDLIESTYGQNAH
SFKRYATKKDTLFERSRLEKFVTQLPNGFELRAIDEKVYNSCLEKEWSQDLVANYATYQYYKKQGIGYVVYYQGNIIAGASSYSTYKNGIEIEVDT
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SEQ ID 963

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ATCCATTGGGTGGACTCTGGTGTGGATACCGGTCAGGTCATCCAACAAGTGCACGTGCCACGCCTAGCAGATGATAGTCTAGAAAGCTTTGAAACC
CGCATCCACGAAACCGAATACCAACTCTACCCAGCTGTCTTAGATAGCTTGGGCATAAAGAGAAAA

SEQ ID 964

MKIAVFASGNGSNFQVIAEQFQVSFVFSDHRDAYVLERAQNLAIPSFAFELKEFENKAAYEQAVVDLLDKHEIDLVCLAGYMKIVGETLLSAYEGR
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SEQ ID 965

ATGAAAATCGCTGTTTTTGCTTCTGGTAATGGTTCCAACTTTCAGGTCATAGCAGAGCAGTTTCCAGTTAGTTTTGTCTTTTCAGATCATCGTGAT
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ATCCACTGGGTTGACTCTGGTGTGGATACCGGTCAGGTCATCCAACAAGTGCGCGTGCCACGCCTAGCAGACGATAGCCTAGAAAGCTTTGAAACC
CGTATCCATGAAACCGAATATCAACTCTACCCAGCTGTCTTAGATAGCTTGGGAGTGGAGAGGAAAGTAATC

SEQ ID 966

MKIAVFASGNGSNFQVIAEQFPVSFVFSDHRDAYVLERAQNLAIPSFAFELKEFENKVAYEQAIVDLLDKHEIDLVCLAGYMKIVGETLLLAYERR
IINIHPAYLPEFPGAHGIEDAWEAGVDQSGVTIHWVDSGVDTGQVIQQVRVPRLADDSLESFETRIHETEYQLYPAVLDSLGVERKVI

SEQ ID 967

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SEQ ID 968

MSEKNAYAQSGVDVEAGYEVVERIKKHVARTERAGVMGALGGFGGMFDLSQTGVKEPVLISGTDGVGTKLMLAIKYDKHDTIGQDCVAMCVNDIIA
AGAEPLYFLDYVATGKNEPAKLEQVVAGVAEGCVQASAALIGGETAEMPGMYGEDDYDLAGFAVGVAEKSQIIDGSKVKEGDILLGLASSGIHSNG
YSLVRRVFADYTGDEVLPELEGKQLKDVLLEPTRIYVKAALPLIKEELVNGIAHITGGGFIENVPRMFADDLAAEIDEDKVPVLPIFKALEKYGDI
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SEQ ID 969

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SEQ ID 970

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YSLVRRVFADYTGKELLPELEGKQLKDVLLEPTRIYVKAALPLIKEELVKGIGHITGGGFIENIPRMFADDLAAEIDEDKVPVLPIFKALEKYGDI
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SEQ ID 971

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CAAAAAGTGAAA

SEQ ID 972

MTYEVKSLNEECGVFGIWGYPQAAQVTYFGLHSLQHRGQEGAGIISNDNGKLYGYRNVGLLSEVFKNQSELDNLTGNAAIGHVRYATAGSADIRNI
QPFLYKFHDGQFALCHNGNLTNAISSRKELEKQGAIFNASSDTEILMHLIRRSHNPSFMGKVKEALSTVKGGFAYLLMTEDKLIAALDPNAFRPLS
IGQMQNGAWVISSETCAFEVVGAKWVRDVEPGEVILIDDSGIQCDRYTDETQLAICSMEYVYFARPDSTIHGVNVHTARKNMGKRLAQEFKQDADI
VIGVPNSSLSAAMGFAEESGLPNEMGLVKNQYTQRTFIQPTQELREQGVRMKLSAVSGVVKGKRVVMIDDSIVRGTTSRRIVGLLREAGATEVHVA
IASPELKYPCFYGIDIQTRRELISANHAVDEVCDIIGADSLTYLSIDGLIKSIGLETKAPNGGLCVAYFDGHYPTPLYDYEEEYLRSLEEKTSFYI
QKVK

SEQ ID 973

TTGTGCGAAAAACTTTCTATTTTCGCTTTACTTGACAGCCTTTGTATCGAGGTAAAAATGACATACGAAGTAAAATCTCTAAATGAAGAATGTGGA
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TCAAATGACAATGGGAAACTCTATGGTTATCGAAATGTTGGGCTCCTTTCTGAAGTTTTTAAGAATCAATCTGAATTAGATAATTTAACTGGGAAT
GCGGCTATTGGACATGTTCGGTATGCTACTGCAGGTTCTGCAGATATTCGCAATATTCAGCCTTTTCTTTATAAATTTCATGACGGGCAATTTGCT
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GCTCGAAAAAATATGGGAAAGCGTCTTGCACAAGAATTTAAACAGGATGCTGATATTGTAATTGGTGTCCCAAATTCGTCCTTATCGGCTGCTATG
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CTGGATGGGTTGATTGAATCAATTGGACTCGAAACAAAAGCACCAAATGGTGGTTTATGCGTAGCTTACTTTGATGGGCATTATCCAACACCGCTT
TATGATTATGAAGAAGAATACCTCAGAAGTTTAGAAGAGAAAACAAGTTTTTATATTCAAAAAGTGAAA

SEQ ID 974

LCEKLSIFALLDSLCIEVKMTYEVKSLNEECGVFGIWGHPQAAQVTYFGLHSLQHRGQEGAGIVSNDNGKLYGYRNVGLLSEVFKNQSELDNLTGN
AAIGHVRYATAGSADIRNIQPFLYKFHDGQFALCHNGNLTNAISLRKELEKQGAIFNASSDTEILMHLIRRSHNSSFMGKVKEALNTVKGGFAYLL
MTENKLIAALDPNAFRPLSIGQMQNGAWVISSETCAFEVVGAKWVRDVEPGEVILIDDRGIQCDRYTDETQLAICSMEYVYFARPDSTIHGVNVHT
ARKNMGKRLAQEFKQDADIVIGVPNSSLSAAMGFAEESGLPNEMGLVKNQYTQRTFIQPTQELREQGVRMKLSAVSGVVKGKRVVMIDDSIVRGTT
SRRIVGLLREAGASEVHVAIASPELKYPCFYGIDIQTRRELISANHSVDEVCDIIGADSLTYLSLDGLIESIGLETKAPNGGLCVAYFDGHYPTPL
YDYEEEYLRSLEEKTSFYIQKVK

SEQ ID 975

GTGAAGGCGAGGTTAGATAGAAATTCGCTATCTTTTGAACGAAGCGAGCTTAACCGTATCTTTCCGCCGTATTGGTATTTGGGAGTCATTGAGACT
AAGGTTCAATGGCTAGCT

SEQ ID 976

MKARLDRNSLSFERSELNRIFPPYWYLGVIETKVQWLA

SEQ ID 977

TTGCGGCTGTCCGCTGTTGTCACACCGAAAGCTACCAAGGTTGGTGGTACTGTCAATTCTTCGAAAGTACCAGACATAGAGTCCTTACCGCCGATT
GATGGCAAACCAAAT

SEQ ID 978

MRLSAVVTPKATKVGGTVNSSKVPDIESLPPIDGKPN

SEQ ID 979

TTGGGCTTACTGAAATCTCAATTTCAGACGTCCTCCTATTTTCGAGTCGCTCCCTTGTCGGACTTGGTATCTTATATGAATAAACGTATTTTTGTT
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GAAACTGAATTGAAAAACATTGATTTTTCGGCCTCTAAATTCCAAAAACAATTGCAGGCGACTTATGACAAATACATTGCCATGCGTGATGAGCTT
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CCAACAGAAATTGAGCCATTTGGTGGAGCGGCGACTTGTATCGGTGGTGCCATTCGTGACCCATTGTCAGGACGTTCATACGTTTATCAGGCTATG
CGTATTTCAGGCGCAGGAGATATCACGACTCCGATTGCGGAAACACGTGCTGGTAAATTGCCACAACAGGTTATTTCTAAGACTGCGGCGCACGGC
TATTCTTCATATGGTAACCAAATTGGGCTTGCGACAACTTATGTGCGTGAGTACTTCCACCCTGGCTTCGTAGCTAAACGCATGGAGCTTGGAGCT